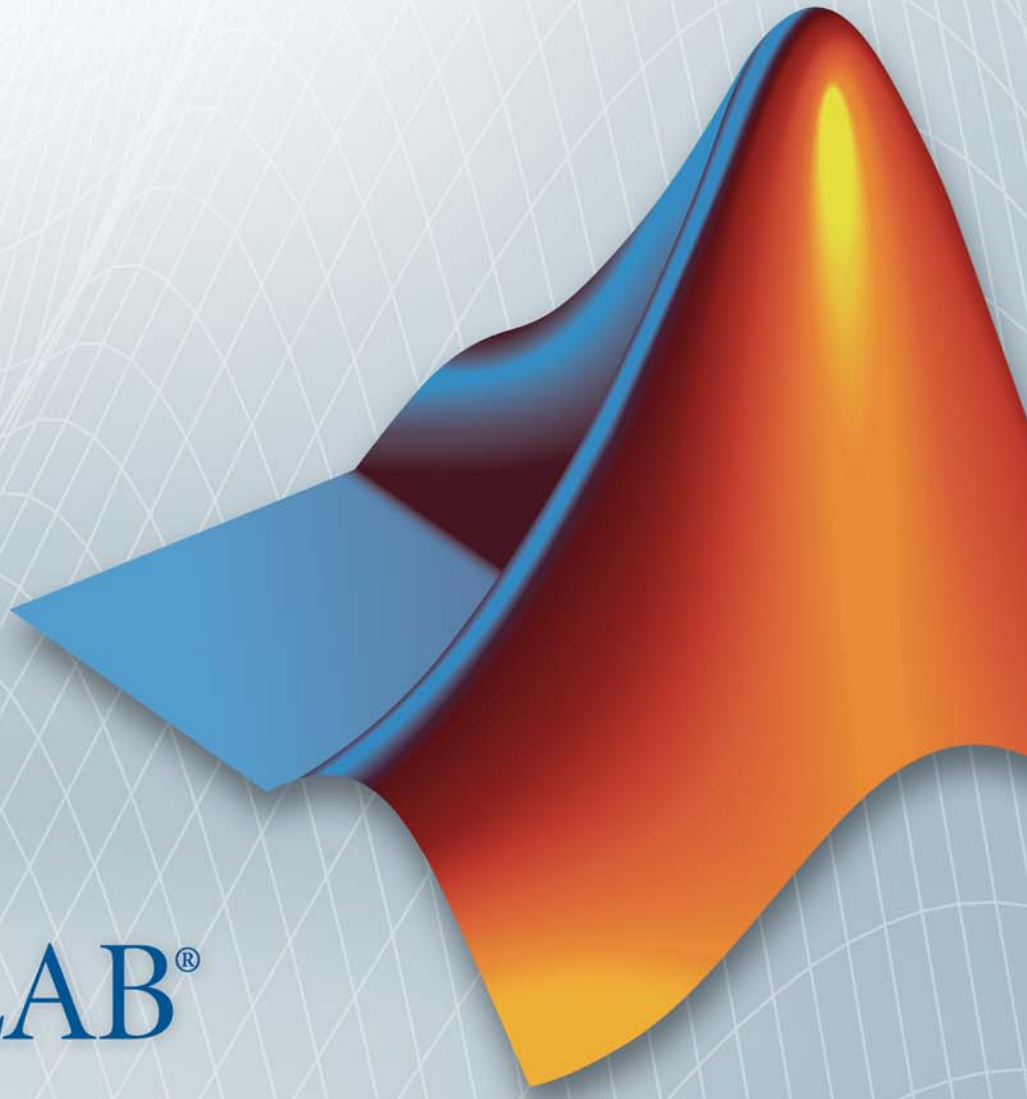
Statistics Toolbox™

User's Guide

R2011b



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Statistics Toolbox™ User's Guide

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1

Getting Started

Product Overview

Statistics Toolbox™ software extends MATLAB® to support a wide range of common statistical tasks. The toolbox contains two categories of tools:

- Building-block statistical functions for use in MATLAB programming
- Graphical user interfaces (GUIs) for interactive data analysis

Code for the building-block functions is open and extensible. Use the MATLAB Editor to review, copy, and edit code for any function. Extend the toolbox by copying code to new files or by writing files that call toolbox functions.

GUIs allow you to perform statistical visualization and analysis without writing code. You interact with the GUIs using sliders, input fields, buttons, etc. and the GUIs automatically call building-block functions.

2

Organizing Data

Introduction to Data Types

MATLAB data is placed into "data containers" in the form of workspace variables. All workspace variables organize data into some form of array. For statistical purposes, arrays are viewed as tables of values.

MATLAB variables use different structures to organize data:

- 2-D numerical arrays (matrices) organize observations and measured variables by rows and columns, respectively. (See "Other Data Structures" in the MATLAB documentation.)
- Multidimensional arrays organize multidimensional observations or experimental designs. (See "Multidimensional Arrays" in the MATLAB documentation.)
- Cell and structure arrays organize heterogeneous data of different types, sizes, units, etc. (See "Cell Arrays" and "Structures" in the MATLAB documentation.)

Data types determine the kind of data variables contain. (See "Classes (Data Types)" in the MATLAB documentation.)

These basic MATLAB container variables are reviewed, in a statistical context, in the section on "MATLAB Arrays" on page 2-4.

These variables are not specifically designed for statistical data, however. Statistical data generally involves observations of multiple variables, with measurements of heterogeneous type and size. Data may be numerical (of type `single` or `double`), categorical, or in the form of descriptive metadata. Fitting statistical data into basic MATLAB variables, and accessing it efficiently, can be cumbersome.

Statistics Toolbox software offers two additional types of container variables specifically designed for statistical data:

- "Categorical Arrays" on page 2-13 accommodate data in the form of discrete levels, together with its descriptive metadata.

- "Dataset Arrays" on page 2-23 encapsulate heterogeneous data and metadata, including categorical data, which is accessed and manipulated using familiar methods analogous to those for numerical matrices.

These statistical container variables are discussed in the section on "Statistical Arrays" on page 2-11.

MATLAB Arrays

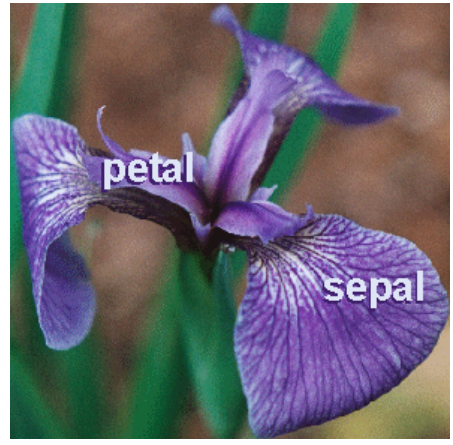
In this section...

Numerical Data

MATLAB two-dimensional numerical arrays (matrices) containing statistical data use rows to represent observations and columns to represent measured variables. For example,

```
load fisheriris % Fisher's iris data (1936)
```

loads the variables `meas` and `species` into the MATLAB workspace. The `meas` variable is a 150-by-4 numerical matrix, representing 150 observations of 4 different measured variables (by column: sepal length, sepal width, petal length, and petal width, respectively).



The observations in `meas` are of three different species of iris (setosa, versicolor, and virginica), which can be separated from one another using the 150-by-1 cell array of strings `species`:

```
setosa_indices = strcmp('setosa',species);
setosa = meas(setosa_indices,:);
```

The resulting `setosa` variable is 50-by-4, representing 50 observations of the 4 measured variables for iris setosa.

To access and display the first five observations in the `setosa` data, use row, column parenthesis indexing:

```
SetosaObs = setosa(1:5,:)
SetosaObs =
    5.1000    3.5000    1.4000    0.2000
    4.9000    3.0000    1.4000    0.2000
    4.7000    3.2000    1.3000    0.2000
    4.6000    3.1000    1.5000    0.2000
    5.0000    3.6000    1.4000    0.2000
```

The data are organized into a table with implicit column headers “Sepal Length,” “Sepal Width,” “Petal Length,” and “Petal Width.” Implicit row headers are “Observation 1,” “Observation 2,” “Observation 3,” etc.

Similarly, 50 observations for iris versicolor and iris virginica can be extracted from the `meas` container variable:

```
versicolor_indices = strcmp('versicolor',species);
versicolor = meas(versicolor_indices,:);

virginica_indices = strcmp('virginica',species);
virginica = meas(virginica_indices,:);
```

Because the data sets for the three species happen to be of the same size, they can be reorganized into a single 50-by-4-by-3 multidimensional array:

```
iris = cat(3,setosa,versicolor,virginica);
```

The `iris` array is a three-layer table with the same implicit row and column headers as the `setosa`, `versicolor`, and `virginica` arrays. The implicit layer names, along the third dimension, are “Setosa,” “Versicolor,” and “Virginica.” The utility of such a multidimensional organization depends on assigning meaningful properties of the data to each dimension.

To access and display data in a multidimensional array, use parenthesis indexing, as for 2-D arrays. The following gives the first five observations of sepal lengths in the setosa data:

```
SetosaSL = iris(1:5,1,1)
SetosaSL =
    5.1000
    4.9000
    4.7000
    4.6000
    5.0000
```

Multidimensional arrays provide a natural way to organize numerical data for which the observations, or experimental designs, have many dimensions. If, for example, data with the structure of `iris` are collected by multiple observers, in multiple locations, over multiple dates, the entirety of the data can be organized into a single higher dimensional array with dimensions for "Observer," "Location," and "Date." Likewise, an experimental design calling for m observations of n p-dimensional variables could be stored in an m-by-n-by-p array.

Numerical arrays have limitations when organizing more general statistical data. One limitation is the implicit nature of the metadata. Another is the requirement that multidimensional data be of commensurate size across all dimensions. If variables have different lengths, or the number of variables differs by layer, then multidimensional arrays must be artificially padded with `NaN`s to indicate "missing values." These limitations are addressed by dataset arrays (see "Dataset Arrays" on page 2-23), which are specifically designed for statistical data.

Heterogeneous Data

MATLAB data types include two container variables—cell arrays and structure arrays—that allow you to combine metadata with variables of different types and sizes.

The data in the variables `setosa`, `versicolor`, and `virginica` created in "Numerical Data" on page 2-4 can be organized in a cell array, as follows:

```
iris1 = cell(51,5,3); % Container variable

obsnames = strcat({'Obs'},num2str((1:50)','%-d'));
iris1(2:end,1,:) = repmat(obsnames,[1 1 3]);

varnames = {'SepalLength','SepalWidth',...
            'PetalLength','PetalWidth'};
iris1(1,2:end,:) = repmat(varnames,[1 1 3]);

iris1(2:end,2:end,1) = num2cell(setosa);
iris1(2:end,2:end,2) = num2cell(versicolor);
iris1(2:end,2:end,3) = num2cell(virginica);

iris1{1,1,1} = 'Setosa';
iris1{1,1,2} = 'Versicolor';
iris1{1,1,3} = 'Virginica';
```

To access and display the cells, use parenthesis indexing. The following displays the first five observations in the setosa sepal data:

```
SetosaSLSW = iris1(1:6,1:3,1)
SetosaSLSW =
    'Setosa'    'SepalLength'    'SepalWidth'
    'Obs1'      [     5.1000]    [    3.5000]
    'Obs2'      [     4.9000]    [         3]
    'Obs3'      [     4.7000]    [    3.2000]
    'Obs4'      [     4.6000]    [    3.1000]
    'Obs5'      [          5]    [    3.6000]
```

Here, the row and column headers have been explicitly labeled with metadata.

To extract the data subset, use row, column curly brace indexing:

```
subset = reshape([iris1{2:6,2:3,1}],5,2)
subset =
    5.1000    3.5000
    4.9000    3.0000
    4.7000    3.2000
    4.6000    3.1000
    5.0000    3.6000
```

While cell arrays are useful for organizing heterogeneous data, they may be cumbersome when it comes to manipulating and analyzing the data. MATLAB and Statistics Toolbox statistical functions do not accept data in the form of cell arrays. For processing, data must be extracted from the cell array to a numerical container variable, as in the preceding example. The indexing can become complicated for large, heterogeneous data sets. This limitation of cell arrays is addressed by dataset arrays (see "Dataset Arrays" on page 2-23), which are designed to store general statistical data and provide easy access.

The data in the preceding example can also be organized in a structure array, as follows:

```
iris2.data = cat(3,setosa,versicolor,virginica);
iris2.varnames = {'SepalLength','SepalWidth',...
                  'PetalLength','PetalWidth'};
iris2.obsnames = strcat({'Obs'},num2str((1:50)','%-d'));
iris2.species = {'setosa','versicolor','virginica'};
```

The data subset is then returned using a combination of dot and parenthesis indexing:

```
subset = iris2.data(1:5,1:2,1)
subset =
    5.1000    3.5000
    4.9000    3.0000
    4.7000    3.2000
    4.6000    3.1000
    5.0000    3.6000
```

For statistical data, structure arrays have many of the same limitations as cell arrays. Once again, dataset arrays (see "Dataset Arrays" on page 2-23), designed specifically for general statistical data, address these limitations.

Statistical Functions

One of the advantages of working in the MATLAB language is that functions operate on entire arrays of data, not just on single scalar values. The functions are said to be *vectorized*. Vectorization allows for both efficient problem formulation, using array-based data, and efficient computation, using vectorized statistical functions.

When MATLAB and Statistics Toolbox statistical functions operate on a vector of numerical data (either a row vector or a column vector), they return a single computed statistic:

```
% Fisher's setosa data:
load fisheriris
setosa_indices = strcmp('setosa',species);
setosa = meas(setosa_indices,:);

% Single variable from the data:
setosa_sepal_length = setosa(:,1);

% Standard deviation of the variable:
std(setosa_sepal_length)
ans =
    0.3525
```

When statistical functions operate on a matrix of numerical data, they treat the columns independently, as separate measured variables, and return a vector of statistics—one for each variable:

```
std(setosa)
ans =
    0.3525    0.3791    0.1737    0.1054
```

The four standard deviations are for measurements of sepal length, sepal width, petal length, and petal width, respectively.

Compare this to

```
std(setosa(:))
ans =
    1.8483
```

which gives the standard deviation across the entire array (all measurements).

Compare the preceding statistical calculations to the more generic mathematical operation

```
sin(setosa)
```

This operation returns a 50-by-4 array the same size as `setosa`. The `sin` function is vectorized in a different way than the `std` function, computing one scalar value for each element in the array.

MATLAB and Statistics Toolbox statistical functions, like `std`, must be distinguished from general mathematical functions like `sin`. Both are vectorized, and both are useful for working with array-based data, but only statistical functions summarize data across observations (rows) while preserving variables (columns). This property of statistical functions may be explicit, as with `std`, or implicit, as with `regress`. To see how a particular function handles array-based data, consult its reference page.

MATLAB statistical functions expect data input arguments to be in the form of numerical arrays. If data is stored in a cell or structure array, it must be extracted to a numerical array, via indexing, for processing. Statistics Toolbox functions are more flexible. Many toolbox functions accept data input arguments in the form of both numerical arrays and dataset arrays (see “Dataset Arrays” on page 2-23), which are specifically designed for storing general statistical data.

Statistical Arrays

In this section...

Introduction to Statistical Arrays

As discussed in "MATLAB Arrays" on page 2-4, MATLAB data types include arrays for numerical, logical, and character data, as well as cell and structure arrays for heterogeneous collections of data.

Statistics Toolbox software offers two additional types of arrays specifically designed for statistical data:

- "Categorical Arrays" on page 2-13
- "Dataset Arrays" on page 2-23

Categorical arrays store data with values in a discrete set of levels. Each level is meant to capture a single, defining characteristic of an observation. If no ordering is encoded in the levels, the data and the array are *nominal*. If an ordering is encoded, the data and the array are *ordinal*.

Categorical arrays also store labels for the levels. Nominal labels typically suggest the type of an observation, while ordinal labels suggest the position or rank.

Dataset arrays collect heterogeneous statistical data and metadata, including categorical data, into a single container variable. Like the numerical matrices discussed in "Numerical Data" on page 2-4, dataset arrays can be viewed as tables of values, with rows representing different observations and columns representing different measured variables. Like the cell and structure arrays discussed in "Heterogeneous Data" on page 2-7, dataset arrays can accommodate variables of different types, sizes, units, etc.

Dataset arrays combine the organizational advantages of these basic MATLAB data types while addressing their shortcomings with respect to storing complex statistical data.

Both categorical and dataset arrays have associated methods for assembling, accessing, manipulating, and processing the collected data. Basic array operations parallel those for numerical, cell, and structure arrays.

Categorical Arrays

Categorical Data

Categorical data take on values from only a finite, discrete set of categories or *levels*. Levels may be determined before the data are collected, based on the application, or they may be determined by the distinct values in the data when converting them to categorical form. Predetermined levels, such as a set of states or numerical intervals, are independent of the data they contain. Any number of values in the data may attain a given level, or no data at all. Categorical data show which measured values share common levels, and which do not.

Levels may have associated *labels*. Labels typically express a defining characteristic of an observation, captured by its level.

If no ordering is encoded in the levels, the data are *nominal*. Nominal labels typically indicate the type of an observation. Examples of nominal labels are {false, true}, {male, female}, and {Afghanistan, ..., Zimbabwe}. For nominal data, the numeric or lexicographic order of the labels is irrelevant—Afghanistan is not considered to be less than, equal to, or greater than Zimbabwe.

If an ordering is encoded in the levels—for example, if levels labeled "red", "green", and "blue" represent wavelengths—the data are *ordinal*. Labels for ordinal levels typically indicate the position or rank of an observation. Examples of ordinal labels are {0, 1}, {mm, cm, m, km}, and {poor, satisfactory, outstanding}. The ordering of the levels may or may not correspond to the numeric or lexicographic order of the labels.

Categorical Arrays

Categorical data can be represented using MATLAB integer arrays, but this method has a number of drawbacks. First, it removes all of the useful metadata that might be captured in labels for the levels. Labels must be stored separately, in character arrays or cell arrays of strings. Secondly, this method suggests that values stored in the integer array have their usual numeric meaning, which, for categorical data, they may not. Finally, integer types have a fixed set of levels (for example, `-128:127` for all `int8` arrays), which cannot be changed.

Categorical arrays, available in Statistics Toolbox software, are specifically designed for storing, manipulating, and processing categorical data and metadata. Unlike integer arrays, each categorical array has its own set of levels, which can be changed. Categorical arrays also accommodate labels for levels in a natural way. Like numerical arrays, categorical arrays take on different shapes and sizes, from scalars to *N*-D arrays.

Organizing data in a categorical array can be an end in itself. Often, however, categorical arrays are used for further statistical processing. They can be used to index into other variables, creating subsets of data based on the category of observation, or they can be used with statistical functions that accept categorical inputs. For examples, see "Grouped Data" on page 2-34.

Categorical arrays come in two types, depending on whether the collected data is understood to be nominal or ordinal. Nominal arrays are constructed with `nominal`; ordinal arrays are constructed with `ordinal`. For example,

```
load fisheriris
ndata = nominal(species,{'A','B','C'});
```

creates a nominal array with levels `A`, `B`, and `C` from the `species` data in `fisheriris.mat`, while

```
odata = ordinal(ndata,{},{'C','A','B'});
```

encodes an ordering of the levels with `C` < `A` < `B`. See "Using Categorical Arrays" on page 2-16, and the reference pages for `nominal` and `ordinal`, for further examples.

Categorical arrays are implemented as objects of the `categorical` class. The class is abstract, defining properties and methods common to both

the `nominal` class and `ordinal` class. Use the corresponding constructors, `nominal` or `ordinal`, to create categorical arrays. Methods of the classes are used to display, summarize, convert, concatenate, and access the collected data. Many of these methods are invoked using operations analogous to those for numerical arrays, and do not need to be called directly (for example, `[]` invokes `horzcat`). Other methods, such as `reorderlevels`, must be called directly.

Using Categorical Arrays

This section provides an extended tutorial example demonstrating the use of categorical arrays with methods of the `nominal` class and `ordinal` class.

Constructing Categorical Arrays.

1. Load the 150-by-4 numerical array `meas` and the 150-by-1 cell array of strings `species`:

   ```
   load fisheriris % Fisher's iris data (1936)
   ```

   The data are 150 observations of four measured variables (by column number: sepal length, sepal width, petal length, and petal width, respectively) over three species of iris (setosa, versicolor, and virginica).

2. Use `nominal` to create a nominal array from `species`:

   ```
   n1 = nominal(species);
   ```

3. Open `species` and `n1` side by side in the Variable Editor (see "Viewing and Editing Workspace Variables with the Variable Editor" in the MATLAB documentation). Note that the string information in `species` has been converted to categorical form, leaving only information on which data share the same values, indicated by the labels for the levels.

   By default, levels are labeled with the distinct values in the data (in this case, the strings in `species`). Give alternate labels with additional input arguments to the `nominal` constructor:

   ```
   n2 = nominal(species,{'species1','species2','species3'});
   ```

4. Open `n2` in the Variable Editor, and compare it with `species` and `n1`. The levels have been relabeled.

5. Suppose that the data are considered to be ordinal. A characteristic of the data that is not reflected in the labels is the diploid chromosome count, which orders the levels corresponding to the three species as follows:

   species1 < species3 < species2

   Use `ordinal` to cast `n2` as an ordinal array:

   ```
   o1 = ordinal(n2,{},{'species1','species3','species2'});
   ```

   The second input argument to `ordinal` is the same as for `nominal`—a list of labels for the levels in the data. If it is unspecified, as above, the labels are inherited from the data, in this case `n2`. The third input argument of `ordinal` indicates the ordering of the levels, in ascending order.

6. When displayed side by side in the Variable Editor, `o1` does not appear any different than `n2`. This is because the data in `o1` have not been sorted. It is important to recognize the difference between the ordering of the levels in an ordinal array and sorting the actual data according to that ordering. Use `sort` to sort ordinal data in ascending order:

   ```
   o2 = sort(o1);
   ```

   When displayed in the Variable Editor, `o2` shows the data sorted by diploid chromosome count.

7. To find which elements moved up in the sort, use the < operator for ordinal arrays:

   ```
   moved_up = (o1 < o2);
   ```

   The operation returns a logical array `moved_up`, indicating which elements have moved up (the data for `species3`).

8. Use `getlabels` to display the labels for the levels in ascending order:

   ```
   labels2 = getlabels(o2)
   labels2 =
       'species1'    'species3'    'species2'
   ```

9. The `sort` function reorders the display of the data, but not the order of the levels. To reorder the levels, use `reorderlevels`:

```
o3 = reorderlevels(o2,labels2([1 3 2]));
labels3 = getlabels(o3)
labels3 =
    'species1'    'species2'    'species3'
o4 = sort(o3);
```

These operations return the levels in the data to their original ordering, by species number, and then sort the data for display purposes.

Accessing Categorical Arrays. Categorical arrays are accessed using parenthesis indexing, with syntax that parallels similar operations for numerical arrays (see "Numerical Data" on page 2-4).

Parenthesis indexing on the right-hand side of an assignment is used to extract the lowest 50 elements from the ordinal array `o4`:

```
low50 = o4(1:50);
```

Suppose you want to categorize the data in `o4` with only two levels: `low` (the data in `low50`) and `high` (the rest of the data). One way to do this is to use an assignment with parenthesis indexing on the left-hand side:

```
o5 = o4; % Copy o4
o5(1:50) = 'low';
Warning: Categorical level 'low' being added.
o5(51:end) = 'high';
Warning: Categorical level 'high' being added.
```

Note the warnings: the assignments move data to new levels. The old levels, though empty, remain:

```
getlabels(o5)
ans =
    'species1' 'species2' 'species3' 'low' 'high'
```

The old levels are removed using `droplevels`:

```
o5 = droplevels(o5,{'species1','species2','species3'});
```

Another approach to creating two categories in `o5` from the three categories in `o4` is to merge levels, using `mergelevels`:

```
o5 = mergelevels(o4,{'species1'},'low');
o5 = mergelevels(o5,{'species2','species3'},'high');

getlabels(o5)
ans =
    'low'    'high'
```

The merged levels are removed and replaced with the new levels.

Combining Categorical Arrays. Categorical arrays are concatenated using square brackets. Again, the syntax parallels similar operations for numerical arrays (see "Numerical Data" on page 2-4). There are, however, restrictions:

- Only categorical arrays of the same type can be combined. You cannot concatenate a nominal array with an ordinal array.
- Only ordinal arrays with the same levels, in the same order, can be combined.
- Nominal arrays with different levels can be combined to produce a nominal array whose levels are the union of the levels in the component arrays.

First use `ordinal` to create ordinal arrays from the variables for sepal length and sepal width in `meas`. Categorize the data as `short` or `long` depending on whether they are below or above the median of the variable, respectively:

```
sl = meas(:,1); % Sepal length data
sw = meas(:,2); % Sepal width data
SL1 = ordinal(sl,{'short','long'},[],...
              [min(sl),median(sl),max(sl)]);
SW1 = ordinal(sw,{'short','long'},[],...
              [min(sw),median(sw),max(sw)]);
```

Because `SL1` and `SW1` are ordinal arrays with the same levels, in the same order, they can be concatenated:

```
S1 = [SL1,SW1];
S1(1:10,:)
ans =
     short      long
     short      long
     short      long
```

```
    short      long
    short      long
    short      long
    short      long
    short      long
    short      short
    short      long
```

The result is an ordinal array `S1` with two columns.

If, on the other hand, the measurements are cast as nominal, different levels can be used for the different variables, and the two nominal arrays can still be combined:

```
SL2 = nominal(sl,{'short','long'},[],...
              [min(sl),median(sl),max(sl)]);
SW2 = nominal(sw,{'skinny','wide'},[],...
              [min(sw),median(sw),max(sw)]);
S2 = [SL2,SW2];
getlabels(S2)
ans =
    'short' 'long' 'skinny' 'wide'
S2(1:10,:)
ans =
     short      wide
     short      wide
     short      wide
     short      wide
     short      wide
     short      wide
     short      wide
     short      wide
     short      skinny
     short      wide
```

Computing with Categorical Arrays. Categorical arrays are used to index into other variables, creating subsets of data based on the category of observation, and they are used with statistical functions that accept categorical inputs, such as those described in “Grouped Data” on page 2-34.

Use `ismember` to create logical variables based on the category of observation. For example, the following creates a logical index the same size as `species` that is `true` for observations of iris setosa and `false` elsewhere. Recall that `n1 = nominal(species)`:

```
SetosaObs = ismember(n1,'setosa');
```

Since the code above compares elements of `n1` to a single value, the same operation is carried out by the equality operator:

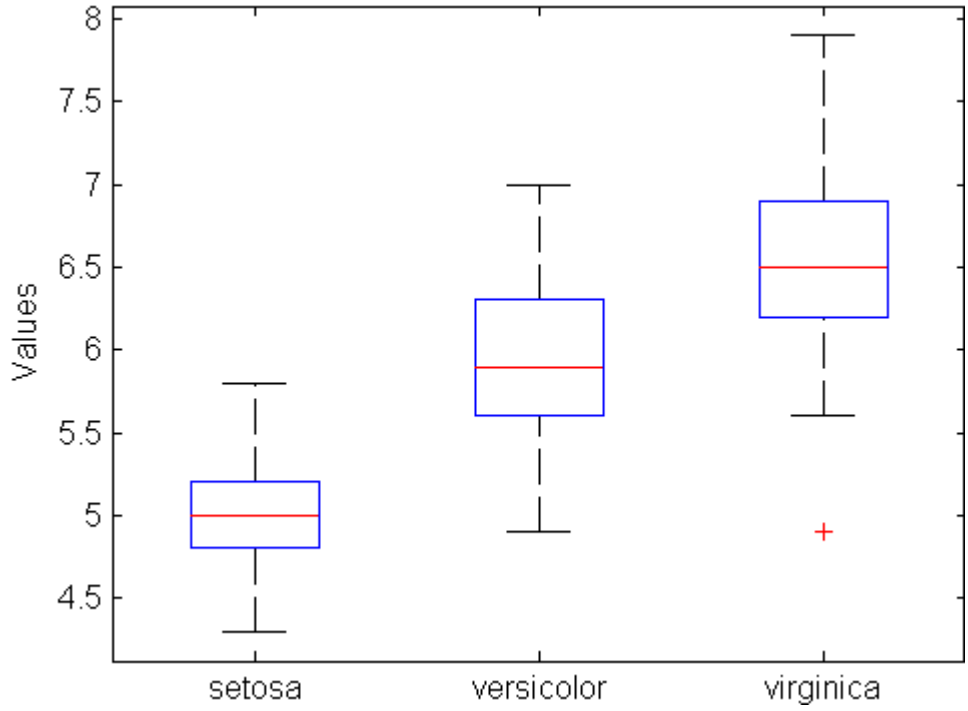
```
SetosaObs = (n1 == 'setosa');
```

The `SetosaObs` variable is used to index into `meas` to extract only the setosa data:

```
SetosaData = meas(SetosaObs,:);
```

Categorical arrays are also used as grouping variables. The following plot summarizes the sepal length data in `meas` by category:

```
boxplot(sl,n1)
```


8
7.5
7
6.5
6
5.5
5
4.5
Values
setosa
versicolor
virginica

Dataset Arrays

Statistical Data

MATLAB data containers (variables) are suitable for completely homogeneous data (numeric, character, and logical arrays) and for completely heterogeneous data (cell and structure arrays). Statistical data, however, are often a mixture of homogeneous variables of heterogeneous types and sizes. Dataset arrays are suitable containers for this kind of data.

Dataset arrays can be viewed as tables of values, with rows representing different observations or cases and columns representing different measured variables. In this sense, dataset arrays are analogous to the numerical arrays for statistical data discussed in "Numerical Data" on page 2-4. Basic methods for creating and manipulating dataset arrays parallel the syntax of corresponding methods for numerical arrays.

While each column of a dataset array must be a variable of a single type, each row may contain an observation consisting of measurements of different types. In this sense, dataset arrays lie somewhere between variables that enforce complete homogeneity on the data and those that enforce nothing. Because of the potentially heterogeneous nature of the data, dataset arrays have indexing methods with syntax that parallels corresponding methods for cell and structure arrays (see "Heterogeneous Data" on page 2-7).

Dataset Arrays

Dataset arrays are variables created with `dataset`. For example, the following creates a dataset array from observations that are a combination of categorical and numerical measurements:

```
load fisheriris
NumObs = size(meas,1);
NameObs = strcat({'Obs'},num2str((1:NumObs)','%-d'));
iris = dataset({nominal(species),'species'},...
               {meas,'SL','SW','PL','PW'},...
               'ObsNames',NameObs);
iris(1:5,:)
ans =
            species    SL     SW     PL     PW
    Obs1    setosa     5.1    3.5    1.4    0.2
    Obs2    setosa     4.9      3    1.4    0.2
    Obs3    setosa     4.7    3.2    1.3    0.2
    Obs4    setosa     4.6    3.1    1.5    0.2
    Obs5    setosa       5    3.6    1.4    0.2
```

When creating a dataset array, variable names and observation names can be assigned together with the data. Other metadata associated with the array can be assigned with `set` and accessed with `get`:

```
iris = set(iris,'Description','Fisher''s Iris Data');
get(iris)
   Description: 'Fisher's Iris Data'
   Units: {}
   DimNames: {'Observations' 'Variables'}
   UserData: []
   ObsNames: {150x1 cell}
   VarNames: {'species' 'SL' 'SW' 'PL' 'PW'}
```

Dataset arrays are implemented as objects of the `dataset` class. Methods of the class are used to display, summarize, convert, concatenate, and access the collected data. Many of these methods are invoked using operations analogous to those for numerical arrays, and do not need to be called directly (for example, `[]` invokes `horzcat`). Other methods, such as `sortrows`, must be called directly.

Using Dataset Arrays

This section provides an extended tutorial example demonstrating the use of dataset arrays with methods of the `dataset` class.

Constructing Dataset Arrays. Load the 150-by-4 numerical array `meas` and the 150-by-1 cell array of strings `species`:

```
load fisheriris % Fisher's iris data (1936)
```

The data are 150 observations of four measured variables (by column number: sepal length, sepal width, petal length, and petal width, respectively) over three species of iris (setosa, versicolor, and virginica).

Use `dataset` to create a dataset array `iris` from the data, assigning variable names `species`, `SL`, `SW`, `PL`, and `PW` and observation names `Obs1`, `Obs2`, `Obs3`, etc.:

```
NumObs = size(meas,1);
NameObs = strcat({'Obs'},num2str((1:NumObs)','%-d'));
iris = dataset({nominal(species),'species'},...
               {meas,'SL','SW','PL','PW'},...
               'ObsNames',NameObs);

iris(1:5,:)
ans =
             species    SL     SW     PL     PW
    Obs1     setosa     5.1    3.5    1.4    0.2
    Obs2     setosa     4.9      3    1.4    0.2
    Obs3     setosa     4.7    3.2    1.3    0.2
    Obs4     setosa     4.6    3.1    1.5    0.2
    Obs5     setosa       5    3.6    1.4    0.2
```

The cell array of strings `species` is first converted to a categorical array of type `nominal` before inclusion in the dataset array. For further information on categorical arrays, see “Categorical Arrays” on page 2-13.

Use `set` to set properties of the array:

```
desc = 'Fisher''s iris data (1936)';
units = [{''} repmat({'cm'},1,4)];
info = 'http://en.wikipedia.org/wiki/R.A._Fisher';

iris = set(iris,'Description',desc,...
                'Units',units,...
                'UserData',info);
```

Use `get` to view properties of the array:

```
get(iris)
    Description: 'Fisher's iris data (1936)'
          Units: {''  'cm'  'cm'  'cm'  'cm'}
       DimNames: {'Observations'  'Variables'}
       UserData: 'http://en.wikipedia.org/wiki/R.A._Fisher'
       ObsNames: {150x1 cell}
       VarNames: {'species'  'SL'  'SW'  'PL'  'PW'}

get(iris(1:5,:),'ObsNames')
ans =
    'Obs1'
    'Obs2'
    'Obs3'
    'Obs4'
    'Obs5'
```

For a table of accessible properties of dataset arrays, with descriptions, see the reference on the `dataset` class.

Accessing Dataset Arrays. Dataset arrays support multiple types of indexing. Like the numerical matrices described in "Numerical Data" on page 2-4, parenthesis `()` indexing is used to access data subsets. Like the cell and structure arrays described in "Heterogeneous Data" on page 2-7, dot `.` indexing is used to access data variables and curly brace `{}` indexing is used to access data elements.

Use parenthesis indexing to assign a subset of the data in `iris` to a new dataset array `iris1`:

```
iris1 = iris(1:5,2:3)
iris1 =
            SL     SW
    Obs1    5.1    3.5
    Obs2    4.9      3
    Obs3    4.7    3.2
    Obs4    4.6    3.1
    Obs5      5    3.6
```

Similarly, use parenthesis indexing to assign new data to the first variable in `iris1`:

```
iris1(:,1) = dataset([5.2;4.9;4.6;4.6;5])
iris1 =
            SL     SW
    Obs1    5.2    3.5
    Obs2    4.9      3
    Obs3    4.6    3.2
    Obs4    4.6    3.1
    Obs5      5    3.6
```

Variable and observation names can also be used to access data:

```
SepalObs = iris1({'Obs1','Obs3','Obs5'},'SL')
SepalObs =
              SL
    Obs1    5.2
    Obs3    4.6
    Obs5      5
```

Dot indexing is used to access variables in a dataset array, and can be combined with other indexing methods. For example, apply `zscore` to the data in `SepalObs` as follows:

```
ScaledSepalObs = zscore(iris1.SL([1 3 5]))
ScaledSepalObs =
    0.8006
   -1.1209
    0.3203
```

The following code extracts the sepal lengths in `iris1` corresponding to sepal widths greater than 3:

```
BigSWLengths = iris1.SL(iris1.SW > 3)
BigSWLengths =
    5.2000
    4.6000
    4.6000
    5.0000
```

Dot indexing also allows entire variables to be deleted from a dataset array:

```
iris1.SL = []
iris1 =
            SW
    Obs  1    3.5
    Obs  2      3
    Obs  3    3.2
    Obs  4    3.1
    Obs  5    3.6
```

Dynamic variable naming works for dataset arrays just as it does for structure arrays. For example, the units of the `SW` variable are changed in `iris1` as follows:

```
varname = 'SW';
iris1.(varname) = iris1.(varname)*10
iris1 =
            SW
    Obs1    35
    Obs2    30
```

```
    Obs3    32
    Obs4    31
    Obs5    36
iris1 = set(iris1,'Units',{'mm'});
```

Curly brace indexing is used to access individual data elements. The following are equivalent:

```
iris1{1,1}
ans =
    35

iris1{'Obs1','SW'}
ans =
    35
```

Combining Dataset Arrays. Combine two dataset arrays into a single dataset array using square brackets:

```
SepalData = iris(:,{'SL','SW'});
PetalData = iris(:,{'PL','PW'});
newiris = [SepalData,PetalData];
size(newiris)
ans =
   150   4
```

For horizontal concatenation, as in the preceding example, the number of observations in the two dataset arrays must agree. Observations are matched up by name (if given), regardless of their order in the two data sets.

The following concatenates variables within a dataset array and then deletes the component variables:

```
newiris.SepalData = [newiris.SL,newiris.SW];
newiris.PetalData = [newiris.PL,newiris.PW];
newiris(:,{'SL','SW','PL','PW'}) = [];
size(newiris)
ans =
   150   2
size(newiris.SepalData)
ans =
```

```
    150   2
```

`newiris` is now a 150-by-2 dataset array containing two 150-by-2 numerical arrays as variables.

Vertical concatenation is also handled in a manner analogous to numerical arrays:

```
newobs = dataset({[5.3 4.2; 5.0 4.1],'PetalData'},...
                 {[5.5 2; 4.8 2.1],'SepalData'});
newiris = [newiris;newobs];
size(newiris)
ans =
   152     2
```

For vertical concatenation, as in the preceding example, the names of the variables in the two dataset arrays must agree. Variables are matched up by name, regardless of their order in the two data sets.

Expansion of variables is also accomplished using direct assignment to new rows:

```
newiris(153,:) = dataset({[5.1 4.0],'PetalData'},...
                         {[5.1 4.2],'SepalData'});
```

A different type of concatenation is performed by `join`, which takes the data in one dataset array and assigns it to the rows of another dataset array, based on matching values in a common key variable. For example, the following creates a dataset array with diploid chromosome counts for each species of iris:

```
snames = nominal({'setosa';'versicolor';'virginica'});
CC = dataset({snames,'species'},{[38;108;70],'cc'})
CC =
    species       cc
    setosa         38
    versicolor    108
    virginica      70
```

This data is broadcast to the rows of `iris` using `join`:

```
iris2 = join(iris,CC);
```

```
iris2([1 2 51 52 101 102],:)
ans =
           species       SL     SW     PL     PW     cc
 Obs1      setosa        5.1    3.5    1.4    0.2     38
 Obs2      setosa        4.9      3    1.4    0.2     38
 Obs51     versicolor      7    3.2    4.7    1.4    108
 Obs52     versicolor    6.4    3.2    4.5    1.5    108
 Obs101    virginica     6.3    3.3      6    2.5     70
 Obs102    virginica     5.8    2.7    5.1    1.9     70
```

Removing Observations from Dataset Arrays. Use one of the following commands to remove observations or variables from a dataset (`ds`):

- Remove a variable by name:

  ```
  ds.var = [];
  ```

- Remove the *j*th variable:

  ```
  ds(:,j) = [];
  ```

- Remove the *j*th variable:

  ```
  ds = ds(:,[1:(j-1) (j+1):end]);
  ```

- Remove the *i*th observation:

  ```
  ds(i,:) = [];
  ```

- Remove the *i*th observation:

  ```
  ds = ds([1:(i-1) (i+1):end],:);
  ```

- Remove the *j*th variable and *i*th observation:

  ```
  ds = ds([1:(i-1) (i+1):end],[1:(j-1) (j+1):end]);
  ```

Computing with Dataset Arrays. Use `summary` to provide summary statistics for the component variables of a dataset array:

```
summary(newiris)
Fisher's iris data (1936)
SepalData: [153x2 double]
```

```
     min         4.3000           2
     1st Q       5.1000      2.8000
     median      5.8000           3
     3rd Q       6.4000      3.3250
     max         7.9000      4.4000
PetalData: [153x2 double]
     min              1      0.1000
     1st Q       1.6000      0.3000
     median      4.4000      1.3000
     3rd Q       5.1000      1.8000
     max         6.9000      4.2000
```

To apply other statistical functions, use dot indexing to access relevant variables:

```
SepalMeans = mean(newiris.SepalData)
SepalMeans =
    5.8294    3.0503
```

The same result is obtained with `datasetfun`, which applies functions to dataset array variables:

```
means = datasetfun(@mean,newiris,'UniformOutput',false)
means =
    [1x2 double]    [1x2 double]
SepalMeans = means{1}
SepalMeans =
    5.8294    3.0503
```

An alternative approach is to cast data in a dataset array as `double` and apply statistical functions directly. Compare the following two methods for computing the covariance of the length and width of the `SepalData` in `newiris`:

```
covs = datasetfun(@cov,newiris,'UniformOutput',false)
covs =
    [2x2 double]    [2x2 double]
SepalCovs = covs{1}
SepalCovs =
    0.6835   -0.0373
   -0.0373    0.2054
```

```
SepalCovs = cov(double(newiris(:,1)))
SepalCovs =
    0.6835   -0.0373
   -0.0373    0.2054
```

Grouped Data

In this section...

Grouping Variables

Grouping variables are utility variables used to indicate which elements in a data set are to be considered together when computing statistics and creating visualizations. Typically, you use grouping variables for classification, where you give or try to infer the group of an observation. Grouping variables may be:

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

Grouping variables have the same length as the variables (columns) in a data set. Observations (rows) *i* and *j* are considered to be in the same group if the values of the corresponding grouping variable are identical at those indices. Grouping variables with multiple columns are used to specify different groups within multiple variables.

For example, the following command loads the 150-by-4 numerical array `meas` and the 150-by-1 cell array of strings `species` into the workspace:

```
load fisheriris % Fisher's iris data (1936)
```

The data are 150 observations of four measured variables (by column number: sepal length, sepal width, petal length, and petal width, respectively) over three species of iris (setosa, versicolor, and virginica). To group the

observations by species, the following are all acceptable (and equivalent) grouping variables:

```
group1 = species;          % Cell array of strings
group2 = grp2idx(species); % Numeric vector
group3 = char(species);    % Character array
group4 = nominal(species); % Categorical array
```

These grouping variables can be supplied as input arguments to any of the functions described in "Functions for Grouped Data" on page 2-35. Examples are given in "Using Grouping Variables" on page 2-36.

Group Definition

Each level of a grouping variable defines a group. The levels and the order of levels are decided as follows:

- For a numeric vector or a logical vector `G`, the set of group levels is the distinct values of `G`. The order is the sorted order of the unique values.
- For a cell array of strings or a character array `G`, the set of group levels is the distinct strings of `G`. The order for strings is the order of their first appearance in `G`.
- For a categorical vector `G`, the set of group levels and their order match the output of the `getlabels (G)` method.

Some functions, such as `grpstats`, can take a cell array of several grouping variables (such as `{G1 G2 G3}`) to group the observations in the data set by each combination of the grouping variable levels. The order is decided first by the order of the first grouping variables, then by the order of the second grouping variable, and so on.

Functions for Grouped Data

The following table lists general Statistics Toolbox functions that accept a grouping variable `group` as an input argument. The grouping variable may be in the form of a numeric or logical vector, string array, cell array of strings, or categorical array, as described in "Grouping Variables" on page 2-34.

For a full description of the syntax of any particular function, and examples of its use, consult its reference page, linked from the table. "Using Grouping Variables" on page 2-36 also includes examples.

Function	Basic Syntax for Grouped Data
gplotmatrix	gplotmatrix(x,y,group)
grp2idx	[G,GN] = grp2idx(group)
grpstats	means = grpstats(X,group)
gscatter	gscatter(x,y,group)

Using Grouping Variables

This section provides an example demonstrating the use of grouping variables and associated functions. Grouping variables are introduced in "Grouping Variables" on page 2-34. A list of general functions accepting grouping variables appears in "Functions for Grouped Data" on page 2-35.

1 Load the 150-by-4 numerical array `meas` and the 150-by-1 cell array of strings `species`:

```
load fisheriris % Fisher's iris data (1936)
```

The data are 150 observations of four measured variables (by column number: sepal length, sepal width, petal length, and petal width, respectively) over three species of iris (setosa, versicolor, and virginica).

2 Compute some basic statistics for the data (median and interquartile range), by group, using the `grpstats` function:

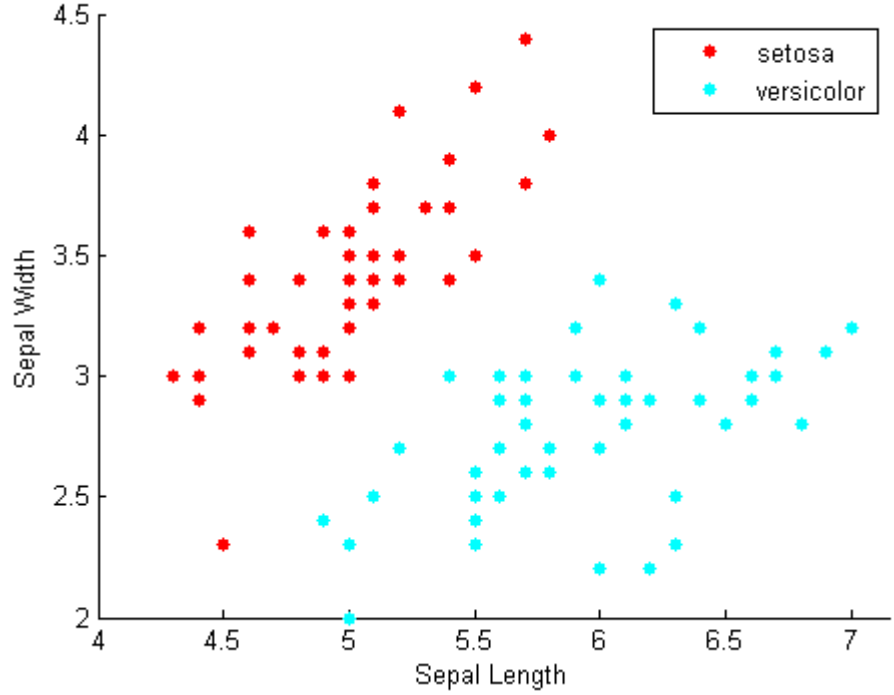
```
[order,number,group_median,group_iqr] = ...
   grpstats(meas,species,{'gname','numel',@median,@iqr})

order =
    'setosa'
    'versicolor'
    'virginica'

number =
    50    50    50    50
```

```
    50    50    50    50
    50    50    50    50

group_median =
    5.0000    3.4000    1.5000    0.2000
    5.9000    2.8000    4.3500    1.3000
    6.5000    3.0000    5.5500    2.0000

group_iqr =
    0.4000    0.5000    0.2000    0.1000
    0.7000    0.5000    0.6000    0.3000
    0.7000    0.4000    0.8000    0.5000
```

The statistics appear in 3-by-4 arrays, corresponding to the 3 groups (categories) and 4 variables in the data. The order of the groups appears in the group names in `order`.

3 You can use grouping variables to create visualizations based on categories of observations. The following scatter plot, created with the `gscatter` function, shows the correlation between sepal length and sepal width in two species of iris. Use `ismember` to subset the two species from `species`:

```
subset = ismember(species,{'setosa','versicolor'});
scattergroup = species(subset);
gscatter(meas(subset,1),...
         meas(subset,2),...
         scattergroup)
xlabel('Sepal Length')
ylabel('Sepal Width')
```


setosa
versicolor
Sepal Width
Sepal Length
4.5
4
3.5
3
2.5
2
4
4.5
5
5.5
6
6.5
7

3

Descriptive Statistics

Introduction to Descriptive Statistics

You may need to summarize large, complex data sets—both numerically and visually—to convey their essence to the data analyst and to allow for further processing. This chapter focuses on numerical summaries; Chapter 4, "Statistical Visualization" focuses on visual summaries.

Measures of Central Tendency

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

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

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

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

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

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

The geometric mean and harmonic mean, like the average, are not robust to outliers. They are useful when the sample is distributed lognormal or heavily skewed.

The following example shows the behavior of the measures of location for a sample with one outlier.

```
x = [ones(1,6) 100]

x =
     1     1     1     1     1     1   100

locate = [geomean(x) harmmean(x) mean(x) median(x)...
          trimmean(x,25)]

locate =
    1.9307    1.1647   15.1429    1.0000    1.0000
```

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

Measures of Dispersion

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

The table gives the function names and descriptions.

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

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

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

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

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

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

The following example shows the behavior of the measures of dispersion for a sample with one outlier.

```
x = [ones(1,6) 100]

x =
     1     1     1     1     1     1   100

stats = [iqr(x) mad(x) range(x) std(x)]

stats =
         0   24.2449   99.0000   37.4185
```

Measures of Shape

Quantiles and percentiles provide information about the shape of data as well as its location and spread.

The *quantile* of order p ($0 \le p \le 1$) is the smallest x value where the cumulative distribution function equals or exceeds p. The function `quantile` computes quantiles as follows:

1. n sorted data points are the $0.5/n$, $1.5/n$, ..., $(n–0.5)/n$ quantiles.
2. Linear interpolation is used to compute intermediate quantiles.
3. The data `min` or `max` are assigned to quantiles outside the range.
4. Missing values are treated as `NaN`, and removed from the data.

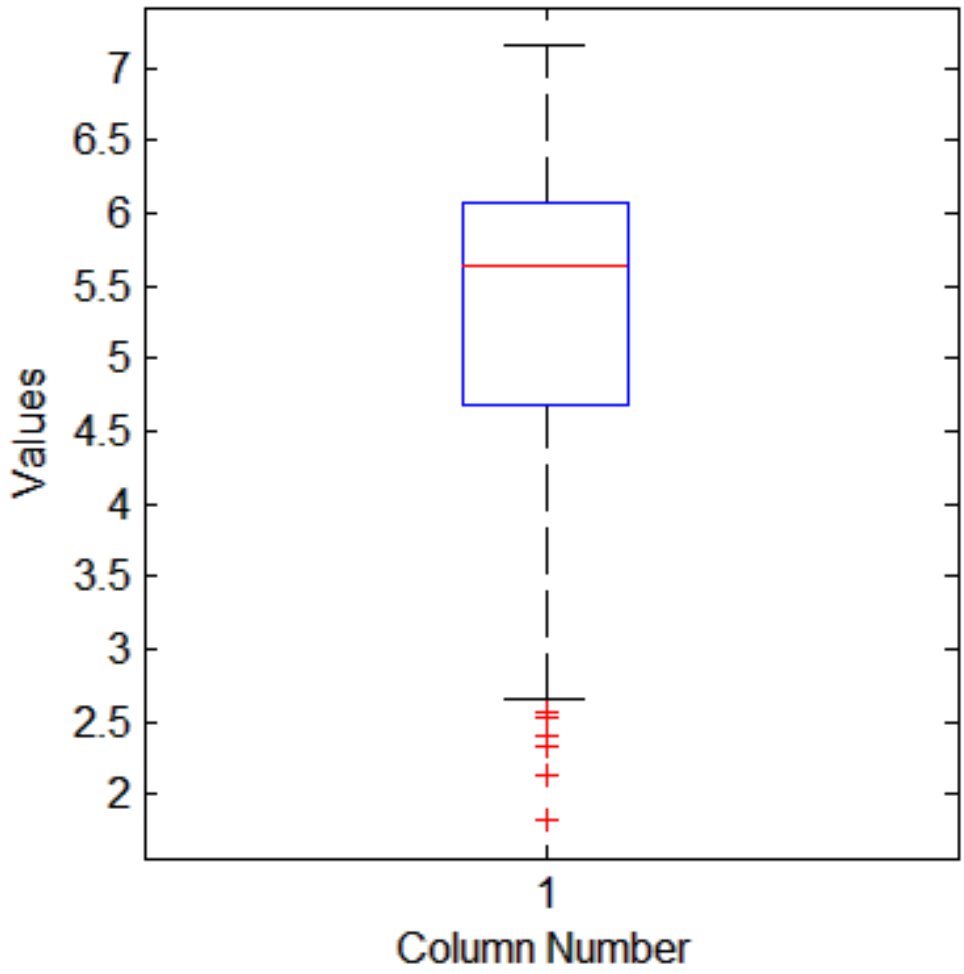
Percentiles, computed by the `prctile` function, are quantiles for a certain percentage of the data, specified for $0 \le p \le 100$.

The following example shows the result of looking at every quartile (quantiles with orders that are multiples of 0.25) of a sample containing a mixture of two distributions.

```
x = [normrnd(4,1,1,100) normrnd(6,0.5,1,200)];
p = 100*(0:0.25:1);
y = prctile(x,p);
z = [p;y]
z =
         0   25.0000   50.0000   75.0000  100.0000
    1.8293    4.6728    5.6459    6.0766    7.1546
```

A box plot helps to visualize the statistics:

```
boxplot(x)
```



The long lower tail and plus signs show the lack of symmetry in the sample values. For more information on box plots, see “Box Plots” on page 4-6.

The shape of a data distribution is also measured by the Statistics Toolbox functions `skewness`, `kurtosis`, and, more generally, `moment`.

Resampling Statistics

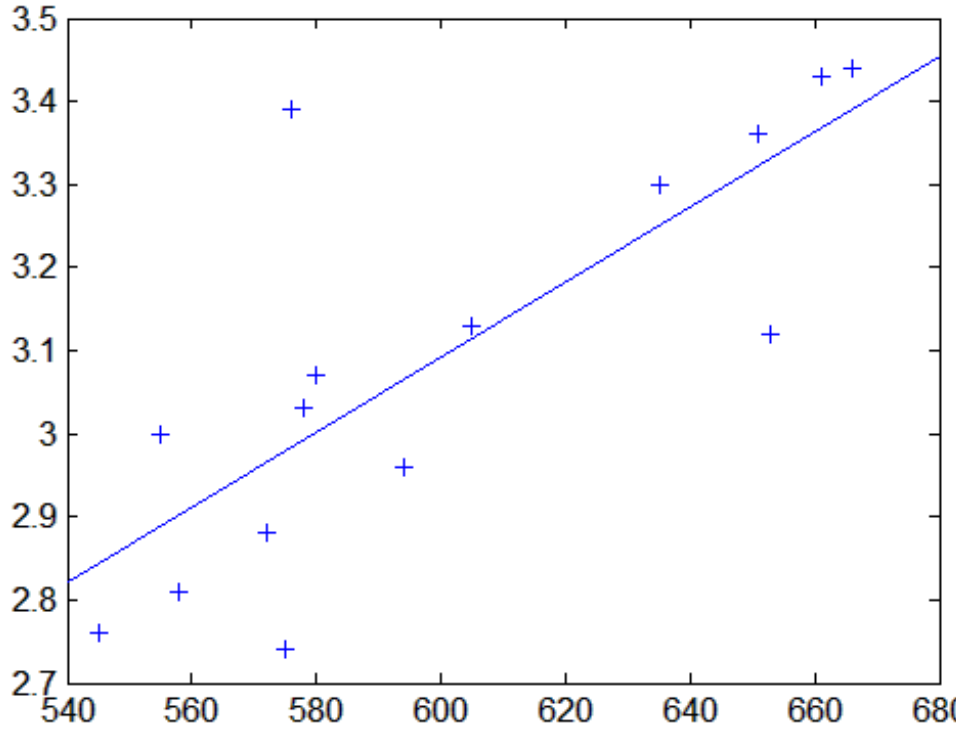
In this section...

The Bootstrap

The *bootstrap* procedure involves choosing random samples with replacement from a data set and analyzing each sample the same way. Sampling with replacement means that each observation is selected separately at random from the original dataset. So a particular data point from the original data set could appear multiple times in a given bootstrap sample. The number of elements in each bootstrap sample equals the number of elements in the original data set. The range of sample estimates you obtain enables you to establish the uncertainty of the quantity you are estimating.

This example from Efron and Tibshirani [33] compares Law School Admission Test (LSAT) scores and subsequent law school grade point average (GPA) for a sample of 15 law schools.

```
load lawdata
plot(lsat,gpa,'+')
lsline
```



The least-squares fit line indicates that higher LSAT scores go with higher law school GPAs. But how certain is this conclusion? The plot provides some intuition, but nothing quantitative.

You can calculate the correlation coefficient of the variables using the `corr` function.

```
rhohat = corr(lsat,gpa)
rhohat =
    0.7764
```

Now you have a number describing the positive connection between LSAT and GPA; though it may seem large, you still do not know if it is statistically significant.

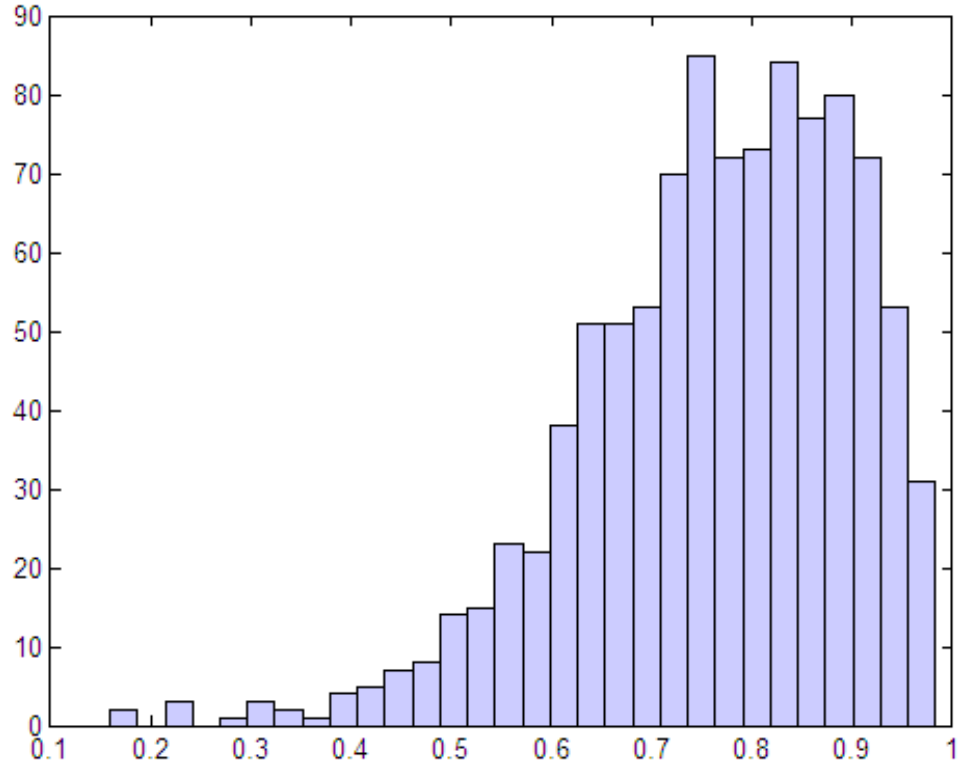
Using the `bootstrp` function you can resample the `lsat` and `gpa` vectors as many times as you like and consider the variation in the resulting correlation coefficients.

Here is an example.

```
rhos1000 = bootstrp(1000,'corr',lsat,gpa);
```

This command resamples the `lsat` and `gpa` vectors 1000 times and computes the `corr` function on each sample. Here is a histogram of the result.

```
hist(rhos1000,30)
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
```



Nearly all the estimates lie on the interval [0.4 1.0].

It is often desirable to construct a confidence interval for a parameter estimate in statistical inferences. Using the `bootci` function, you can use bootstrapping to obtain a confidence interval. The confidence interval for the `lsat` and `gpa` data is computed as:

```
ci = bootci(5000,@corr,lsat,gpa)

ci =

    0.3313
    0.9427
```

Therefore, a 95% confidence interval for the correlation coefficient between LSAT and GPA is [0.33 0.94]. This is strong quantitative evidence that LSAT and subsequent GPA are positively correlated. Moreover, this evidence does not require any strong assumptions about the probability distribution of the correlation coefficient.

Although the `bootci` function computes the Bias Corrected and accelerated (BCa) interval as the default type, it is also able to compute various other types of bootstrap confidence intervals, such as the studentized bootstrap confidence interval.

The Jackknife

Similar to the bootstrap is the *jackknife*, which uses resampling to estimate the bias of a sample statistic. Sometimes it is also used to estimate standard error of the sample statistic. The jackknife is implemented by the Statistics Toolbox function `jackknife`.

The jackknife resamples systematically, rather than at random as the bootstrap does. For a sample with `n` points, the jackknife computes sample statistics on `n` separate samples of size `n`-1. Each sample is the original data with a single observation omitted.

In the previous bootstrap example you measured the uncertainty in estimating the correlation coefficient. You can use the jackknife to estimate the bias, which is the tendency of the sample correlation to over-estimate or under-estimate the true, unknown correlation. First compute the sample correlation on the data:

```
load lawdata
rhohat = corr(lsat,gpa)

rhohat =

    0.7764
```

Next compute the correlations for jackknife samples, and compute their mean:

```
jackrho = jackknife(@corr,lsat,gpa);
meanrho = mean(jackrho)

meanrho =

    0.7759
```

Now compute an estimate of the bias:

```
n = length(lsat);
biasrho = (n-1) * (meanrho-rhohat)

biasrho =

   -0.0065
```

The sample correlation probably underestimates the true correlation by about this amount.

Parallel Computing Support for Resampling Methods

For information on computing resampling statistics in parallel, see Chapter 17, “Parallel Statistics”.

Data with Missing Values

Many data sets have one or more missing values. It is convenient to code missing values as `NaN` (Not a Number) to preserve the structure of data sets across multiple variables and observations.

For example:

```
X = magic(3);
X([1 5]) = [NaN NaN]
X =
   NaN    1    6
     3  NaN    7
     4    9    2
```

Normal MATLAB arithmetic operations yield `NaN` values when operands are `NaN`:

```
s1 = sum(X)
s1 =
   NaN   NaN   15
```

Removing the `NaN` values would destroy the matrix structure. Removing the rows containing the `NaN` values would discard data. Statistics Toolbox functions in the following table remove `NaN` values only for the purposes of computation.

Function	Description
`nancov`	Covariance matrix, ignoring `NaN` values
`nanmax`	Maximum, ignoring `NaN` values
`nanmean`	Mean, ignoring `NaN` values
`nanmedian`	Median, ignoring `NaN` values
`nanmin`	Minimum, ignoring `NaN` values
`nanstd`	Standard deviation, ignoring `NaN` values
`nansum`	Sum, ignoring `NaN` values
`nanvar`	Variance, ignoring `NaN` values

For example:

```
s2 = nansum(X)
s2 =
     7    10    15
```

Other Statistics Toolbox functions also ignore `NaN` values. These include `iqr`, `kurtosis`, `mad`, `prctile`, `range`, `skewness`, and `trimmean`.

4

Statistical Visualization

Introduction to Statistical Visualization

Statistics Toolbox data visualization functions add to the extensive graphics capabilities already in MATLAB.

- Scatter plots are a basic visualization tool for multivariate data. They are used to identify relationships among variables. Grouped versions of these plots use different plotting symbols to indicate group membership. The `gname` function is used to label points on these plots with a text label or an observation number.
- Box plots display a five-number summary of a set of data: the median, the two ends of the interquartile range (the box), and two extreme values (the whiskers) above and below the box. Because they show less detail than histograms, box plots are most useful for side-by-side comparisons of two distributions.
- Distribution plots help you identify an appropriate distribution family for your data. They include normal and Weibull probability plots, quantile-quantile plots, and empirical cumulative distribution plots.

Advanced Statistics Toolbox visualization functions are available for specialized statistical analyses.

Note For information on creating visualizations of data by group, see "Grouped Data" on page 2-34.

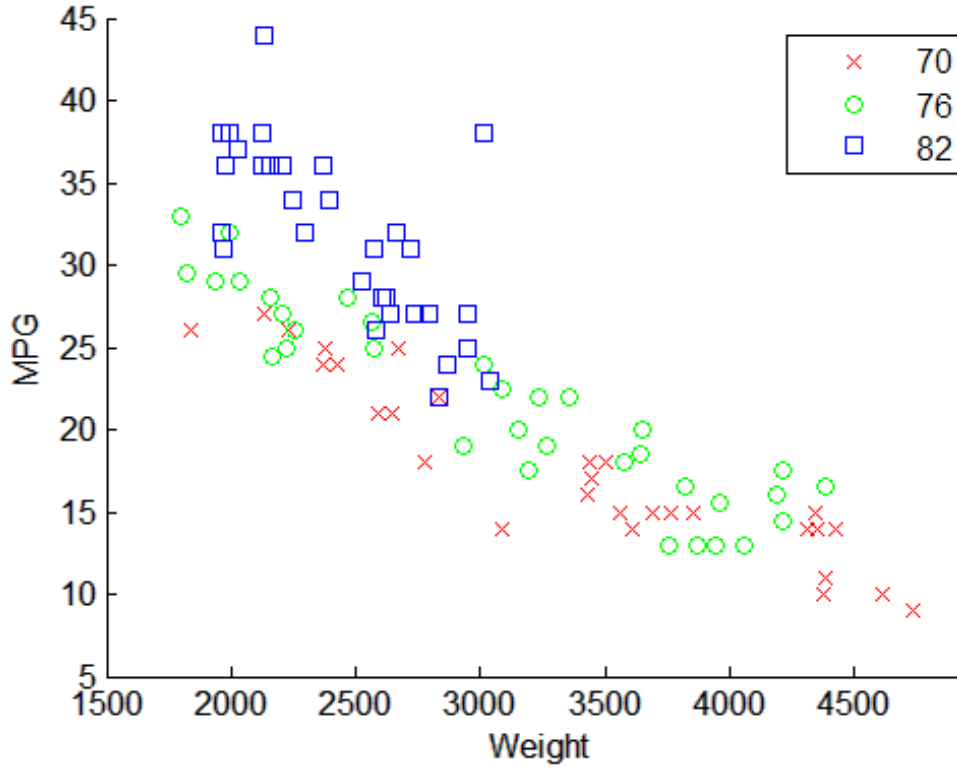
Scatter Plots

A scatter plot is a simple plot of one variable against another. The MATLAB functions `plot` and `scatter` produce scatter plots. The MATLAB function `plotmatrix` can produce a matrix of such plots showing the relationship between several pairs of variables.

Statistics Toolbox functions `gscatter` and `gplotmatrix` produce grouped versions of these plots. These are useful for determining whether the values of two variables or the relationship between those variables is the same in each group.

Suppose you want to examine the weight and mileage of cars from three different model years.

```
load carsmall
gscatter(Weight,MPG,Model_Year,'','xos')
```



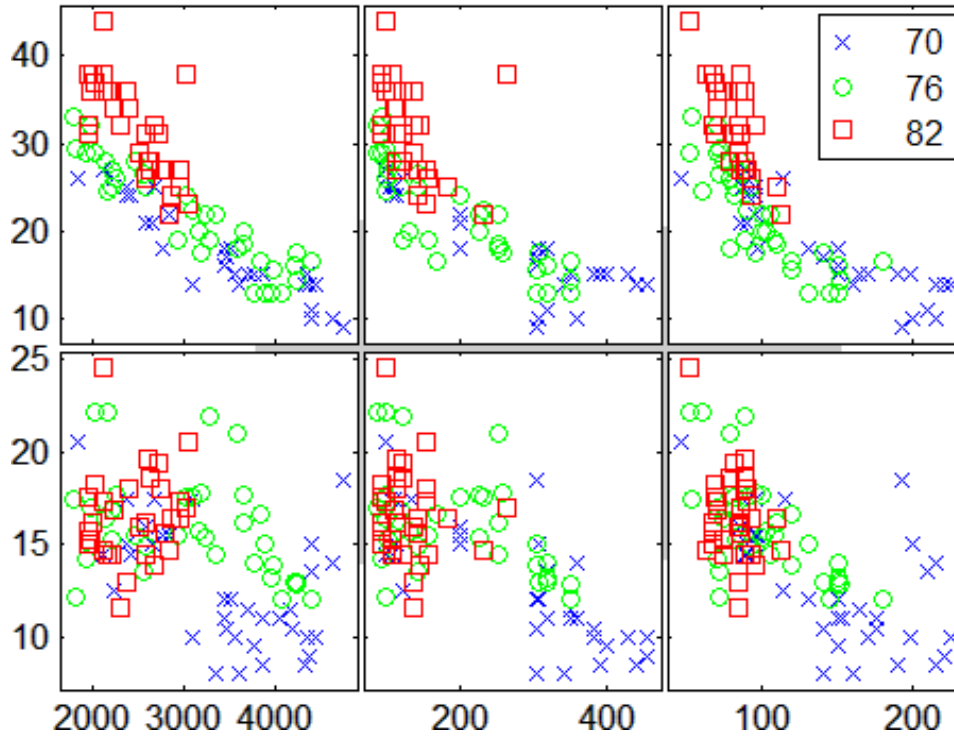
This shows that not only is there a strong relationship between the weight of a car and its mileage, but also that newer cars tend to be lighter and have better gas mileage than older cars.

The default arguments for `gscatter` produce a scatter plot with the different groups shown with the same symbol but different colors. The last two arguments above request that all groups be shown in default colors and with different symbols.

The `carsmall` data set contains other variables that describe different aspects of cars. You can examine several of them in a single display by creating a grouped plot matrix.

```
xvars = [Weight Displacement Horsepower];
yvars = [MPG Acceleration];
```

```
gplotmatrix(xvars,yvars,Model_Year,'','xos')
```



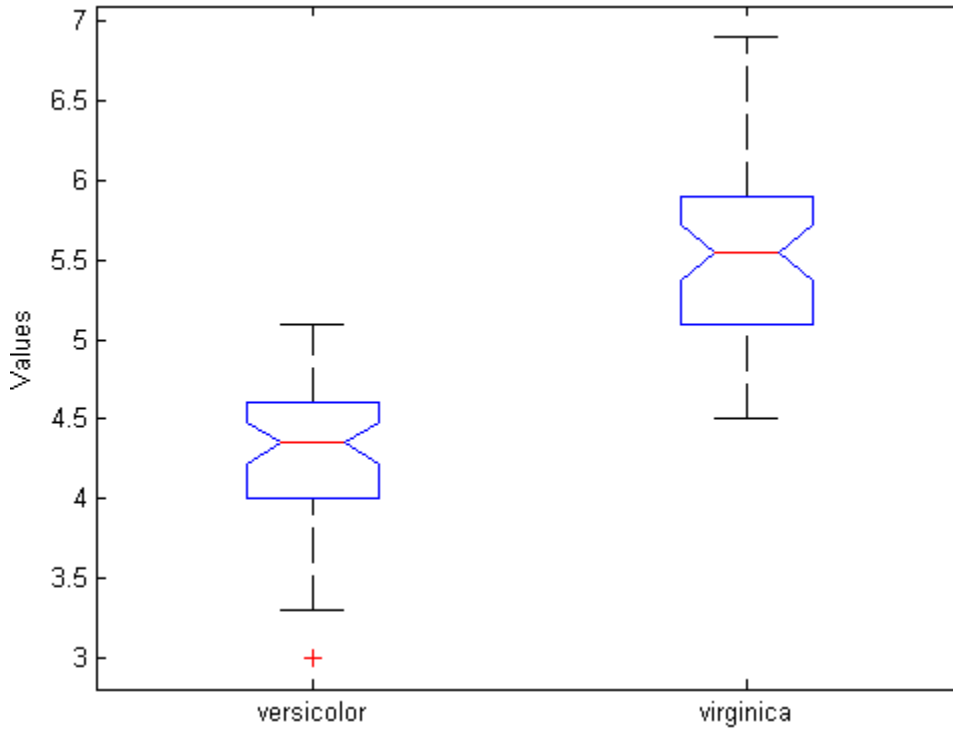
The upper right subplot displays `MPG` against `Horsepower`, and shows that over the years the horsepower of the cars has decreased but the gas mileage has improved.

The `gplotmatrix` function can also graph all pairs from a single list of variables, along with histograms for each variable. See “MANOVA” on page 8-39.

Box Plots

The graph below, created with the `boxplot` command, compares petal lengths in samples from two species of iris.

```
load fisheriris
s1 = meas(51:100,3);
s2 = meas(101:150,3);
boxplot([s1 s2],'notch','on',...
        'labels',{'versicolor','virginica'})
```



This plot has the following features:

- The tops and bottoms of each "box" are the 25th and 75th percentiles of the samples, respectively. The distances between the tops and bottoms are the interquartile ranges.

- The line in the middle of each box is the sample median. If the median is not centered in the box, it shows sample skewness.
- The whiskers are lines extending above and below each box. Whiskers are drawn from the ends of the interquartile ranges to the furthest observations within the whisker length (the *adjacent values*).
- Observations beyond the whisker length are marked as outliers. By default, an outlier is a value that is more than 1.5 times the interquartile range away from the top or bottom of the box, but this value can be adjusted with additional input arguments. Outliers are displayed with a red + sign.
- Notches display the variability of the median between samples. The width of a notch is computed so that box plots whose notches do not overlap (as above) have different medians at the 5% significance level. The significance level is based on a normal distribution assumption, but comparisons of medians are reasonably robust for other distributions. Comparing box-plot medians is like a visual hypothesis test, analogous to the t test used for means.

Distribution Plots

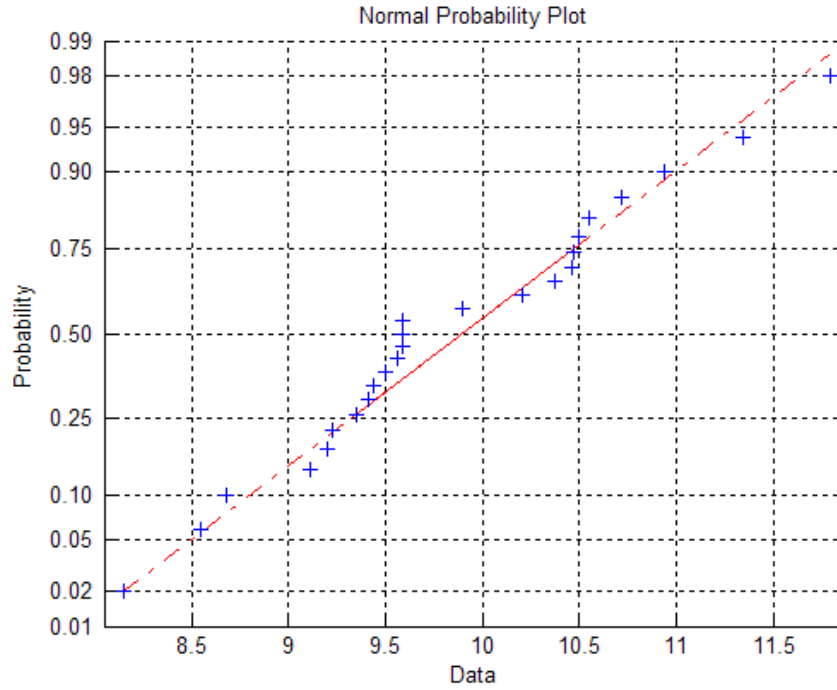
In this section...

Normal Probability Plots

Normal probability plots are used to assess whether data comes from a normal distribution. Many statistical procedures make the assumption that an underlying distribution is normal, so normal probability plots can provide some assurance that the assumption is justified, or else provide a warning of problems with the assumption. An analysis of normality typically combines normal probability plots with hypothesis tests for normality, as described in Chapter 7, "Hypothesis Tests".

The following example shows a normal probability plot created with the `normplot` function.

```
x = normrnd(10,1,25,1);
normplot(x)
```



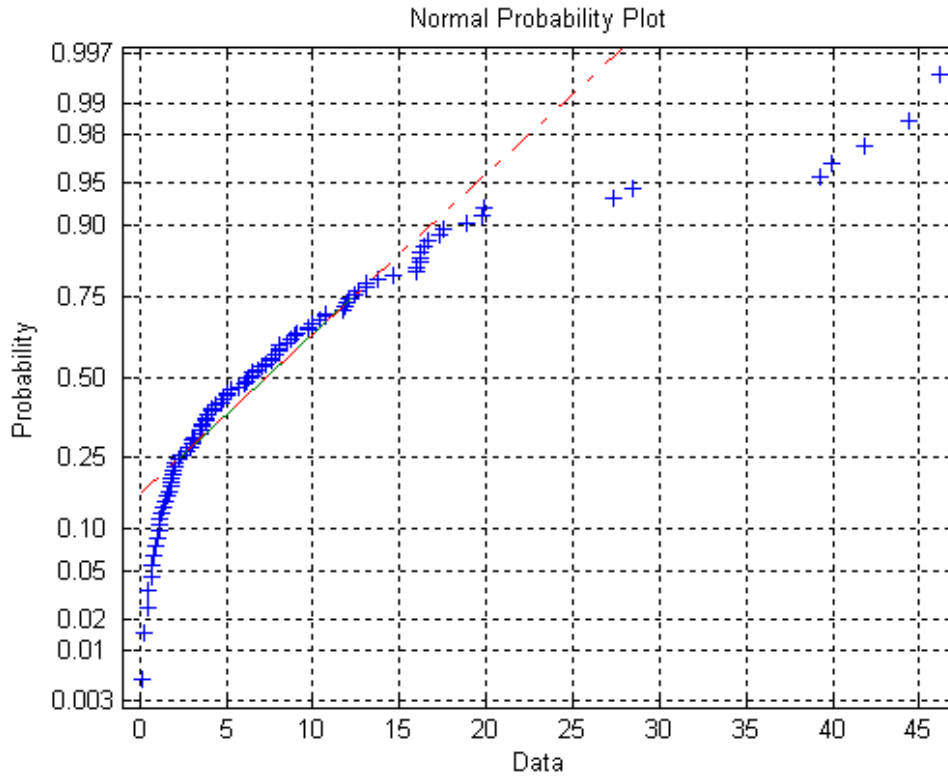
The plus signs plot the empirical probability versus the data value for each point in the data. A solid line connects the 25th and 75th percentiles in the data, and a dashed line extends it to the ends of the data. The *y*-axis values are probabilities from zero to one, but the scale is not linear. The distance between tick marks on the *y*-axis matches the distance between the quantiles of a normal distribution. The quantiles are close together near the median (probability = 0.5) and stretch out symmetrically as you move away from the median.

In a normal probability plot, if all the data points fall near the line, an assumption of normality is reasonable. Otherwise, the points will curve away from the line, and an assumption of normality is not justified.

For example:

```
x = exprnd(10,100,1);
```

```
normplot(x)
```



The plot is strong evidence that the underlying distribution is not normal.

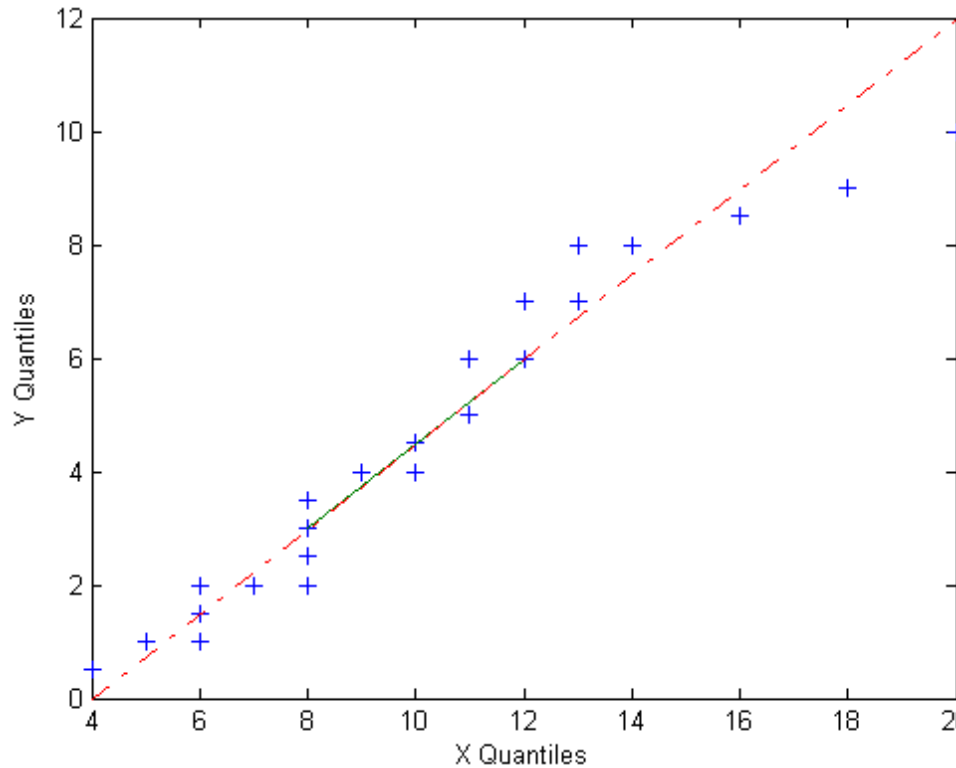
Quantile-Quantile Plots

Quantile-quantile plots are used to determine whether two samples come from the same distribution family. They are scatter plots of quantiles computed from each sample, with a line drawn between the first and third quartiles. If the data falls near the line, it is reasonable to assume that the two samples come from the same distribution. The method is robust with respect to changes in the location and scale of either distribution.

To create a quantile-quantile plot, use the `qqplot` function.

The following example shows a quantile-quantile plot of two samples from Poisson distributions.

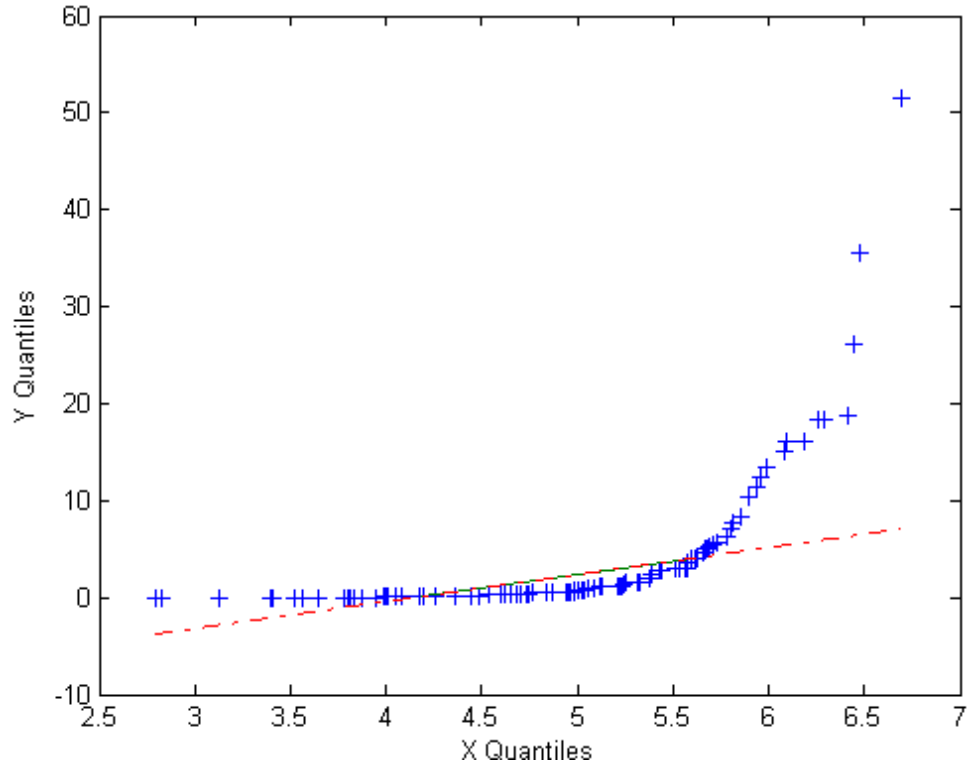
```
x = poissrnd(10,50,1);
y = poissrnd(5,100,1);
qqplot(x,y);
```



Even though the parameters and sample sizes are different, the approximate linear relationship suggests that the two samples may come from the same distribution family. As with normal probability plots, hypothesis tests, as described in Chapter 7, "Hypothesis Tests", can provide additional justification for such an assumption. For statistical procedures that depend on the two samples coming from the same distribution, however, a linear quantile-quantile plot is often sufficient.

The following example shows what happens when the underlying distributions are not the same.

```
x = normrnd(5,1,100,1);
y = wblrnd(2,0.5,100,1);
qqplot(x,y);
```



These samples clearly are not from the same distribution family.

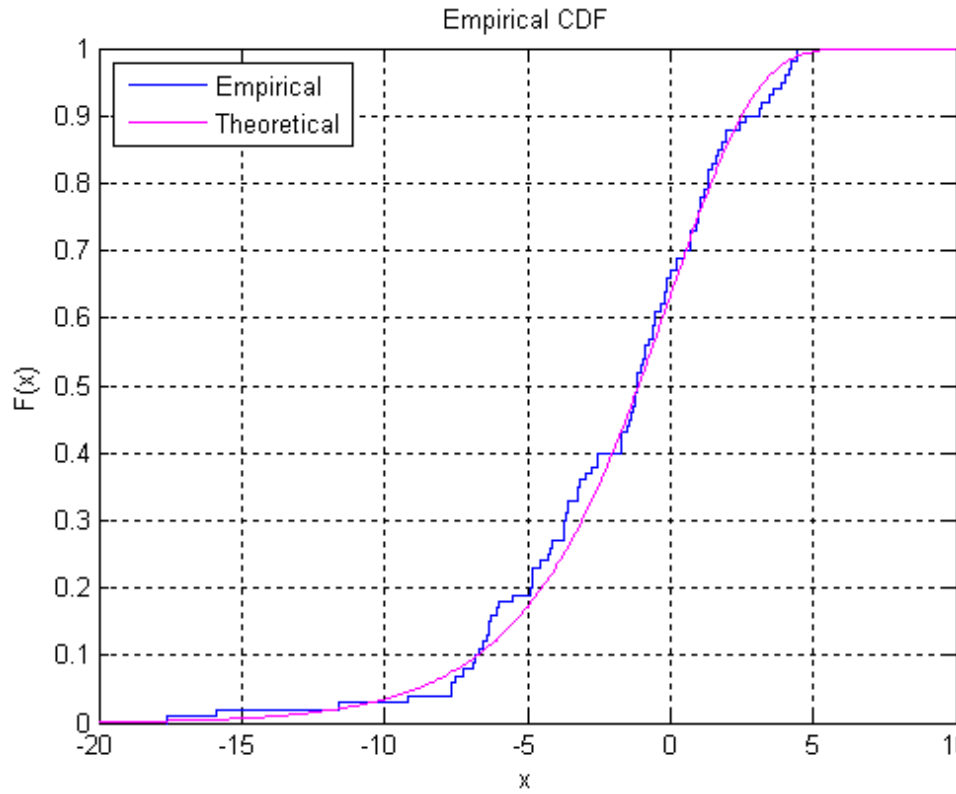
Cumulative Distribution Plots

An empirical cumulative distribution function (cdf) plot shows the proportion of data less than each *x* value, as a function of *x*. The scale on the *y*-axis is linear; in particular, it is not scaled to any particular distribution. Empirical cdf plots are used to compare data cdfs to cdfs for particular distributions.

To create an empirical cdf plot, use the `cdfplot` function (or `ecdf` and `stairs`).

The following example compares the empirical cdf for a sample from an extreme value distribution with a plot of the cdf for the sampling distribution. In practice, the sampling distribution would be unknown, and would be chosen to match the empirical cdf.

```
y = evrnd(0,3,100,1);
cdfplot(y)
hold on
x = -20:0.1:10;
f = evcdf(x,0,3);
plot(x,f,'m')
legend('Empirical','Theoretical','Location','NW')
```



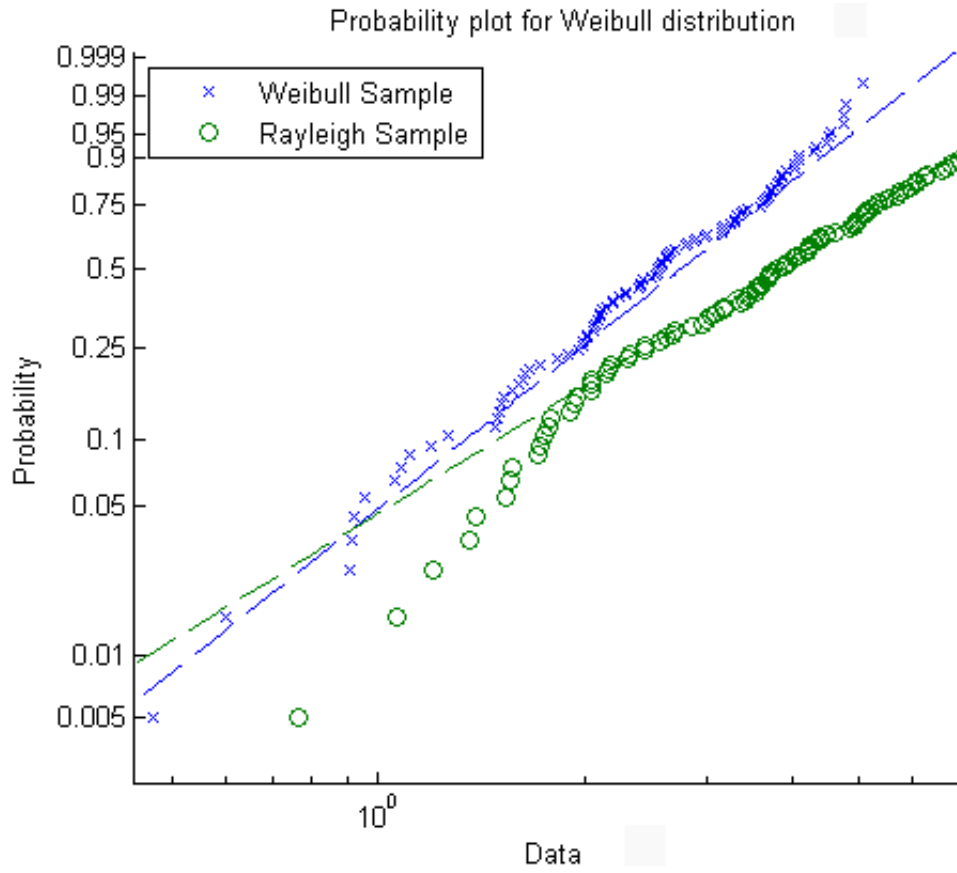
Other Probability Plots

A probability plot, like the normal probability plot, is just an empirical cdf plot scaled to a particular distribution. The *y*-axis values are probabilities from zero to one, but the scale is not linear. The distance between tick marks is the distance between quantiles of the distribution. In the plot, a line is drawn between the first and third quartiles in the data. If the data falls near the line, it is reasonable to choose the distribution as a model for the data.

To create probability plots for different distributions, use the `probplot` function.

For example, the following plot assesses two samples, one from a Weibull distribution and one from a Rayleigh distribution, to see if they may have come from a Weibull population.

```
x1 = wblrnd(3,3,100,1);
x2 = raylrnd(3,100,1);
probplot('weibull',[x1 x2])
legend('Weibull Sample','Rayleigh Sample','Location','NW')
```



The plot gives justification for modeling the first sample with a Weibull distribution; much less so for the second sample.

A distribution analysis typically combines probability plots with hypothesis tests for a particular distribution, as described in Chapter 7, “Hypothesis Tests”.

5

Probability Distributions

Using Probability Distributions

Probability distributions are theoretical distributions based on assumptions about a source population. They assign probability to the event that a random variable takes on a specific, discrete value, or falls within a specified range of continuous values. There are two main types of models:

- **Parametric Models**—Choose a model based on a parametric family of probability distributions and then adjust the parameters to fit the data. For information on supported parametric distributions, see "Parametric Distributions" on page 5-4.
- **Nonparametric Models**—When data or statistics do not follow any standard probability distribution, *nonparametric models* may be appropriate. For information on supported nonparametric distributions, see "Nonparametric Distributions" on page 5-8.

The Statistics Toolbox provides several ways of working with both parametric and nonparametric probability distributions:

- **Graphic User Interfaces (GUIs)**—Interact with the distributions to visualize distributions, fit a distribution to your data, or generate random data using a specific distribution. For more information, see "Working with Distributions Through GUIs" on page 5-9.
- **Command Line Functions**—Use command-line functions to further explore the distributions, fit relevant models to your data, or generate random data. For more information on using functions, see "Statistics Toolbox Distribution Functions" on page 5-52.
- **Distribution Objects**—Use objects to explore and fit your data to a distribution, save the results to a single entity, and generate random data from the resulting parameters. For more information, see "Using Probability Distribution Objects" on page 5-84.

Supported Distributions

In this section...

Probability distributions supported by the Statistics Toolbox are cross-referenced with their supporting functions and GUIs in the following tables. The tables use the following abbreviations for distribution functions:

- **pdf** — Probability density functions
- **cdf** — Cumulative distribution functions
- **inv** — Inverse cumulative distribution functions
- **stat** — Distribution statistics functions
- **fit** — Distribution fitting functions
- **like** — Negative log-likelihood functions
- **rnd** — Random number generators

For more detailed explanations of each supported distribution, see Appendix B, “Distribution Reference”.

Parametric Distributions

Continuous Distributions (Data)

Name	pdf	cdf	inv	stat	fit	like	rnd
Beta	betapdf, pdf	betacdf, cdf	betainv, icdf	betastat	betafit, fitdist, mle, dfittool	betalike	betarnd, random, randtool
Birnbaum-Saunders					mle, fitdist, dfittool		
Exponential	exppdf, pdf	expcdf, cdf	expinv, icdf	expstat	expfit, mle, fitdist, dfittool	explike	exprnd, random, randtool
Extreme value	evpdf, pdf	evcdf, cdf	evinv, icdf	evstat	evfit, mle, fitdist, dfittool	evlike	evrnd, random, randtool
Gamma	gampdf, pdf	gamcdf, cdf	gaminv, icdf	gamstat	gamfit, mle, fitdist, dfittool	gamlike	gamrnd, randg, random, randtool
Generalized extreme value	gevpdf, pdf	gevcdf, cdf	gevinv, icdf	gevstat	gevfit, mle, fitdist, dfittool	gevlike	gevrnd, random, randtool
Generalized Pareto	gppdf, pdf	gpcdf, cdf	gpinv, icdf	gpstat	gpfit, mle, fitdist, dfittool	gplike	gprnd, random, randtool
Inverse Gaussian					mle, fitdist, dfittool		
Johnson system					johnsrnd		johnsrnd

Name	pdf	cdf	inv	stat	fit	like	rnd
Logistic					mle, fitdist, dfittool		
Loglogistic					mle, fitdist, dfittool		
Lognormal	lognpdf, pdf	logncdf, cdf	logninv, icdf	lognstat	lognfit, mle, fitdist, dfittool	lognlike	lognrnd, random, randtool
Nakagami					mle, fitdist, dfittool		
Normal (Gaussian)	normpdf, pdf	normcdf, cdf	norminv, icdf	normstat	normfit, mle, fitdist, dfittool	normlike	normrnd, randn, random, randtool
Pearson system					pearsrnd		pearsrnd
Piecewise	pdf	cdf	icdf		paretotails		random
Rayleigh	raylpdf, pdf	raylcdf, cdf	raylinv, icdf	raylstat	raylfit, mle, fitdist, dfittool		raylrnd, random, randtool
Rician					mle, fitdist, dfittool		
Uniform (continuous)	unifpdf, pdf	unifcdf, cdf	unifinv, icdf	unifstat	unifit, mle		unifrnd, rand, random
Weibull	wblpdf, pdf	wblcdf, cdf	wblinv, icdf	wblstat	wblfit, mle, fitdist, dfittool	wbllike	wblrnd, random

Continuous Distributions (Statistics)

Name	pdf	cdf	inv	stat	fit	like	rnd
Chi-square	`chi2pdf`, `pdf`	`chi2cdf`, `cdf`	`chi2inv`, `icdf`	`chi2stat`			`chi2rnd`, `random`, `randtool`
F	`fpdf`, `pdf`	`fcdf`, `cdf`	`finv`, `icdf`	`fstat`			`frnd`, `random`, `randtool`
Noncentral chi-square	`ncx2pdf`, `pdf`	`ncx2cdf`, `cdf`	`ncx2inv`, `icdf`	`ncx2stat`			`ncx2rnd`, `random`, `randtool`
Noncentral *F*	`ncfpdf`, `pdf`	`ncfcdf`, `cdf`	`ncfinv`, `icdf`	`ncfstat`			`ncfrnd`, `random`, `randtool`
Noncentral *t*	`nctpdf`, `pdf`	`nctcdf`, `cdf`	`nctinv`, `icdf`	`nctstat`			`nctrnd`, `random`, `randtool`
Student's *t*	`tpdf`, `pdf`	`tcdf`, `cdf`	`tinv`, `icdf`	`tstat`			`trnd`, `random`, `randtool`
t location-scale					`mle`, `fitdist`, `dfittool`		

Discrete Distributions

Name	pdf	cdf	inv	stat	fit	like	rnd
Binomial	`binopdf`, `pdf`	`binocdf`, `cdf`	`binoinv`, `icdf`	`binostat`	`binofit`, `mle`, `fitdist`, `dfittool`		`binornd`, `random`, `randtool`
Bernoulli					`mle`		
Geometric	`geopdf`, `pdf`	`geocdf`, `cdf`	`geoinv`, `icdf`	`geostat`	`mle`		`geornd`, `random`, `randtool`
Hypergeometric	`hygepdf`, `pdf`	`hygecdf`, `cdf`	`hygeinv`, `icdf`	`hygestat`			`hygernd`, `random`
Multinomial	`mnpdf`						`mnrnd`
Negative binomial	`nbinpdf`, `pdf`	`nbincdf`, `cdf`	`nbininv`, `icdf`	`nbinstat`	`nbinfit`, `mle`, `fitdist`, `dfittool`		`nbinrnd`, `random`, `randtool`
Poisson	`poisspdf`, `pdf`	`poisscdf`, `cdf`	`poissinv`, `icdf`	`poisstat`	`poissfit`, `mle`, `fitdist`, `dfittool`		`poissrnd`, `random`, `randtool`
Uniform (discrete)	`unidpdf`, `pdf`	`unidcdf`, `cdf`	`unidinv`, `icdf`	`unidstat`	`mle`		`unidrnd`, `random`, `randtool`

Multivariate Distributions

Name	pdf	cdf	inv	stat	fit	like	rnd
Gaussian copula	copulapdf	copulacdf		copulastat	copulafit		copularnd
Gaussian mixture	pdf	cdf			fit		random
t copula	copulapdf	copulacdf		copulastat	copulafit		copularnd
Clayton copula	copulapdf	copulacdf		copulastat	copulafit		copularnd
Frank copula	copulapdf	copulacdf		copulastat	copulafit		copularnd
Gumbel copula	copulapdf	copulacdf		copulastat	copulafit		copularnd
Inverse Wishart							iwishrnd
Multivariate normal	mvnpdf	mvncdf					mvnrnd
Multivariate *t*	mvtpdf	mvtcdf					mvtrnd
Wishart							wishrnd

Nonparametric Distributions

Name	pdf	cdf	inv	stat	fit	like	rnd
Nonparametric	ksdensity	ksdensity	ksdensity		ksdensity, fitdist, dfittool		

Working with Distributions Through GUIs

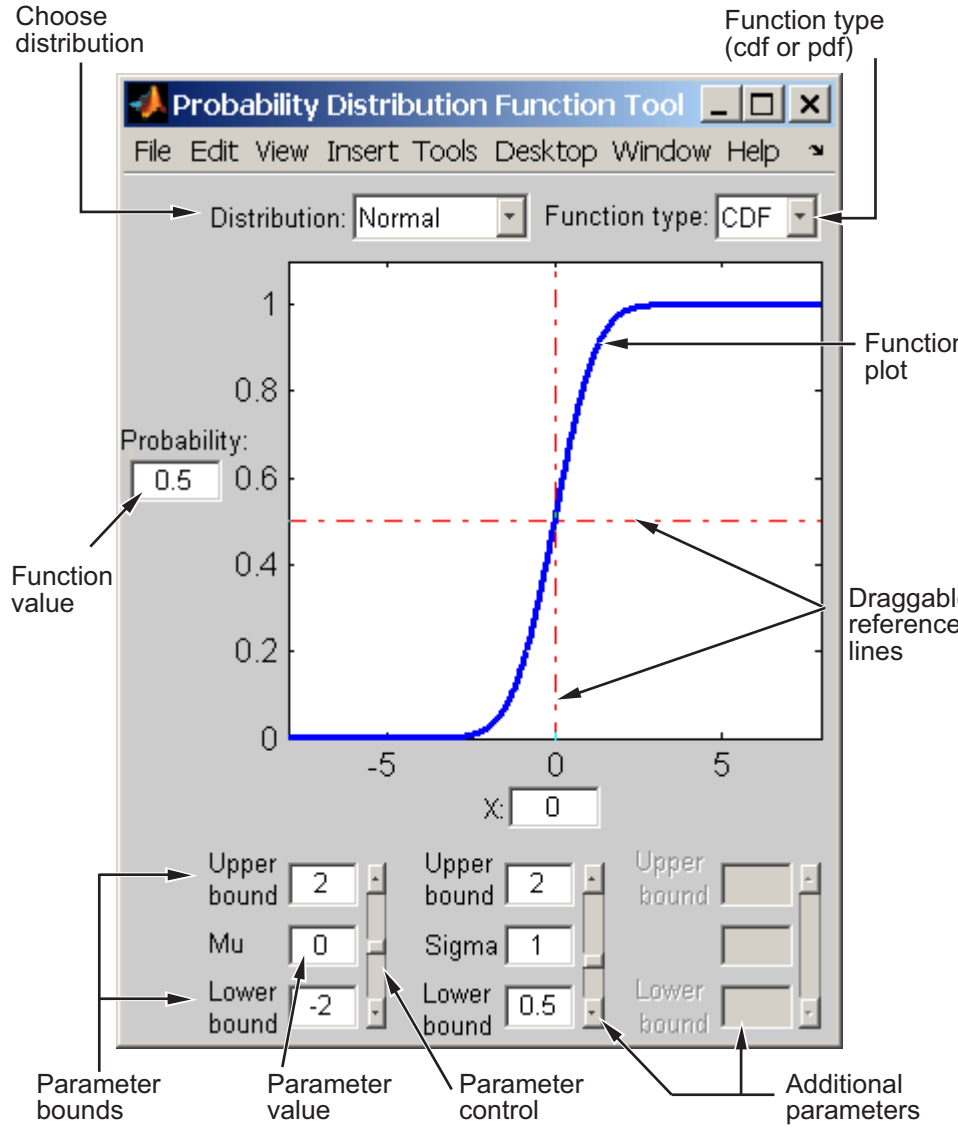
In this section...

This section describes Statistics Toolbox GUIs that provide convenient, interactive access to the distribution functions described in "Statistics Toolbox Distribution Functions" on page 5-52.

Exploring Distributions

To interactively see the influence of parameter changes on the shapes of the pdfs and cdfs of supported Statistics Toolbox distributions, use the Probability Distribution Function Tool.

Run the tool by typing `disttool` at the command line.



Start by selecting a distribution. Then choose the function type: probability density function (pdf) or cumulative distribution function (cdf).

After the plot appears, you can

- Calculate a new function value by
  - Typing a new x value in the text box on the *x*-axis
  - Dragging the vertical reference line.
  - Clicking in the figure where you want the line to be.

  The new function value appears in the text box to the left of the plot.
- For cdf plots, find critical values corresponding to a specific probability by typing the desired probability in the text box on the *y*-axis or by dragging the horizontal reference line.
- Use the controls at the bottom of the window to set parameter values for the distribution and to change their upper and lower bounds.

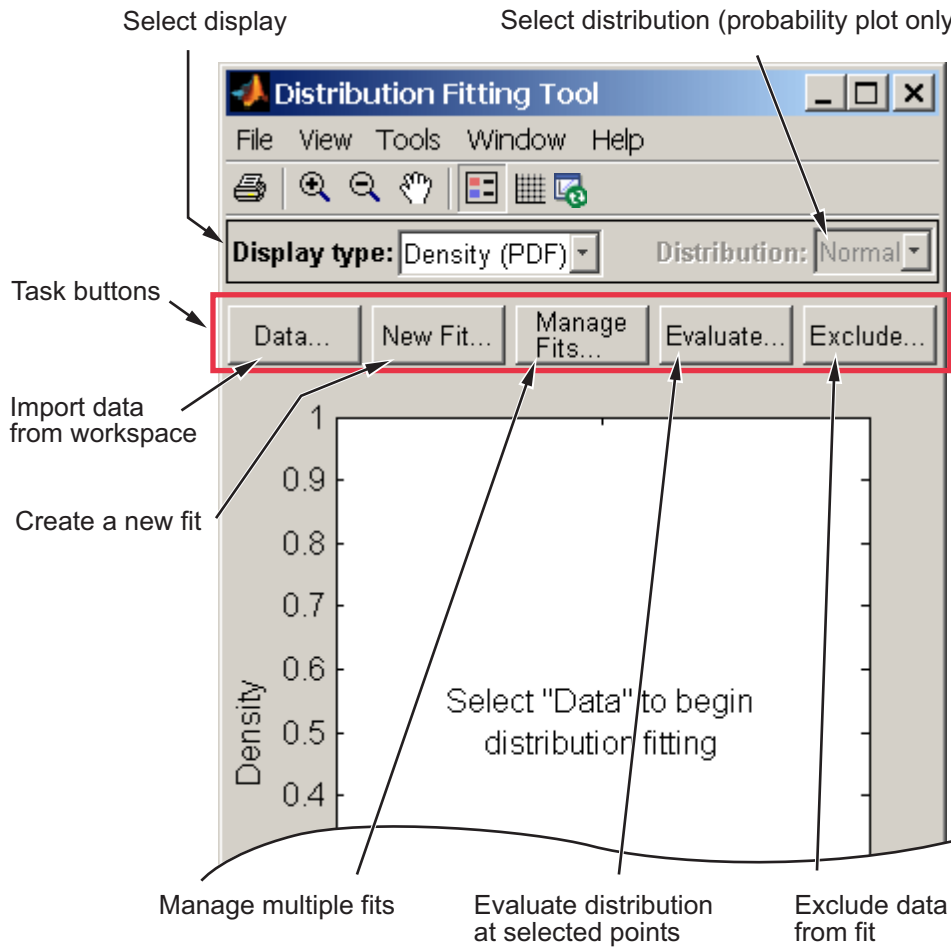
Modeling Data Using the Distribution Fitting Tool

The Distribution Fitting Tool is a GUI for fitting univariate distributions to data. This section describes how to use the Distribution Fitting Tool this tool and covers the following topics:

Opening the Distribution Fitting Tool

To open the Distribution Fitting Tool, enter the command

```
dfittool
```



Adjusting the Plot. Buttons at the top of the tool allow you to adjust the plot displayed in this window:

- — Toggle the legend on (default) or off.

-  — Toggle grid lines on or off (default).
-  — Restore default axes limits.

Displaying the Data. The **Display type** field specifies the type of plot displayed in the main window. Each type corresponds to a probability function, for example, a probability density function. The following display types are available:

- `Density (PDF)` — Display a probability density function (PDF) plot for the fitted distribution.
- `Cumulative probability (CDF)` — Display a cumulative probability plot of the data.
- `Quantile (inverse CDF)` — Display a quantile (inverse CDF) plot.
- `Probability plot` — Display a probability plot.
- `Survivor function` — Display a survivor function plot of the data.
- `Cumulative hazard` — Display a cumulative hazard plot of the data.

Inputting and Fitting Data. The task buttons enable you to perform the tasks necessary to fit distributions to data. Each button opens a new dialog box in which you perform the task. The buttons include:

- **Data** — Import and manage data sets. See “Creating and Managing Data Sets” on page 5-14.
- **New Fit** — Create new fits. See “Creating a New Fit” on page 5-19.
- **Manage Fits** — Manage existing fits. See “Managing Fits” on page 5-26.
- **Evaluate** — Evaluate fits at any points you choose. See “Evaluating Fits” on page 5-28.
- **Exclude** — Create rules specifying which values to exclude when fitting a distribution. See “Excluding Data” on page 5-32.

The display pane displays plots of the data sets and fits you create. Whenever you make changes in one of the dialog boxes, the results in the display pane update.

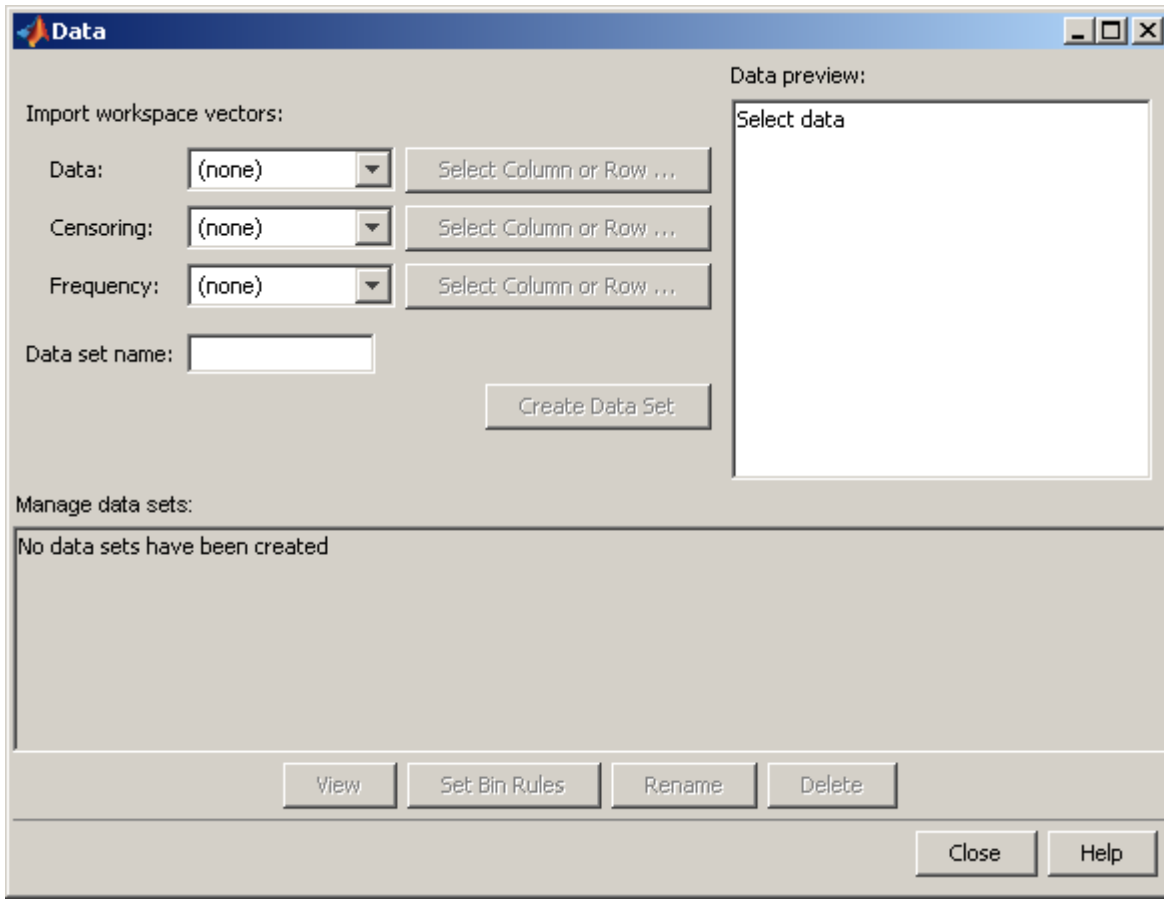
Saving and Customizing Distributions. The Distribution Fitting Tool menus contain items that enable you to do the following:

- Save and load sessions. See "Saving and Loading Sessions" on page 5-38.
- Generate a file with which you can fit distributions to data and plot the results independently of the Distribution Fitting Tool. See "Generating a File to Fit and Plot Distributions" on page 5-46.
- Define and import custom distributions. See "Using Custom Distributions" on page 5-47.

Creating and Managing Data Sets

This section describes how to create and manage data sets.

To begin, click the **Data** button in the Distribution Fitting Tool to open the Data dialog box shown in the following figure.



Importing Data. The **Import workspace vectors** pane enables you to create a data set by importing a vector from the MATLAB workspace. The following sections describe the fields in this pane and give appropriate values for vectors imported from the MATLAB workspace:

- **Data** — The drop-down list in the **Data** field contains the names of all matrices and vectors, other than 1-by-1 matrices (scalars) in the MATLAB workspace. Select the array containing the data you want to fit. The actual data you import must be a vector. If you select a matrix in the **Data** field, the first column of the matrix is imported by default. To select a different column or row of the matrix, click **Select Column or Row**. This displays

the matrix in the Variable Editor, where you can select a row or column by highlighting it with the mouse.

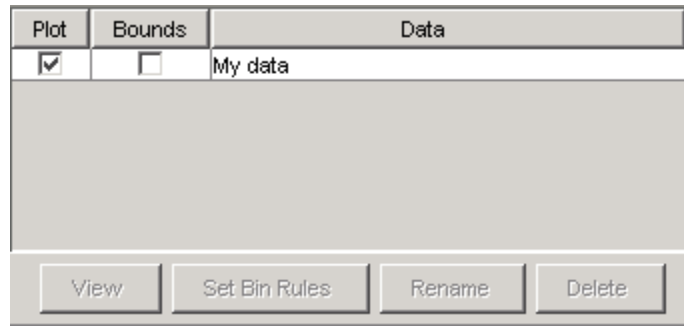
Alternatively, you can enter any valid MATLAB expression in the **Data** field.

When you select a vector in the **Data** field, a histogram of the data appears in the **Data preview** pane.

- **Censoring** — If some of the points in the data set are censored, enter a Boolean vector, of the same size as the data vector, specifying the censored entries of the data. A `1` in the censoring vector specifies that the corresponding entry of the data vector is censored, while a `0` specifies that the entry is not censored. If you enter a matrix, you can select a column or row by clicking **Select Column or Row**. If you do not want to censor any data, leave the **Censoring** field blank.
- **Frequency** — Enter a vector of positive integers of the same size as the data vector to specify the frequency of the corresponding entries of the data vector. For example, a value of `7` in the 15th entry of frequency vector specifies that there are 7 data points corresponding to the value in the 15th entry of the data vector. If all entries of the data vector have frequency 1, leave the **Frequency** field blank.
- **Data set name** — Enter a name for the data set you import from the workspace, such as `My data`.

After you have entered the information in the preceding fields, click **Create Data Set** to create the data set `My data`.

Managing Data Sets. The **Manage data sets** pane enables you to view and manage the data sets you create. When you create a data set, its name appears in the **Data sets** list. The following figure shows the **Manage data sets** pane after creating the data set `My data`.



For each data set in the **Data sets** list, you can:

- Select the **Plot** check box to display a plot of the data in the main Distribution Fitting Tool window. When you create a new data set, **Plot** is selected by default. Clearing the **Plot** check box removes the data from the plot in the main window. You can specify the type of plot displayed in the **Display type** field in the main window.
- If **Plot** is selected, you can also select **Bounds** to display confidence interval bounds for the plot in the main window. These bounds are pointwise confidence bounds around the empirical estimates of these functions. The bounds are only displayed when you set **Display Type** in the main window to one of the following:
  - `Cumulative probability (CDF)`
  - `Survivor function`
  - `Cumulative hazard`

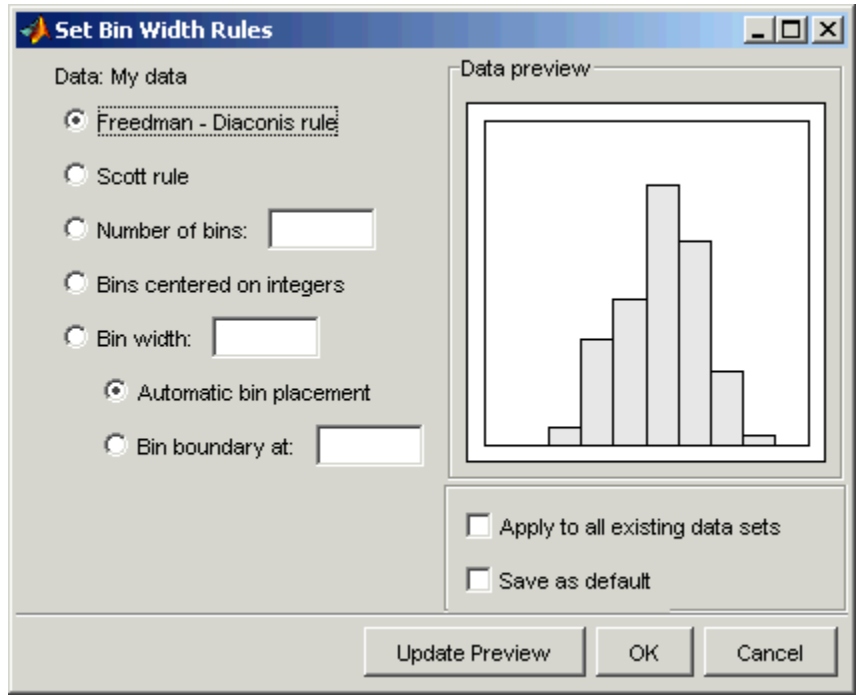
The Distribution Fitting Tool cannot display confidence bounds on density (PDF), quantile (inverse CDF), or probability plots. Clearing the **Bounds** check box removes the confidence bounds from the plot in the main window.

When you select a data set from the list, the following buttons are enabled:

- **View** — Display the data in a table in a new window.
- **Set Bin Rules** — Defines the histogram bins used in a density (PDF) plot.
- **Rename** — Rename the data set.

- **Delete** — Delete the data set.

Setting Bin Rules. To set bin rules for the histogram of a data set, click **Set Bin Rules**. This opens the **Set Bin Width Rules** dialog box.



You can select from the following rules:

- **Freedman-Diaconis rule** — Algorithm that chooses bin widths and locations automatically, based on the sample size and the spread of the data. This rule, which is the default, is suitable for many kinds of data.
- **Scott rule** — Algorithm intended for data that are approximately normal. The algorithm chooses bin widths and locations automatically.
- **Number of bins** — Enter the number of bins. All bins have equal widths.
- **Bins centered on integers** — Specifies bins centered on integers.

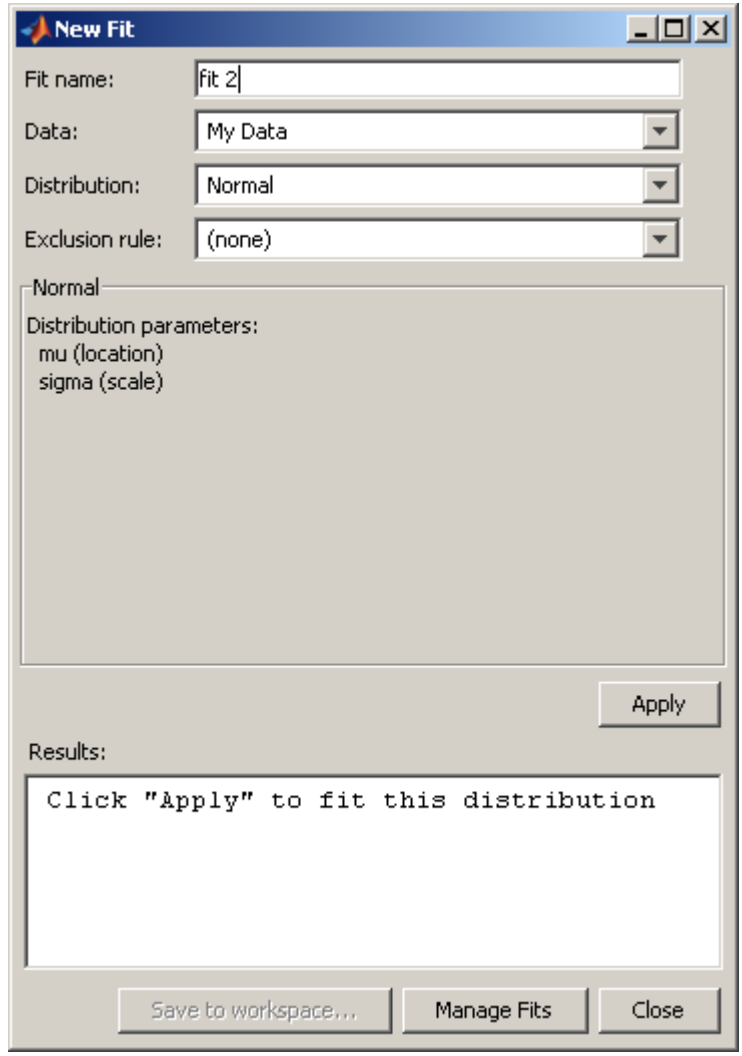
- **Bin width** — Enter the width of each bin. If you select this option, you can also select:
  - **Automatic bin placement** — Place the edges of the bins at integer multiples of the **Bin width**.
  - **Bin boundary at** — Enter a scalar to specify the boundaries of the bins. The boundary of each bin is equal to this scalar plus an integer multiple of the **Bin width**.

The Set Bin Width Rules dialog box also provides the following options:

- **Apply to all existing data sets** — Apply the rule to all data sets. Otherwise, the rule is only applied to the data set currently selected in the Data dialog box.
- **Save as default** — Apply the current rule to any new data sets that you create. You can also set default bin width rules by selecting **Set Default Bin Rules** from the **Tools** menu in the main window.

Creating a New Fit

This section describes how to create a new fit. To begin, click the **New Fit** button at the top of the main window to open the New Fit dialog box. If you created the data set `My data`, it appears in the **Data** field.



Field Name	Description
Fit Name	Enter a name for the fit in the **Fit Name** field.
Data	The **Data** field contains a drop-down list of the data sets you have created. Select the data set to which you want to fit a distribution.

Field Name	Description
Distribution	Select the type of distribution to fit from the **Distribution** drop-down list. See "Available Distributions" on page 5-22 for a list of distributions supported by the Distribution Fitting Tool. Only the distributions that apply to the values of the selected data set appear in the **Distribution** field. For example, positive distributions are not displayed when the data include values that are zero or negative. You can specify either a parametric or a nonparametric distribution. When you select a parametric distribution from the drop-down list, a description of its parameters appears in the Normal pane. The Distribution Fitting Tool estimates these parameters to fit the distribution to the data set. When you select `Nonparametric fit`, options for the fit appear in the pane, as described in "Further Options for Nonparametric Fits" on page 5-23.
Exclusion rule	Specify a rule to exclude some data in the **Exclusion rule** field. Create an exclusion rule by clicking **Exclude** in the Distribution Fitting Tool. For more information, see "Excluding Data" on page 5-32.

Apply the New Fit. Click **Apply** to fit the distribution. For a parametric fit, the **Results** pane displays the values of the estimated parameters. For a nonparametric fit, the **Results** pane displays information about the fit.

When you click **Apply**, the Distribution Fitting Tool displays a plot of the distribution, along with the corresponding data.

Note When you click **Apply**, the title of the dialog box changes to Edit Fit. You can now make changes to the fit you just created and click **Apply** again to save them. After closing the Edit Fit dialog box, you can reopen it from the Fit Manager dialog box at any time to edit the fit.

After applying the fit, you can save the information to the workspace using probability distribution objects by clicking **Save to workspace**. See "Using Probability Distribution Objects" on page 5-84 for more information.

Available Distributions. This section lists the distributions available in the Distribution Fitting Tool.

Most, but not all, of the distributions available in the Distribution Fitting Tool are supported elsewhere in Statistics Toolbox software (see "Supported Distributions" on page 5-3), and have dedicated distribution fitting functions. These functions compute the majority of the fits in the Distribution Fitting Tool, and are referenced in the list below.

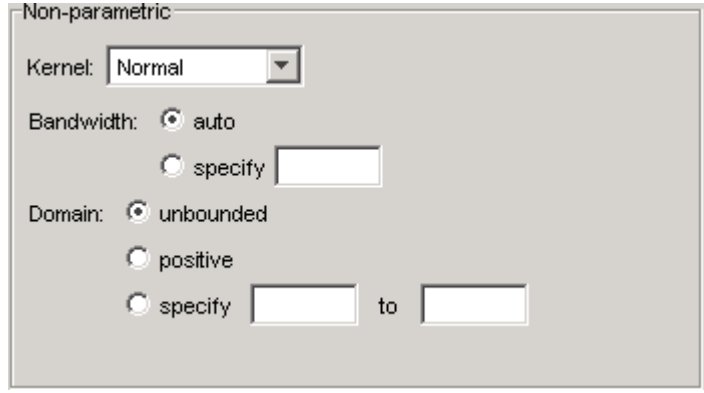
Other fits are computed using functions internal to the Distribution Fitting Tool. Distributions that do not have corresponding Statistics Toolbox fitting functions are described in "Additional Distributions Available in the Distribution Fitting Tool" on page 5-49.

Not all of the distributions listed below are available for all data sets. The Distribution Fitting Tool determines the extent of the data (nonnegative, unit interval, etc.) and displays appropriate distributions in the **Distribution** drop-down list. Distribution data ranges are given parenthetically in the list below.

- Beta (unit interval values) distribution, fit using the function `betafit`.
- Binomial (nonnegative values) distribution, fit using the function `binopdf`.
- Birnbaum-Saunders (positive values) distribution.
- Exponential (nonnegative values) distribution, fit using the function `expfit`.
- Extreme value (all values) distribution, fit using the function `evfit`.
- Gamma (positive values) distribution, fit using the function `gamfit`.
- Generalized extreme value (all values) distribution, fit using the function `gevfit`.
- Generalized Pareto (all values) distribution, fit using the function `gpfit`.
- Inverse Gaussian (positive values) distribution.

- Logistic (all values) distribution.
- Loglogistic (positive values) distribution.
- Lognormal (positive values) distribution, fit using the function `lognfit`.
- Nakagami (positive values) distribution.
- Negative binomial (nonnegative values) distribution, fit using the function `nbinpdf`.
- Nonparametric (all values) distribution, fit using the function `ksdensity`. See "Further Options for Nonparametric Fits" on page 5-23 for a description of available options.
- Normal (all values) distribution, fit using the function `normfit`.
- Poisson (nonnegative integer values) distribution, fit using the function `poisspdf`.
- Rayleigh (positive values) distribution using the function `raylfit`.
- Rician (positive values) distribution.
- *t* location-scale (all values) distribution.
- Weibull (positive values) distribution using the function `wblfit`.

Further Options for Nonparametric Fits. When you select `Non-parametric` in the **Distribution** field, a set of options appears in the **Non-parametric** pane, as shown in the following figure.



The options for nonparametric distributions are:

- **Kernel** — Type of kernel function to use.
  - `Normal`
  - `Box`
  - `Triangle`
  - `Epanechnikov`
- **Bandwidth** — The bandwidth of the kernel smoothing window. Select **auto** for a default value that is optimal for estimating normal densities. This value appears in the **Fit results** pane after you click **Apply**. Select **specify** and enter a smaller value to reveal features such as multiple modes or a larger value to make the fit smoother.
- **Domain** — The allowed x-values for the density.
  - **unbounded** — The density extends over the whole real line.
  - **positive** — The density is restricted to positive values.
  - **specify** — Enter lower and upper bounds for the domain of the density.

  When you select **positive** or **specify**, the nonparametric fit has zero probability outside the specified domain.

Displaying Results

This section explains the different ways to display results in the Distribution Fitting Tool window. This window displays plots of:

- The data sets for which you select **Plot** in the Data dialog box
- The fits for which you select **Plot** in the Fit Manager dialog box
- Confidence bounds for:
  - Data sets for which you select **Bounds** in the Data dialog box
  - Fits for which you select **Bounds** in the Fit Manager dialog box

The following fields are available.

Display Type. The **Display Type** field in the main window specifies the type of plot displayed. Each type corresponds to a probability function, for example, a probability density function. The following display types are available:

- `Density (PDF)` — Display a probability density function (PDF) plot for the fitted distribution. The main window displays data sets using a probability histogram, in which the height of each rectangle is the fraction of data points that lie in the bin divided by the width of the bin. This makes the sum of the areas of the rectangles equal to 1.
- `Cumulative probability (CDF)` — Display a cumulative probability plot of the data. The main window displays data sets using a cumulative probability step function. The height of each step is the cumulative sum of the heights of the rectangles in the probability histogram.
- `Quantile (inverse CDF)` — Display a quantile (inverse CDF) plot.
- `Probability plot` — Display a probability plot of the data. You can specify the type of distribution used to construct the probability plot in the **Distribution** field, which is only available when you select `Probability plot`. The choices for the distribution are:
  - `Exponential`
  - `Extreme value`
  - `Logistic`
  - `Log-Logistic`
  - `Lognormal`
  - `Normal`
  - `Rayleigh`
  - `Weibull`

  In addition to these choices, you can create a probability plot against a parametric fit that you create in the **New Fit** pane. These fits are added at the bottom of the **Distribution** drop-down list when you create them.
- `Survivor function` — Display survivor function plot of the data.
- `Cumulative hazard` — Display cumulative hazard plot of the data.

Note Some distributions are unavailable if the plotted data includes `0` or negative values.

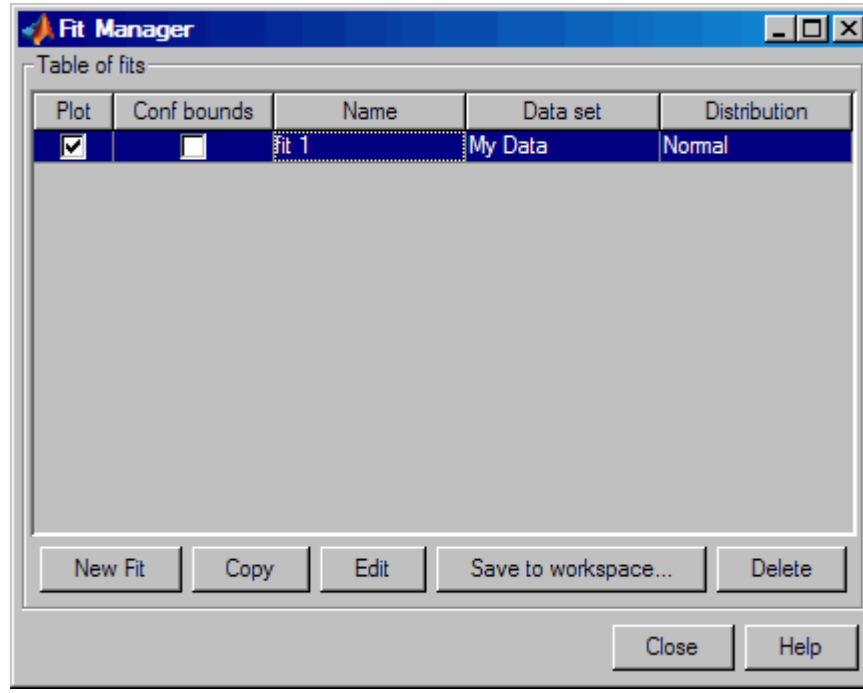
Confidence Bounds. You can display confidence bounds for data sets and fits when you set **Display Type** to `Cumulative probability (CDF)`, `Survivor function`, `Cumulative hazard`, or, for fits only, `Quantile (inverse CDF)`.

- To display bounds for a data set, select **Bounds** next to the data set in the **Data sets** pane of the Data dialog box.
- To display bounds for a fit, select **Bounds** next to the fit in the Fit Manager dialog box. Confidence bounds are not available for all fit types.

To set the confidence level for the bounds, select `Confidence Level` from the **View** menu in the main window and choose from the options.

Managing Fits

This section describes how to manage fits that you have created. To begin, click the **Manage Fits** button in the Distribution Fitting Tool. This opens the Fit Manager dialog box as shown in the following figure.



The **Table of fits** displays a list of the fits you create, with the following options:

- **Plot** — Select **Plot** to display a plot of the fit in the main window of the Distribution Fitting Tool. When you create a new fit, **Plot** is selected by default. Clearing the **Plot** check box removes the fit from the plot in the main window.
- **Bounds** — If **Plot** is selected, you can also select **Bounds** to display confidence bounds in the plot. The bounds are displayed when you set **Display Type** in the main window to one of the following:
  - `Cumulative probability (CDF)`
  - `Quantile (inverse CDF)`
  - `Survivor function`
  - `Cumulative hazard`

The Distribution Fitting Tool cannot display confidence bounds on density (PDF) or probability plots. In addition, bounds are not supported for nonparametric fits and some parametric fits.

Clearing the **Bounds** check box removes the confidence intervals from the plot in the main window.

When you select a fit in the **Table of fits**, the following buttons are enabled below the table:

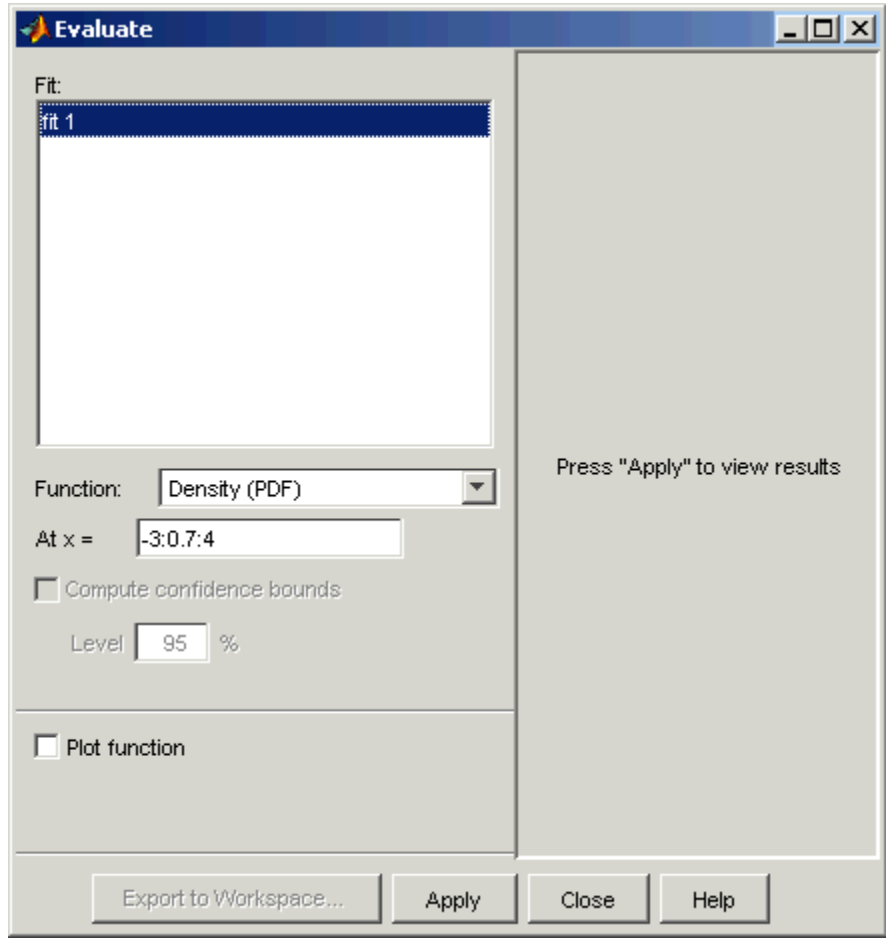
- **New Fit** — Open a New Fit window.
- **Copy** — Create a copy of the selected fit.
- **Edit** — Open an Edit Fit dialog box, where you can edit the fit.

Note You can only edit the currently selected fit in the Edit Fit dialog box. To edit a different fit, select it in the **Table of fits** and click **Edit** to open another Edit Fit dialog box.

- **Save to workspace** — Save the selected fit as a distribution object. See "Using Probability Distribution Objects" on page 5-84 for more information.
- **Delete** — Delete the selected fit.

Evaluating Fits

The Evaluate dialog box enables you to evaluate any fit at whatever points you choose. To open the dialog box, click the **Evaluate** button in the Distribution Fitting Tool. The following figure shows the Evaluate dialog box.



The Evaluate dialog box contains the following items:

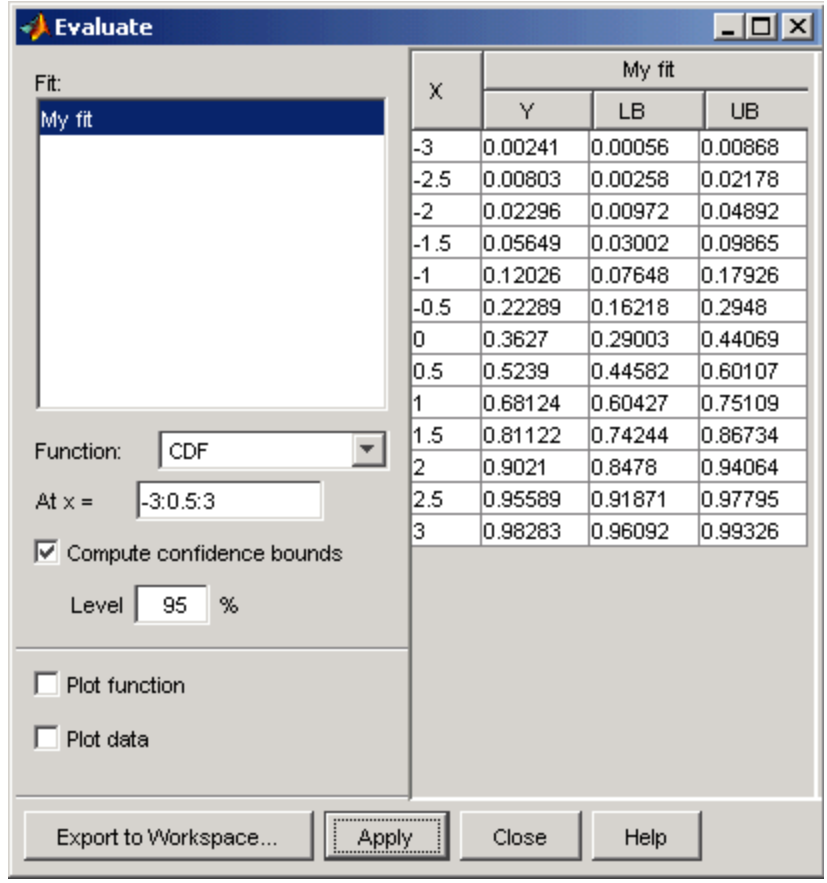
- **Fit** pane — Display the names of existing fits. Select one or more fits that you want to evaluate. Using your platform specific functionality, you can select multiple fits.
- **Function** — Select the type of probability function you want to evaluate for the fit. The available functions are
  - `Density (PDF)` — Computes a probability density function.

  - `Cumulative probability (CDF)` — Computes a cumulative probability function.
  - `Quantile (inverse CDF)` — Computes a quantile (inverse CDF) function.
  - `Survivor function` — Computes a survivor function.
  - `Cumulative hazard` — Computes a cumulative hazard function.
  - `Hazard rate` — Computes the hazard rate.
- **At x =** — Enter a vector of points or the name of a workspace variable containing a vector of points at which you want to evaluate the distribution function. If you change **Function** to `Quantile (inverse CDF)`, the field name changes to **At p =** and you enter a vector of probability values.
- **Compute confidence bounds** — Select this box to compute confidence bounds for the selected fits. The check box is only enabled if you set **Function** to one of the following:
  - `Cumulative probability (CDF)`
  - `Quantile (inverse CDF)`
  - `Survivor function`
  - `Cumulative hazard`

  The Distribution Fitting Tool cannot compute confidence bounds for nonparametric fits and for some parametric fits. In these cases, the tool returns `NaN` for the bounds.
- **Level** — Set the level for the confidence bounds.
- **Plot function** — Select this box to display a plot of the distribution function, evaluated at the points you enter in the **At x =** field, in a new window.

Note The settings for **Compute confidence bounds**, **Level**, and **Plot function** do not affect the plots that are displayed in the main window of the Distribution Fitting Tool. The settings only apply to plots you create by clicking **Plot function** in the Evaluate window.

Click **Apply** to apply these settings to the selected fit. The following figure shows the results of evaluating the cumulative density function for the fit `My fit`, created in "Example: Fitting a Distribution" on page 5-39, at the points in the vector `-3:0.5:3`.



X	My fit		
	Y	LB	UB
-3	0.00241	0.00056	0.00868
-2.5	0.00803	0.00258	0.02178
-2	0.02296	0.00972	0.04892
-1.5	0.05649	0.03002	0.09865
-1	0.12026	0.07648	0.17926
-0.5	0.22289	0.16218	0.2948
0	0.3627	0.29003	0.44069
0.5	0.5239	0.44582	0.60107
1	0.68124	0.60427	0.75109
1.5	0.81122	0.74244	0.86734
2	0.9021	0.8478	0.94064
2.5	0.95589	0.91871	0.97795
3	0.98283	0.96092	0.99326

The window displays the following values in the columns of the table to the right of the **Fit** pane:

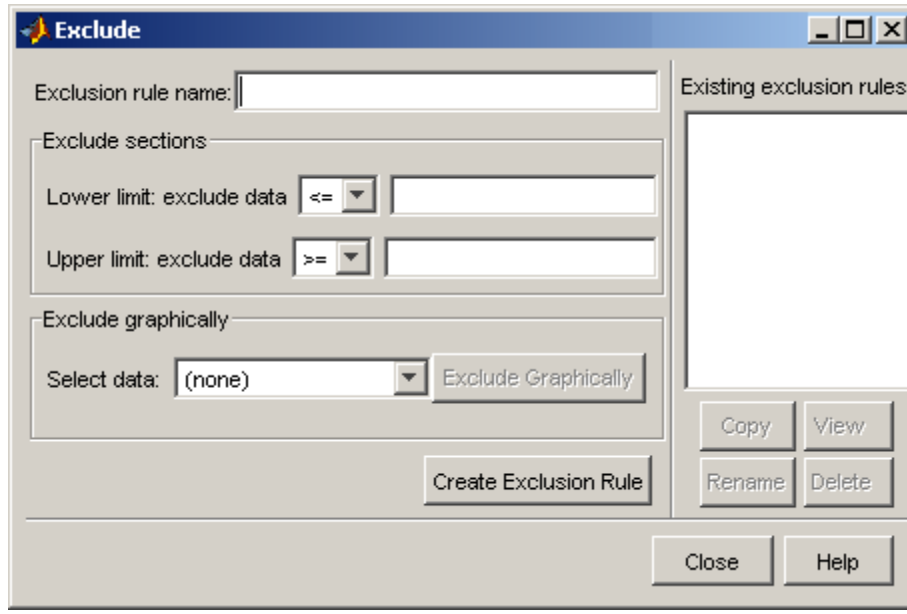
- X — The entries of the vector you enter in **At x =** field
- Y — The corresponding values of the CDF at the entries of X

- LB — The lower bounds for the confidence interval, if you select **Compute confidence bounds**
- UB — The upper bounds for the confidence interval, if you select **Compute confidence bounds**

To save the data displayed in the Evaluate window, click **Export to Workspace**. This saves the values in the table to a matrix in the MATLAB workspace.

Excluding Data

To exclude values from fit, click the **Exclude** button in the main window of the Distribution Fitting Tool. This opens the Exclude window, in which you can create rules for excluding specified values. You can use these rules to exclude data when you create a new fit in the New Fit window. The following figure shows the Exclude window.



To create an exclusion rule:

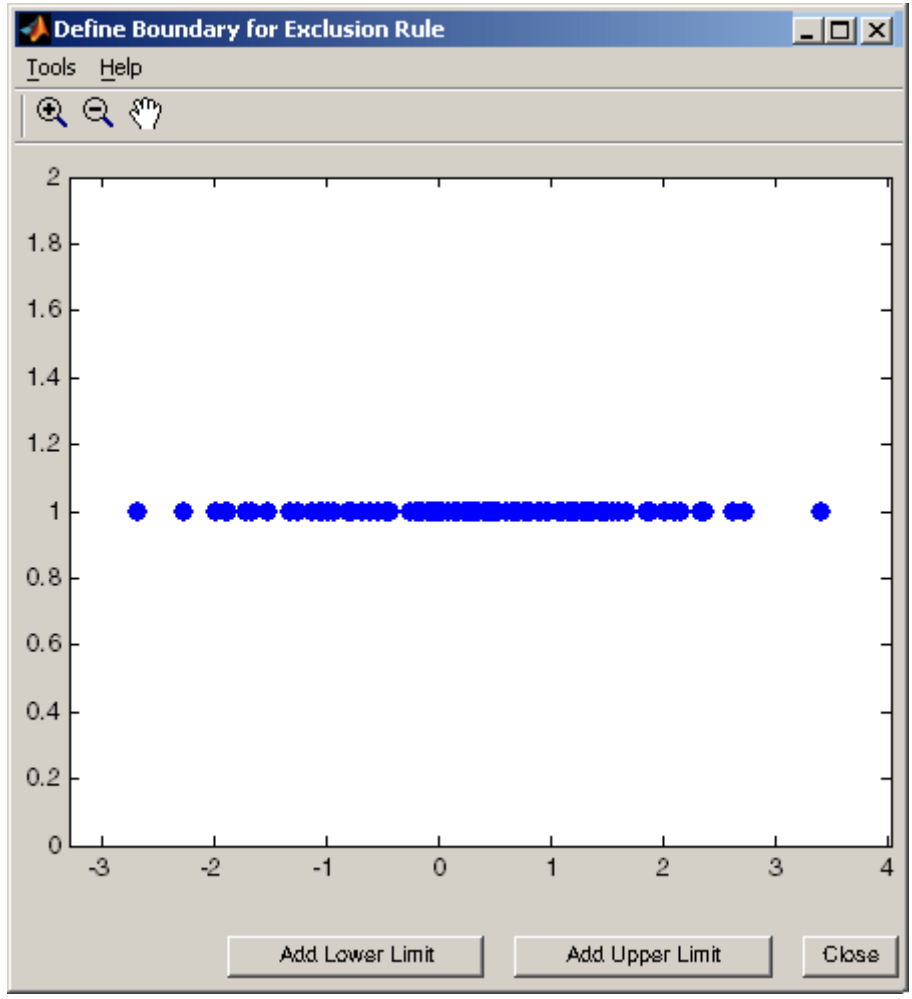
1 **Exclusion Rule Name**—Enter a name for the exclusion rule in the **Exclusion rule name** field.

2 **Exclude Sections**—In the **Exclude sections** pane, you can specify bounds for the excluded data:

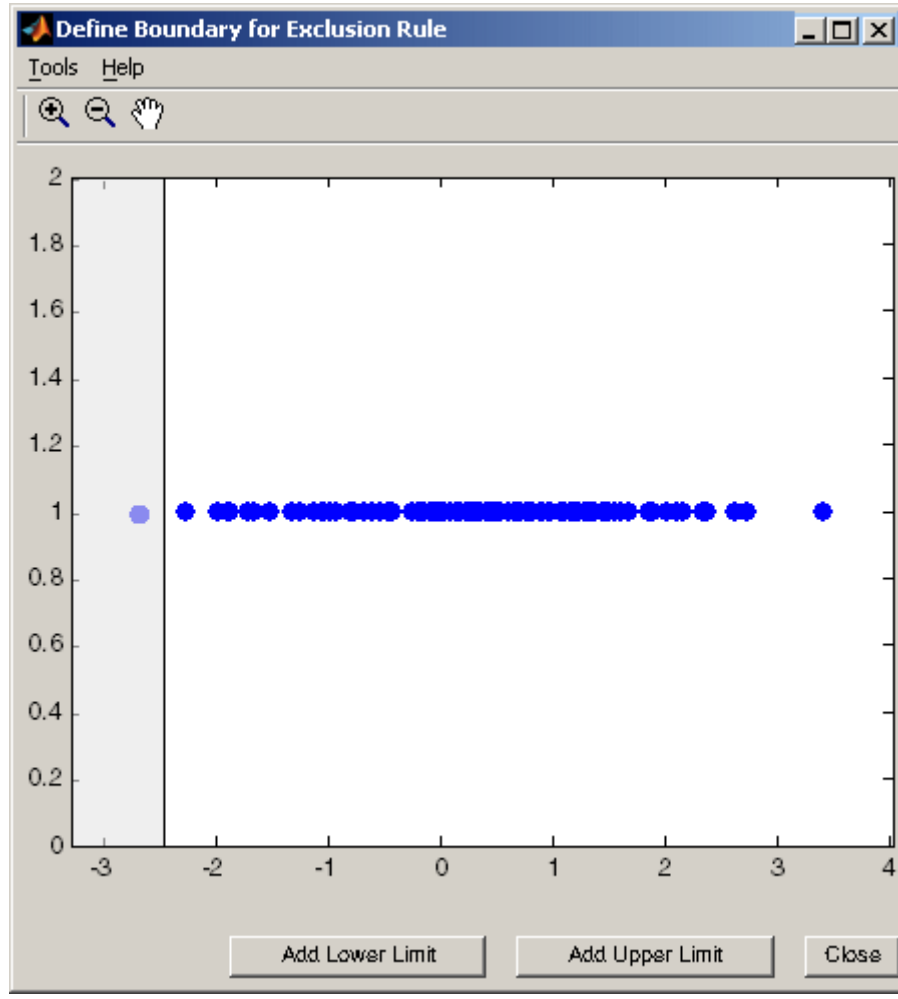
- In the **Lower limit: exclude Y** drop-down list, select <= or < from the drop-down list and enter a scalar in the field to the right. This excludes values that are either less than or equal to or less than that scalar, respectively.
- In the **Upper limit: exclude Y** drop-down list, select >= or > from the drop-down list and enter a scalar in the field to the right to exclude values that are either greater than or equal to or greater than the scalar, respectively.

OR

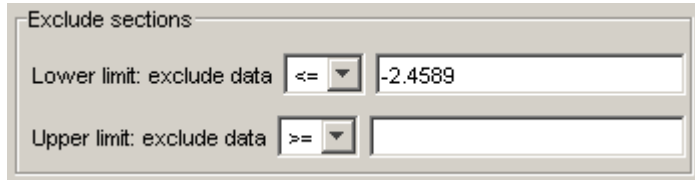
Exclude Graphically—The **Exclude Graphically** button enables you to define the exclusion rule by displaying a plot of the values in a data set and selecting the bounds for the excluded data with the mouse. For example, if you created the data set `My data`, described in "Creating and Managing Data Sets" on page 5-14, select it from the drop-down list next to **Exclude graphically** and then click the **Exclude graphically** button. This displays the values in `My data` in a new window as shown in the following figure.



To set a lower limit for the boundary of the excluded region, click **Add Lower Limit**. This displays a vertical line on the left side of the plot window. Move the line with the mouse to the point you where you want the lower limit, as shown in the following figure.



Moving the vertical line changes the value displayed in the **Lower limit: exclude data** field in the Exclude window, as shown in the following figure.



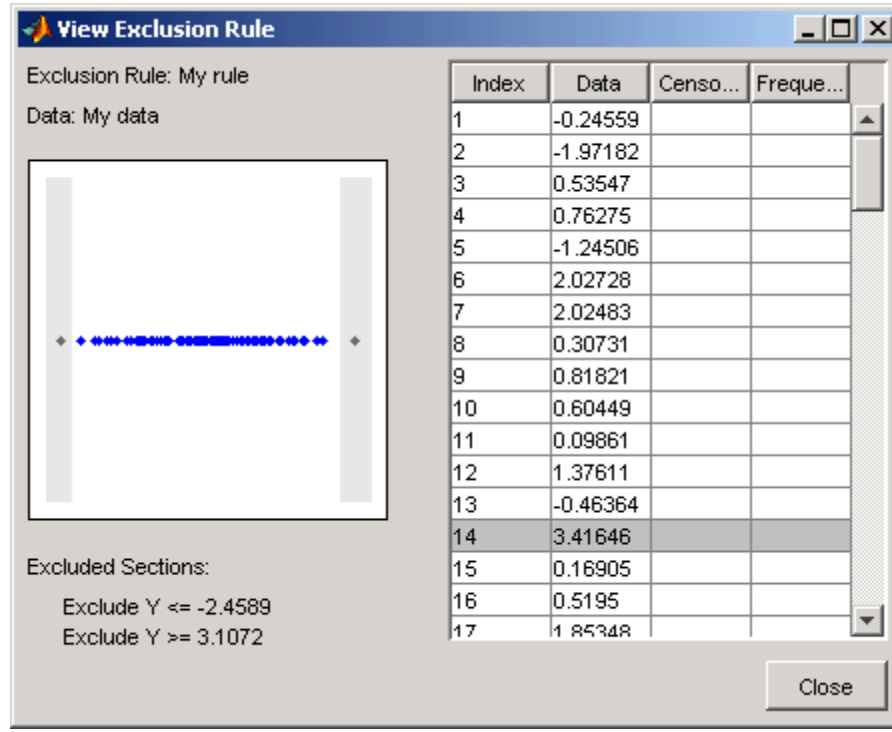
The value displayed corresponds to the *x*-coordinate of the vertical line.

Similarly, you can set the upper limit for the boundary of the excluded region by clicking **Add Upper Limit** and moving the vertical line that appears at the right side of the plot window. After setting the lower and upper limits, click **Close** and return to the Exclude window.

3 **Create Exclusion Rule**—Once you have set the lower and upper limits for the boundary of the excluded data, click **Create Exclusion Rule** to create the new rule. The name of the new rule now appears in the **Existing exclusion rules** pane.

When you select an exclusion rule in the **Existing exclusion rules** pane, the following buttons are enabled:

- **Copy** — Creates a copy of the rule, which you can then modify. To save the modified rule under a different name, click **Create Exclusion Rule**.
- **View** — Opens a new window in which you can see which data points are excluded by the rule. The following figure shows a typical example.



The shaded areas in the plot graphically display which data points are excluded. The table to the right lists all data points. The shaded rows indicate excluded points:

- **Rename** — Renames the rule
- **Delete** — Deletes the rule

Once you define an exclusion rule, you can use it when you fit a distribution to your data. The rule does not exclude points from the display of the data set.

Saving and Loading Sessions

This section explains how to save your work in the current Distribution Fitting Tool session and then load it in a subsequent session, so that you can continue working where you left off.

Saving a Session. To save the current session, select `Save Session` from the **File** menu in the main window. This opens a dialog box that prompts you to enter a filename, such as `my_session.dfit`, for the session. Clicking **Save** saves the following items created in the current session:

- Data sets
- Fits
- Exclusion rules
- Plot settings
- Bin width rules

Loading a Session. To load a previously saved session, select `Load Session` from the **File** menu in the main window and enter the name of a previously saved session. Clicking **Open** restores the information from the saved session to the current session of the Distribution Fitting Tool.

Example: Fitting a Distribution

This section presents an example that illustrates how to use the Distribution Fitting Tool. The example involves the following steps:

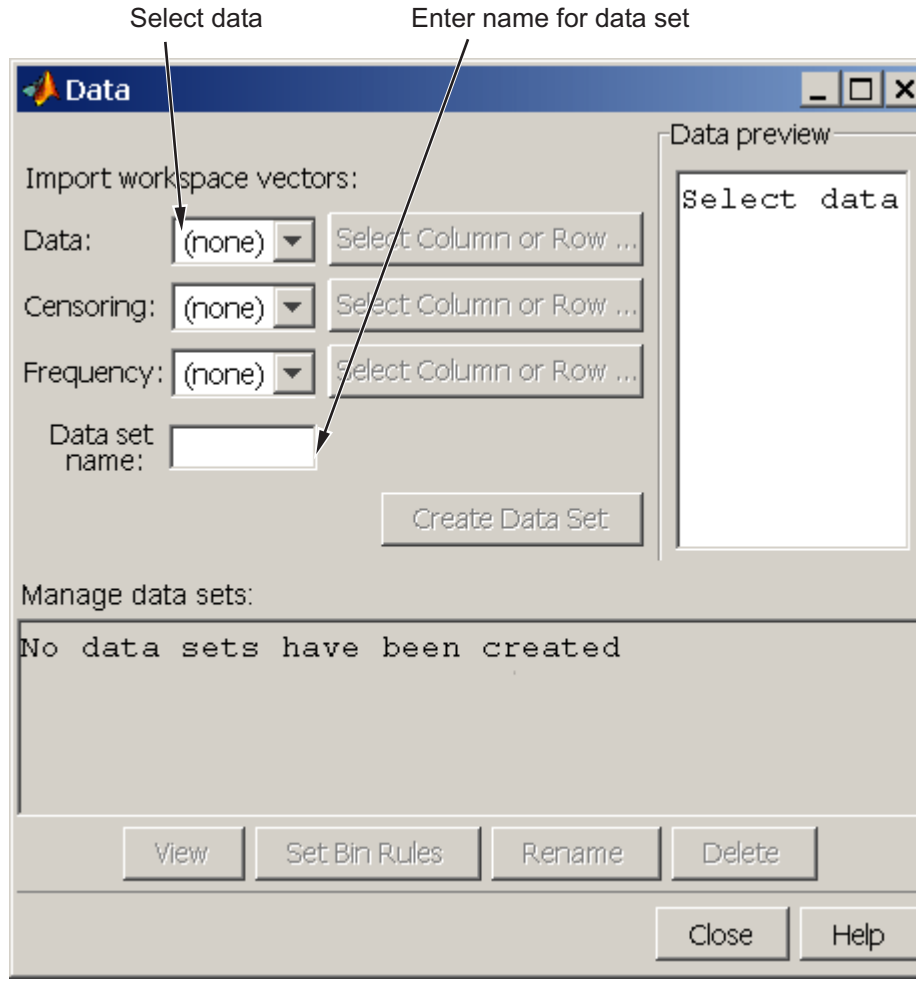
Step 1: Generate Random Data. To try the example, first generate some random data to which you will fit a distribution. The following command generates a vector `data`, of length `100`, whose entries are random numbers from a normal distribution with mean `.36` and standard deviation `1.4`.

```
data = normrnd(.36, 1.4, 100, 1);
```

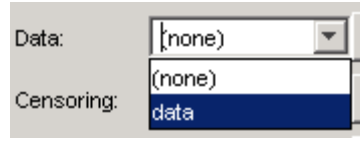
Step 2: Import Data. Open the distribution fitting tool:

```
dfittool
```

To import the vector `data` into the Distribution Fitting Tool, click the **Data** button in main window. This opens the window shown in the following figure.

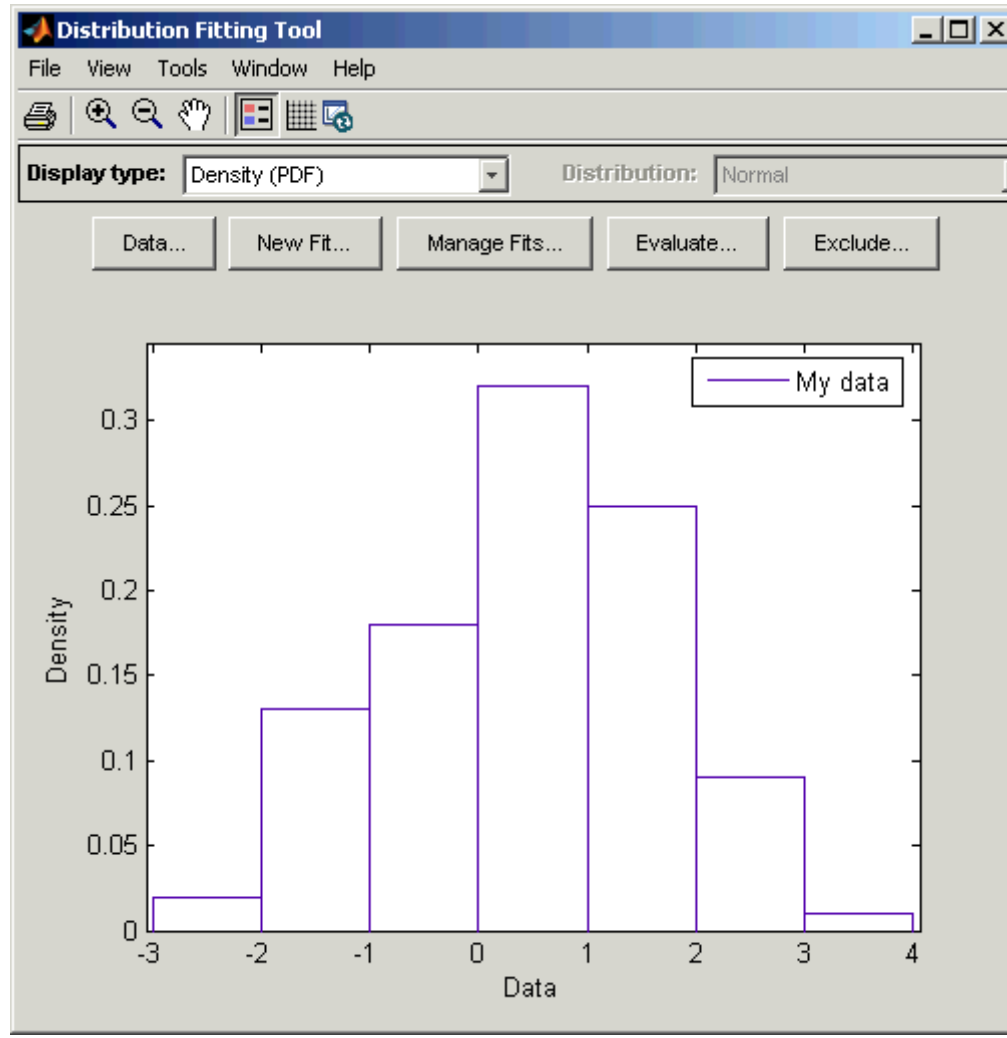


The **Data** field displays all numeric arrays in the MATLAB workspace. Select `data` from the drop-down list, as shown in the following figure.



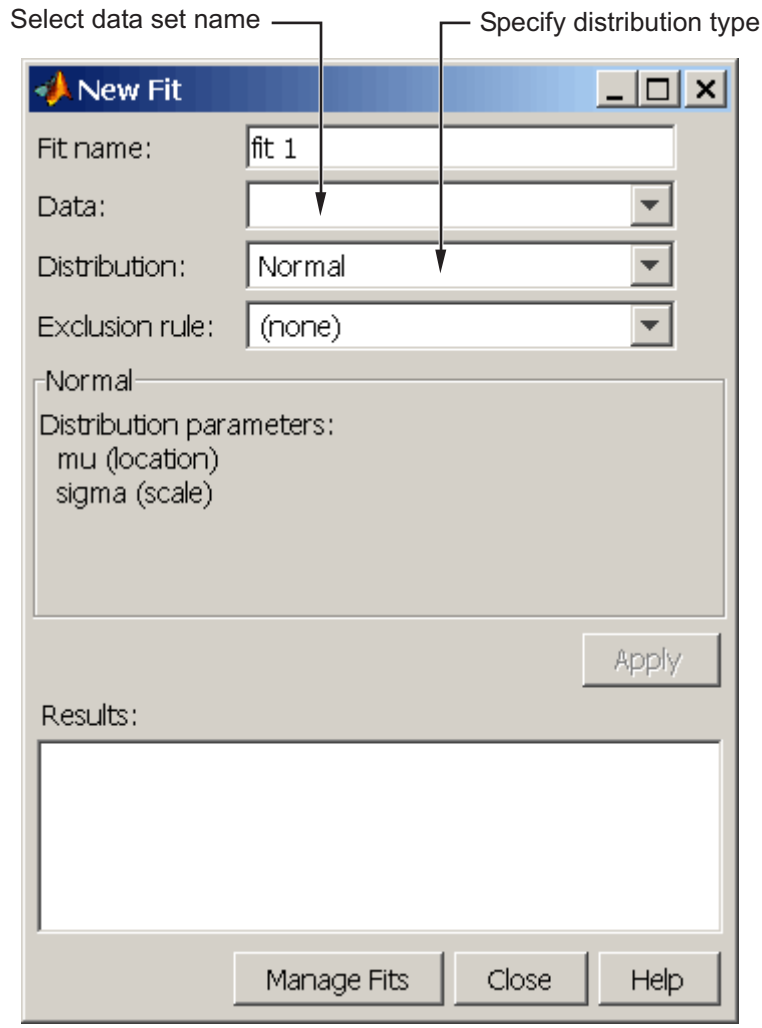
This displays a histogram of the data in the **Data preview** pane.

In the **Data set name** field, type a name for the data set, such as `My data`, and click **Create Data Set** to create the data set. The main window of the Distribution Fitting Tool now displays a larger version of the histogram in the **Data preview** pane, as shown in the following figure.



Note Because the example uses random data, you might see a slightly different histogram if you try this example for yourself.

Step 3: Create a New Fit. To fit a distribution to the data, click **New Fit** in the main window of the Distribution Fitting Tool. This opens the window shown in the following figure.

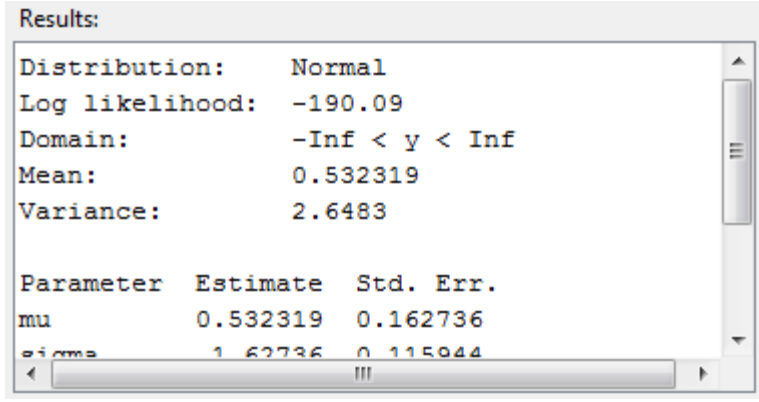


To fit a normal distribution, the default entry of the **Distribution** field, to `My data`:

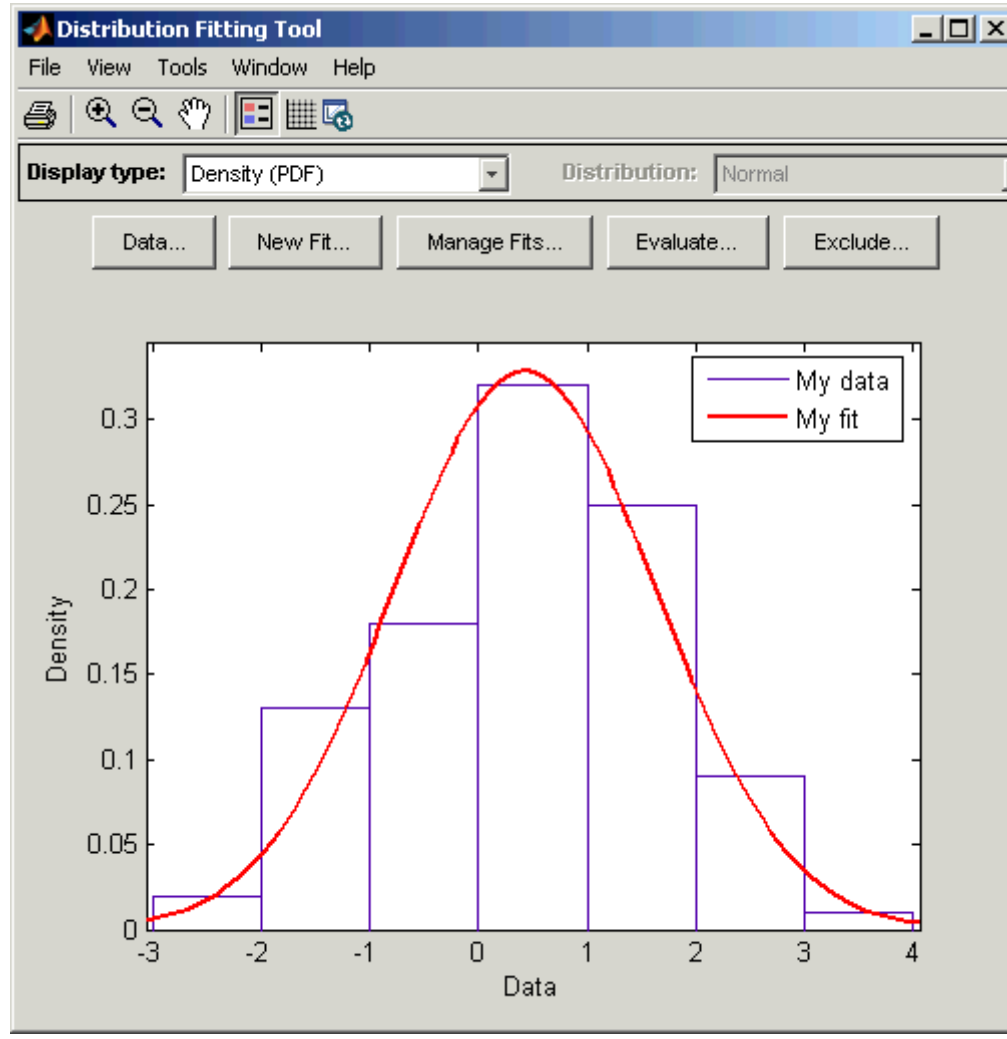
1. Enter a name for the fit, such as `My fit`, in the **Fit name** field.
2. Select `My data` from the drop-down list in the **Data** field.

3 Click **Apply**.

The **Results** pane displays the mean and standard deviation of the normal distribution that best fits `My data`, as shown in the following figure.



The main window of the Distribution Fitting Tool displays a plot of the normal distribution with this mean and standard deviation, as shown in the following figure.


Distribution Fitting Tool
File View Tools Window Help
Display type: Density (PDF)
Distribution: Normal
Data... New Fit... Manage Fits... Evaluate... Exclude...
My data
My fit
Density
0.3
0.25
0.2
0.15
0.1
0.05
0
-3 -2 -1 0 1 2 3 4
Data

Generating a File to Fit and Plot Distributions

The `Generate Code` option in the **File** menu enables you to create a file that

- Fits the distributions used in the current session to any data vector in the MATLAB workspace.
- Plots the data and the fits.

After you end the current session, you can use the file to create plots in a standard MATLAB figure window, without having to reopen the Distribution Fitting Tool.

As an example, assuming you created the fit described in "Creating a New Fit" on page 5-19, do the following steps:

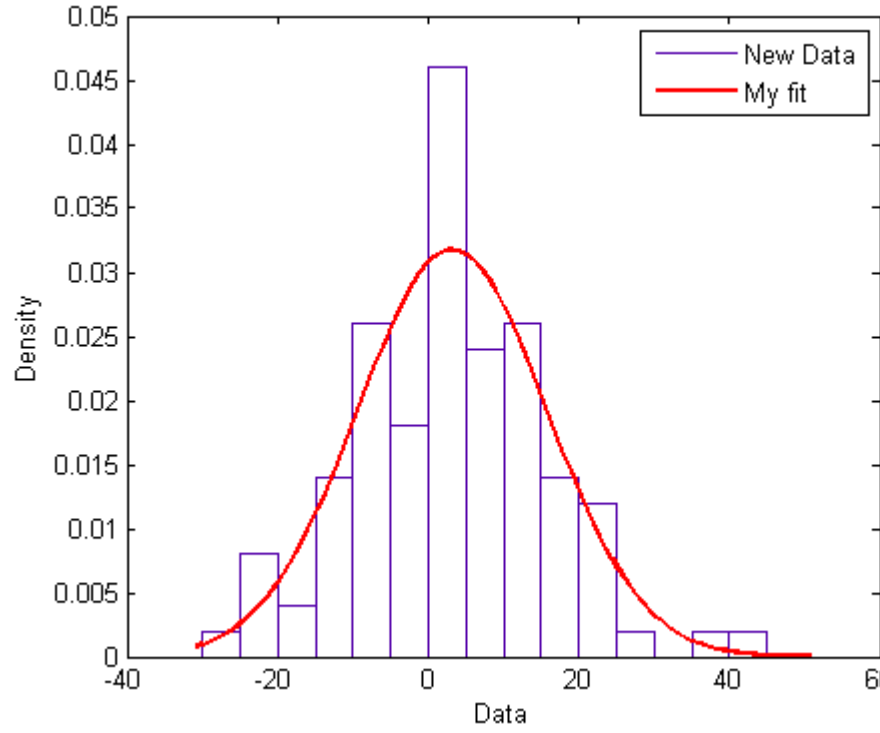
1. Select `Generate Code` from the **File** menu.
2. Choose **File > Save as** in the MATLAB Editor window. Save the file as `normal_fit.m` in a folder on the MATLAB path.

You can then apply the function `normal_fit` to any vector of data in the MATLAB workspace. For example, the following commands

```
new_data = normrnd(4.1, 12.5, 100, 1);
newfit = normal_fit(new_data)
legend('New Data', 'My fit')
```

generate `newfit`, a fitted normal distribution of the data, and generates a plot of the data and the fit.

```
newfit =

normal distribution

    mu = 3.19148
    sigma = 12.5631
```



Note By default, the file labels the data in the legend using the same name as the data set in the Distribution Fitting Tool. You can change the label using the `legend` command, as illustrated by the preceding example.

Using Custom Distributions

This section explains how to use custom distributions with the Distribution Fitting Tool.

Defining Custom Distributions. To define a custom distribution, select `Define Custom Distribution` from the **File** menu. This opens a file template in the MATLAB editor. You then edit this file so that it computes the distribution you want.

The template includes example code that computes the Laplace distribution, beginning at the lines

```
%                               -
%    Remove the following return statement to define the
%    Laplace distributon
%                               -
return
```

To use this example, simply delete the command `return` and save the file. If you save the template in a folder on the MATLAB path, under its default name `dfittooldists.m`, the Distribution Fitting Tool reads it in automatically when you start the tool. You can also save the template under a different name, such as `laplace.m`, and then import the custom distribution as described in the following section.

Importing Custom Distributions. To import a custom distribution, select `Import Custom Distributions` from the **File** menu. This opens a dialog box in which you can select the file that defines the distribution. For example, if you created the file `laplace.m`, as described in the preceding section, you can enter `laplace.m` and select **Open** in the dialog box. The **Distribution** field of the New Fit window now contains the option `Laplace`.

Additional Distributions Available in the Distribution Fitting Tool

The following distributions are available in the Distribution Fitting Tool, but do not have dedicated distribution functions as described in "Statistics Toolbox Distribution Functions" on page 5-52. The distributions can be used with the functions `pdf`, `cdf`, `icdf`, and `mle` in a limited capacity. See the reference pages for these functions for details on the limitations.

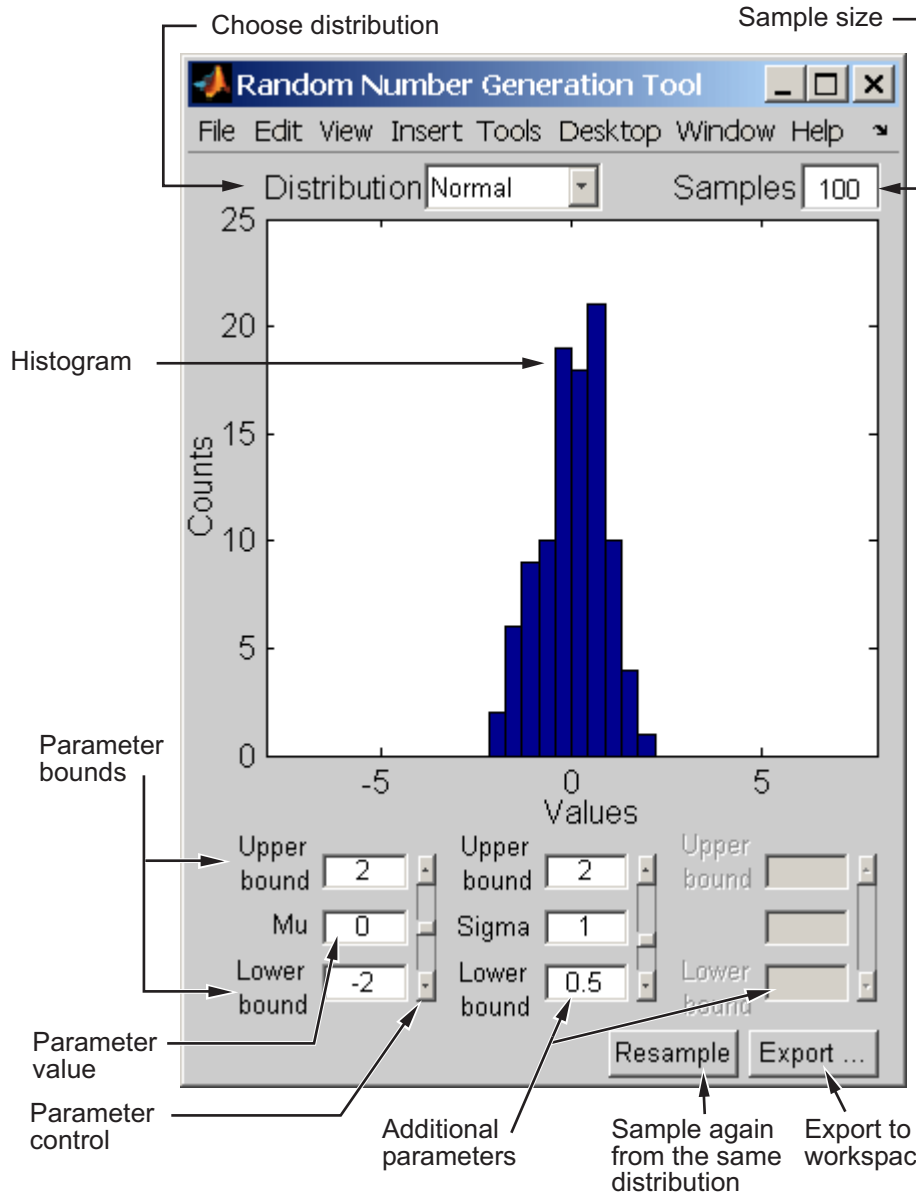
- "Birnbaum-Saunders Distribution" on page B-10
- "Inverse Gaussian Distribution" on page B-45
- "Loglogistic Distribution" on page B-50
- "Logistic Distribution" on page B-49
- "Nakagami Distribution" on page B-70
- "Rician Distribution" on page B-93
- "t Location-Scale Distribution" on page B-97

For a complete list of the distributions available for use with the Distribution Fitting Tool, see "Supported Distributions" on page 5-3. Distributions listing `dfittool` in the **fit** column of the tables in that section can be used with the Distribution Fitting Tool.

Visually Exploring Random Number Generation

The Random Number Generation Tool is a graphical user interface that generates random samples from specified probability distributions and displays the samples as histograms. Use the tool to explore the effects of changing parameters and sample size on the distributions.

Run the tool by typing `randtool` at the command line.



Start by selecting a distribution, then enter the desired sample size.

You can also

- Use the controls at the bottom of the window to set parameter values for the distribution and to change their upper and lower bounds.
- Draw another sample from the same distribution, with the same size and parameters.
- Export the current sample to your workspace. A dialog box enables you to provide a name for the sample.

Statistics Toolbox Distribution Functions

In this section...

For each distribution supported by Statistics Toolbox software, a selection of the distribution functions described in this section is available for statistical programming. This section gives a general overview of the use of each type of function, independent of the particular distribution. For specific functions available for specific distributions, see "Supported Distributions" on page 5-3.

Probability Density Functions

Estimating PDFs with Parameters

Probability density functions (pdfs) for supported Statistics Toolbox distributions all end with `pdf`, as in `binopdf` or `exppdf`. For more information on specific function names for specific distributions see "Supported Distributions" on page 5-3.

Each function represents a parametric family of distributions. Input arguments are arrays of outcomes followed by a list of parameter values specifying a particular member of the distribution family.

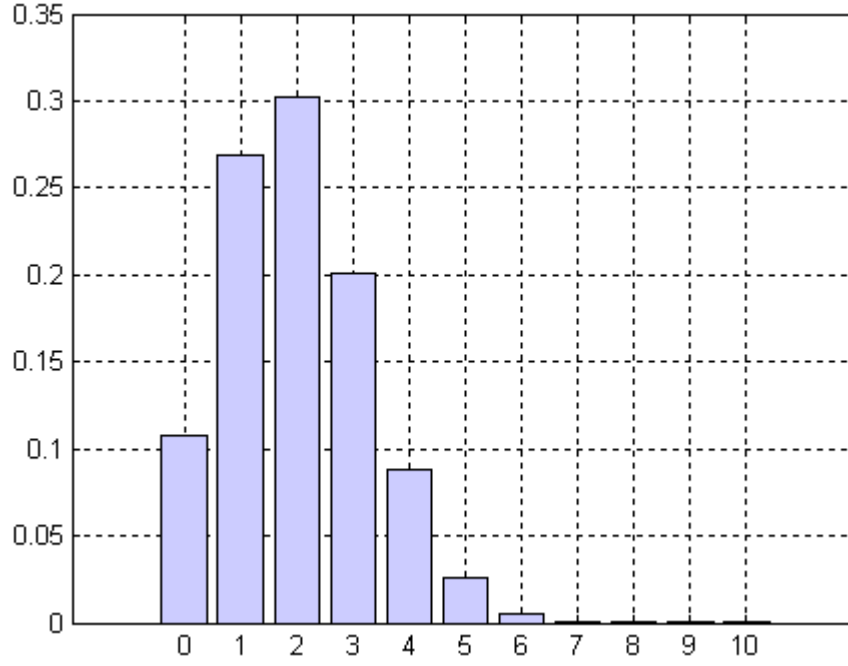
For discrete distributions, the pdf assigns a probability to each outcome. In this context, the pdf is often called a *probability mass function* (*pmf*).

For example, the discrete binomial pdf

$$f(k) = \binom{n}{k} p^k (1-p)^{n-k}$$

assigns probability to the event of k successes in n trials of a Bernoulli process (such as coin flipping) with probability p of success at each trial. Each of the integers $k = 0, 1, 2, \ldots, n$ is assigned a positive probability, with the sum of the probabilities equal to 1. Compute the probabilities with the `binopdf` function:

```
p = 0.2; % Probability of success for each trial
n = 10; % Number of trials
k = 0:n; % Outcomes
m = binopdf(k,n,p); % Probability mass vector
bar(k,m) % Visualize the probability distribution
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
grid on
```



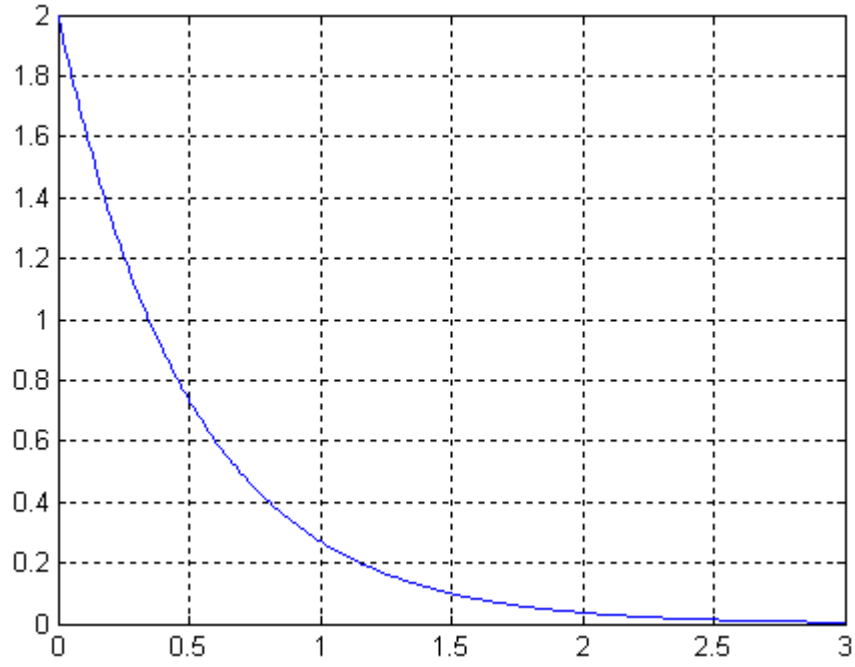
For continuous distributions, the pdf assigns a probability *density* to each outcome. The probability of any single outcome is zero. The pdf must be integrated over a set of outcomes to compute the probability that an outcome falls within that set. The integral over the entire set of outcomes is 1.

For example, the continuous exponential pdf

$$f(t) = \lambda e^{-\lambda t}$$

is used to model the probability that a process with constant failure rate λ will have a failure within time t . Each time $t > 0$ is assigned a positive probability density. Densities are computed with the `exppdf` function:

```
lambda = 2; % Failure rate
t = 0:0.01:3; % Outcomes
f = exppdf(t,1/lambda); % Probability density vector
plot(t,f) % Visualize the probability distribution
grid on
```



Probabilities for continuous pdfs can be computed with the quad function. In the example above, the probability of failure in the time interval [0,1] is computed as follows:

```
f_lambda = @(t)exppdf(t,1/lambda); % Pdf with fixed lambda
P = quad(f_lambda,0,1) % Integrate from 0 to 1
P =
    0.8647
```

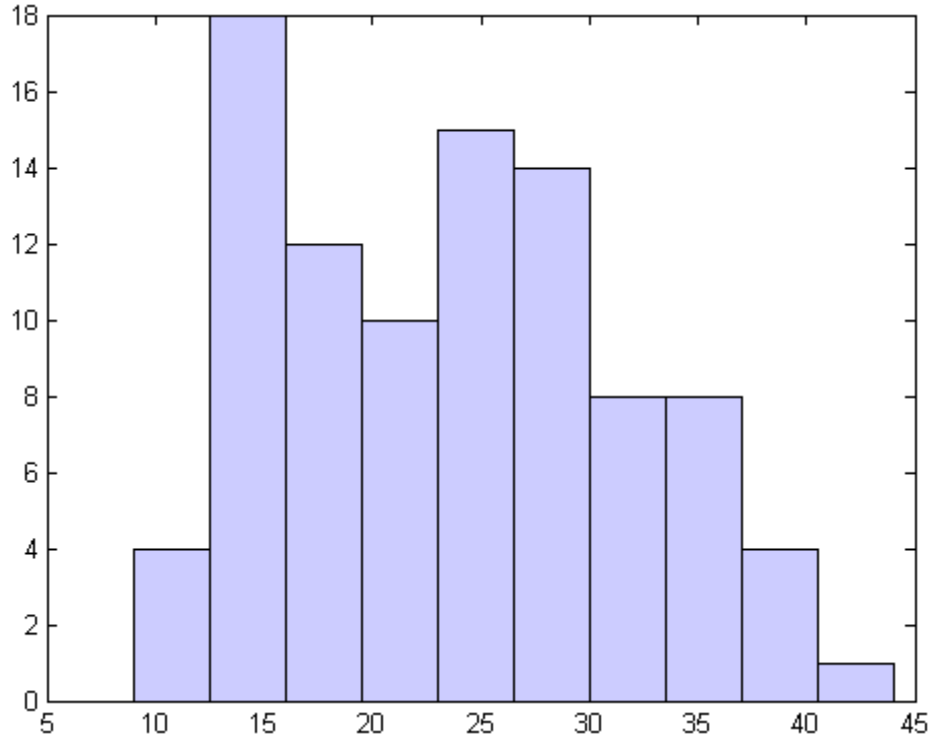
Alternatively, the cumulative distribution function (cdf) for the exponential function, expcdf, can be used:

```
P = expcdf(1,1/lambda) % Cumulative probability from 0 to 1
P =
    0.8647
```

Estimating PDFs without Parameters

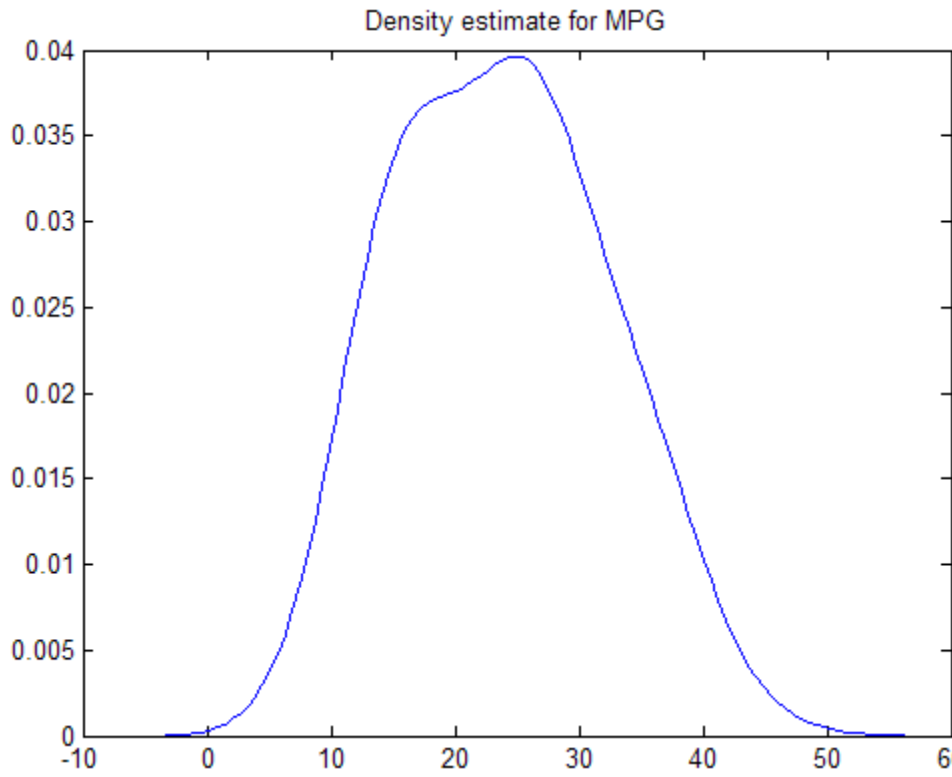
A distribution of data can be described graphically with a histogram:

```
cars = load('carsmall','MPG','Origin');
MPG = cars.MPG;
hist(MPG)
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
```



You can also describe a data distribution by estimating its density. The `ksdensity` function does this using a kernel smoothing method. A nonparametric density estimate of the previous data, using the default kernel and bandwidth, is given by:

```
[f,x] = ksdensity(MPG);
plot(x,f);
title('Density estimate for MPG')
```

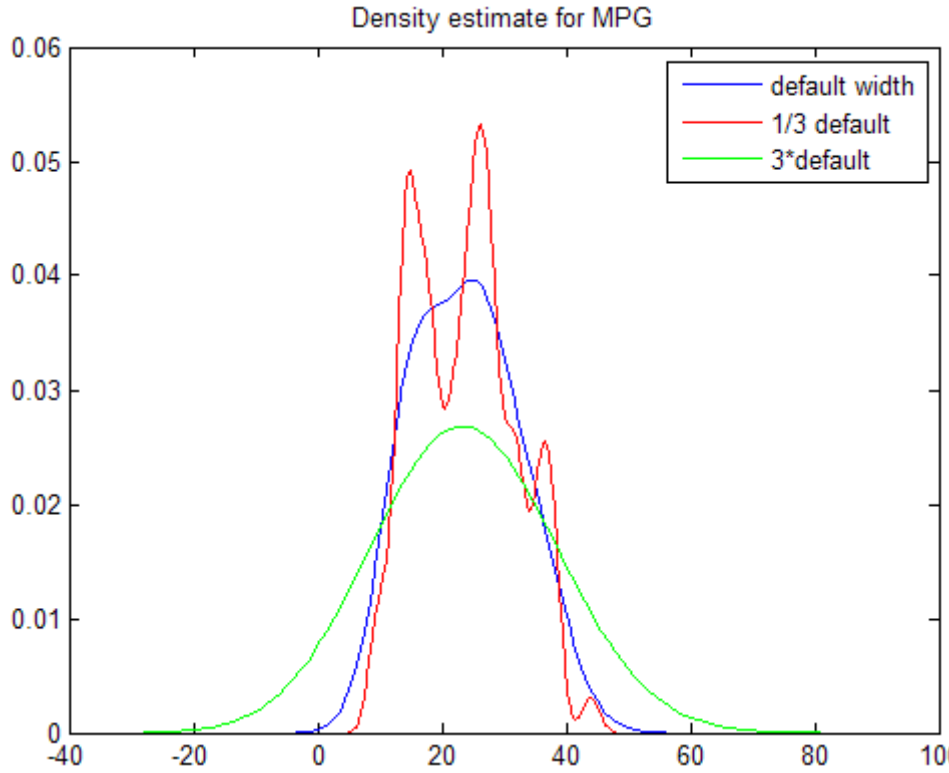


Controlling Probability Density Curve Smoothness. The choice of kernel bandwidth controls the smoothness of the probability density curve. The following graph shows the density estimate for the same mileage data using different bandwidths. The default bandwidth is in blue and looks like the preceding graph. Estimates for smaller and larger bandwidths are in red and green.

The first call to `ksdensity` returns the default bandwidth, `u`, of the kernel smoothing function. Subsequent calls modify this bandwidth.

```
[f,x,u] = ksdensity(MPG);
plot(x,f)
title('Density estimate for MPG')
hold on
```

```
[f,x] = ksdensity(MPG,'width',u/3);
plot(x,f,'r');

[f,x] = ksdensity(MPG,'width',u*3);
plot(x,f,'g');

legend('default width','1/3 default','3*default')
hold off
```



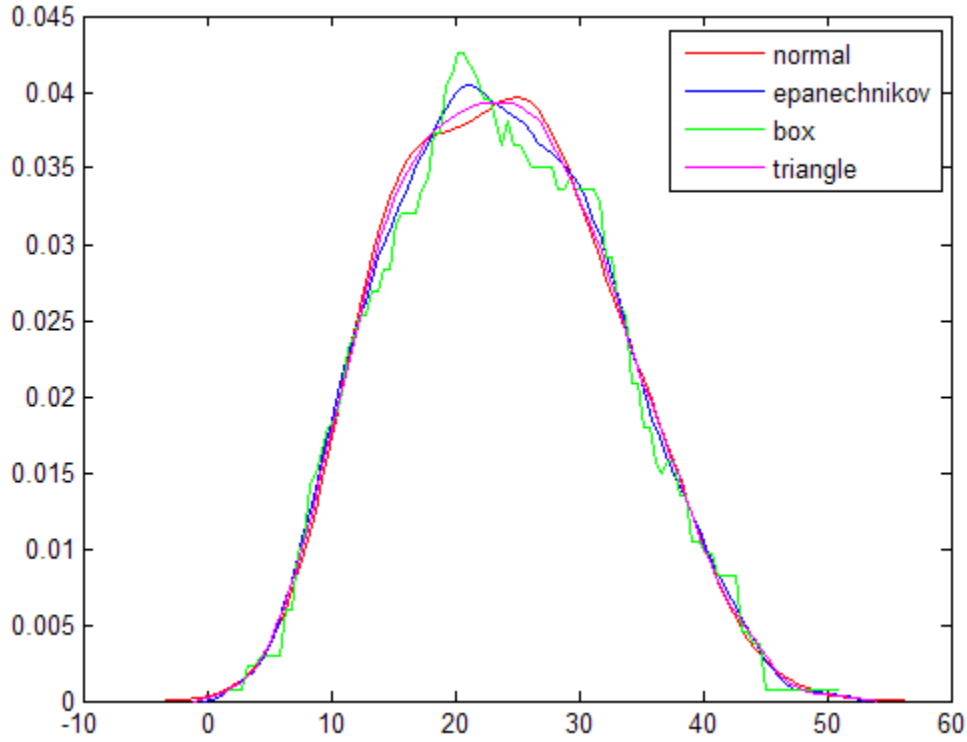
The default bandwidth seems to be doing a good job—reasonably smooth, but not so smooth as to obscure features of the data. This bandwidth is the one that is theoretically optimal for estimating densities for the normal distribution.

The green curve shows a density with the kernel bandwidth set too high. This curve smooths out the data so much that the end result looks just like the kernel function. The red curve has a smaller bandwidth and is rougher looking than the blue curve. It may be too rough, but it does provide an indication that there might be two major peaks rather than the single peak of the blue curve. A reasonable choice of width might lead to a curve that is intermediate between the red and blue curves.

Specifying Kernel Smoothing Functions. You can also specify a kernel function by supplying either the function name or a function handle. The four preselected functions, `'normal'`, `'epanechnikov'`, `'box'`, and `'triangle'`, are all scaled to have standard deviation equal to 1, so they perform a comparable degree of smoothing.

Using default bandwidths, you can now plot the same mileage data, using each of the available kernel functions.

```
hname = {'normal' 'epanechnikov' 'box' 'triangle'};
colors = {'r' 'b' 'g' 'm'};
for j=1:4
    [f,x] = ksdensity(MPG,'kernel',hname{j});
    plot(x,f,colors{j});
    hold on;
end
legend(hname{:});
hold off
```

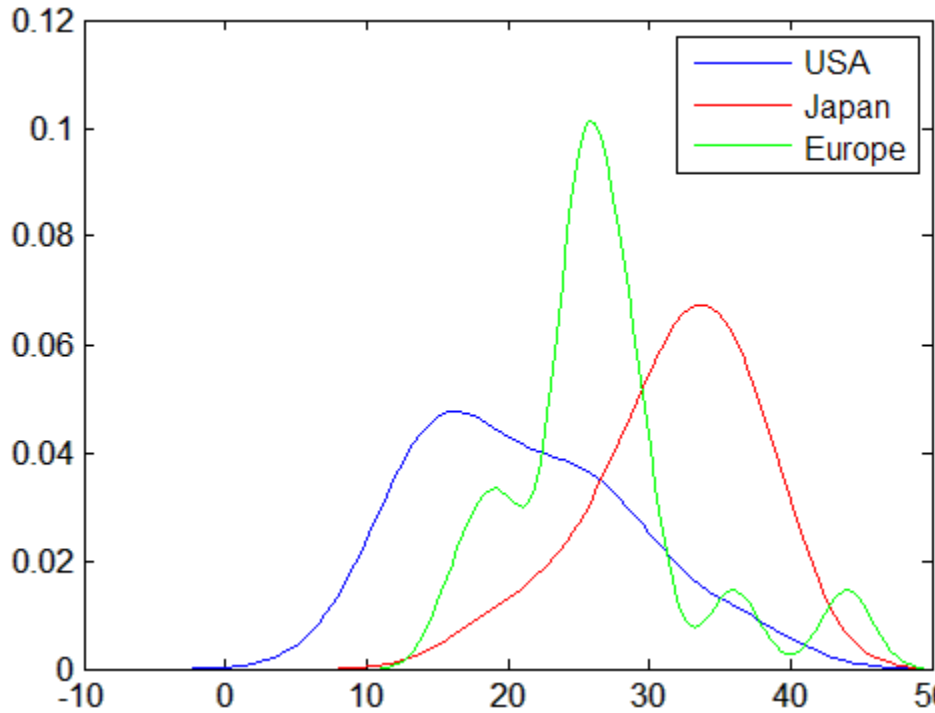


The density estimates are roughly comparable, but the box kernel produces a density that is rougher than the others.

Comparing Density Estimates. While it is difficult to overlay two histograms to compare them, you can easily overlay smooth density estimates. For example, the following graph shows the MPG distributions for cars from different countries of origin:

```
Origin = cellstr(cars.Origin);

I = strcmp('USA',Origin);
J = strcmp('Japan',Origin);
K = ~(I|J);
MPG_USA = MPG(I);
MPG_Japan = MPG(J);
MPG_Europe = MPG(K);
```

```
[fI,xI] = ksdensity(MPG_USA);
plot(xI,fI,'b')
hold on

[fJ,xJ] = ksdensity(MPG_Japan);
plot(xJ,fJ,'r')

[fK,xK] = ksdensity(MPG_Europe);
plot(xK,fK,'g')

legend('USA','Japan','Europe')
hold off
```



For piecewise probability density estimation, using kernel smoothing in the center of the distribution and Pareto distributions in the tails, see “Fitting Piecewise Distributions” on page 5-72.

Cumulative Distribution Functions

Estimating Parametric CDFs

Cumulative distribution functions (cdfs) for supported Statistics Toolbox distributions all end with `cdf`, as in `binocdf` or `expcdf`. Specific function names for specific distributions can be found in "Supported Distributions" on page 5-3.

Each function represents a parametric family of distributions. Input arguments are arrays of outcomes followed by a list of parameter values specifying a particular member of the distribution family.

For discrete distributions, the cdf F is related to the pdf f by

$$F(x) = \sum_{y \le x} f(y)$$

For continuous distributions, the cdf F is related to the pdf f by

$$F(x) = \int_{-\infty}^{x} f(y)dy$$

Cdfs are used to compute probabilities of events. In particular, if F is a cdf and x and y are outcomes, then

- $P(y \le x) = F(x)$
- $P(y > x) = 1 - F(x)$
- $P(x_1 < y \le x_2) = F(x_2) - F(x_1)$

For example, the t-statistic

$$t = \frac{\bar{x} - \mu}{s/\sqrt{n}}$$

follows a Student's t distribution with $n - 1$ degrees of freedom when computed from repeated random samples from a normal population with mean μ. Here $\bar{x}$ is the sample mean, s is the sample standard deviation, and n is the sample size. The probability of observing a t-statistic greater than or equal to the value computed from a sample can be found with the `tcdf` function:

```
mu = 1; % Population mean
sigma = 2; % Population standard deviation
n = 100; % Sample size
x = normrnd(mu,sigma,n,1); % Random sample from population
xbar = mean(x); % Sample mean
s = std(x); % Sample standard deviation
t = (xbar-mu)/(s/sqrt(n)) % t-statistic
t =
    0.2489
p = 1-tcdf(t,n-1) % Probability of larger t-statistic
p =
    0.4020
```

This probability is the same as the p value returned by a t-test of the null hypothesis that the sample comes from a normal population with mean μ:

```
[h,ptest] = ttest(x,mu,0.05,'right')
h =
     0
ptest =
    0.4020
```

Estimating Empirical CDFs

The `ksdensity` function produces an empirical version of a probability density function (pdf). That is, instead of selecting a density with a particular parametric form and estimating the parameters, it produces a nonparametric density estimate that adapts itself to the data.

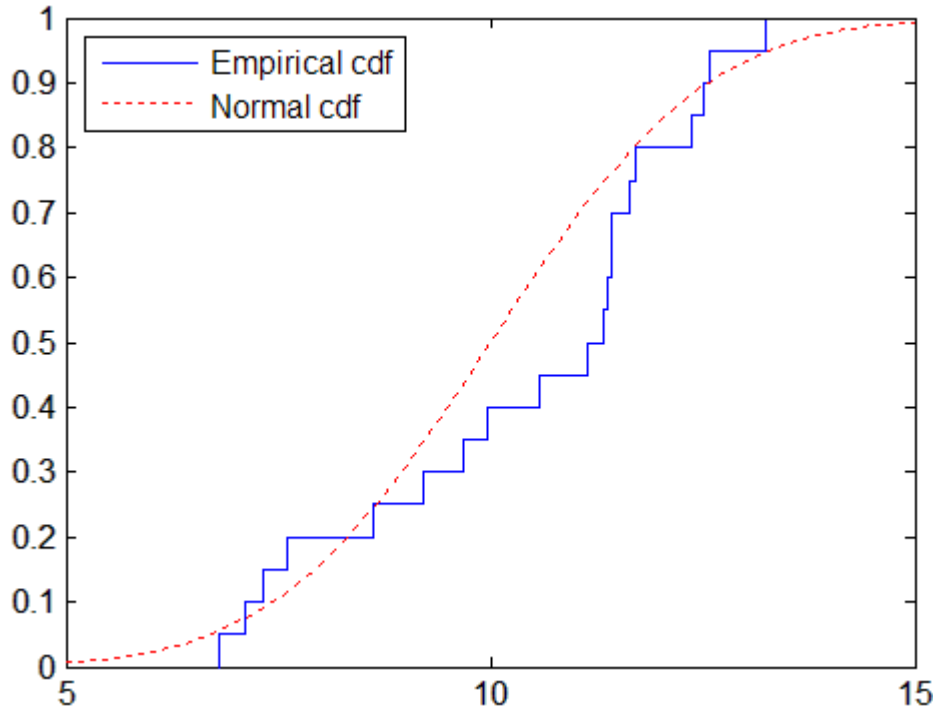
Similarly, it is possible to produce an empirical version of the cumulative distribution function (cdf). The `ecdf` function computes this empirical cdf. It

returns the values of a function F such that $F(x)$ represents the proportion of observations in a sample less than or equal to x.

The idea behind the empirical cdf is simple. It is a function that assigns probability $1/n$ to each of n observations in a sample. Its graph has a stair-step appearance. If a sample comes from a distribution in a parametric family (such as a normal distribution), its empirical cdf is likely to resemble the parametric distribution. If not, its empirical distribution still gives an estimate of the cdf for the distribution that generated the data.

The following example generates 20 observations from a normal distribution with mean 10 and standard deviation 2. You can use `ecdf` to calculate the empirical cdf and `stairs` to plot it. Then you overlay the normal distribution curve on the empirical function.

```
x = normrnd(10,2,20,1);
[f,xf] = ecdf(x);

stairs(xf,f)
hold on
xx=linspace(5,15,100);
yy = normcdf(xx,10,2);
plot(xx,yy,'r:')
hold off
legend('Empirical cdf','Normal cdf',2)
```



The empirical cdf is especially useful in survival analysis applications. In such applications the data may be censored, that is, not observed exactly. Some individuals may fail during a study, and you can observe their failure time exactly. Other individuals may drop out of the study, or may not fail until after the study is complete. The `ecdf` function has arguments for dealing with censored data. In addition, you can use the `coxphfit` function with individuals that have predictors that are not the same.

For piecewise probability density estimation, using the empirical cdf in the center of the distribution and Pareto distributions in the tails, see “Fitting Piecewise Distributions” on page 5-72.

Inverse Cumulative Distribution Functions

Inverse cumulative distribution functions for supported Statistics Toolbox distributions all end with `inv`, as in `binoinv` or `expinv`. Specific function names for specific distributions can be found in "Supported Distributions" on page 5-3.

Each function represents a parametric family of distributions. Input arguments are arrays of cumulative probabilities from 0 to 1 followed by a list of parameter values specifying a particular member of the distribution family.

For continuous distributions, the inverse cdf returns the unique outcome whose cdf value is the input cumulative probability.

For example, the `expinv` function can be used to compute inverses of exponential cumulative probabilities:

```
x = 0.5:0.2:1.5 % Outcomes
x =
    0.5000  0.7000  0.9000  1.1000  1.3000  1.5000
p = expcdf(x,1) % Cumulative probabilities
p =
    0.3935  0.5034  0.5934  0.6671  0.7275  0.7769
expinv(p,1) % Return original outcomes
ans =
    0.5000  0.7000  0.9000  1.1000  1.3000  1.5000
```

For discrete distributions, there may be no outcome whose cdf value is the input cumulative probability. In these cases, the inverse cdf returns the first outcome whose cdf value equals or exceeds the input cumulative probability.

For example, the `binoinv` function can be used to compute inverses of binomial cumulative probabilities:

```
x = 0:5               % Some possible outcomes
p = binocdf(x,10,0.2) % Their cumulative probabilities

p =

    0.1074    0.3758    0.6778    0.8791    0.9672    0.9936
q = [.1 .2 .3 .4]     % New trial probabilities
```

```
q =

    0.1000    0.2000    0.3000    0.4000

binoinv(q,10,0.2)     % Their corresponding outcomes
ans =

     0     1     1     2
```

The inverse cdf is useful in hypothesis testing, where critical outcomes of a test statistic are computed from cumulative significance probabilities. For example, `norminv` can be used to compute a 95% confidence interval under the assumption of normal variability:

```
p = [0.025 0.975]; % Interval containing 95% of [0,1]
x = norminv(p,0,1) % Assume standard normal variability
x =
   -1.9600  1.9600 % 95% confidence interval

n = 20; % Sample size
y = normrnd(8,1,n,1); % Random sample (assume mean is unknown)
ybar = mean(y);
ci = ybar + (1/sqrt(n))*x % Confidence interval for mean
ci =
    7.6779  8.5544
```

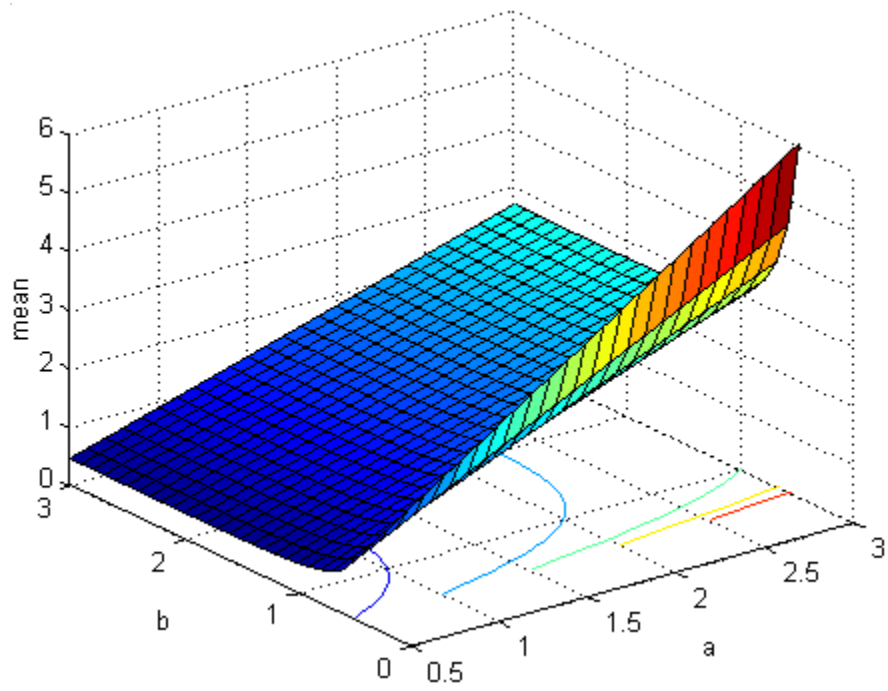
Distribution Statistics Functions

Distribution statistics functions for supported Statistics Toolbox distributions all end with `stat`, as in `binostat` or `expstat`. Specific function names for specific distributions can be found in "Supported Distributions" on page 5-3.

Each function represents a parametric family of distributions. Input arguments are lists of parameter values specifying a particular member of the distribution family. Functions return the mean and variance of the distribution, as a function of the parameters.

For example, the `wblstat` function can be used to visualize the mean of the Weibull distribution as a function of its two distribution parameters:

```
a = 0.5:0.1:3;
b = 0.5:0.1:3;
[A,B] = meshgrid(a,b);
M = wblstat(A,B);
surfc(A,B,M)
```


mean
6
5
4
3
2
1
0
3
2
1
0
b
0.5
1
1.5
2
2.5
3
a

Distribution Fitting Functions

Fitting Regular Distributions

Distribution fitting functions for supported Statistics Toolbox distributions all end with `fit`, as in `binofit` or `expfit`. Specific function names for specific distributions can be found in "Supported Distributions" on page 5-3.

Each function represents a parametric family of distributions. Input arguments are arrays of data, presumed to be samples from some member of the selected distribution family. Functions return maximum likelihood estimates (MLEs) of distribution parameters, that is, parameters for the distribution family member with the maximum likelihood of producing the data as a random sample.

The Statistics Toolbox function `mle` is a convenient front end to the individual distribution fitting functions, and more. The function computes MLEs for distributions beyond those for which Statistics Toolbox software provides specific pdf functions.

For some pdfs, MLEs can be given in closed form and computed directly. For other pdfs, a search for the maximum likelihood must be employed. The search can be controlled with an `options` input argument, created using the `statset` function. For efficient searches, it is important to choose a reasonable distribution model and set appropriate convergence tolerances.

MLEs can be heavily biased, especially for small samples. As sample size increases, however, MLEs become unbiased minimum variance estimators with approximate normal distributions. This is used to compute confidence bounds for the estimates.

For example, consider the following distribution of means from repeated random samples of an exponential distribution:

```
mu = 1; % Population parameter
n = 1e3; % Sample size
ns = 1e4; % Number of samples
```

```
samples = exprnd(mu,n,ns); % Population samples
means = mean(samples); % Sample means
```

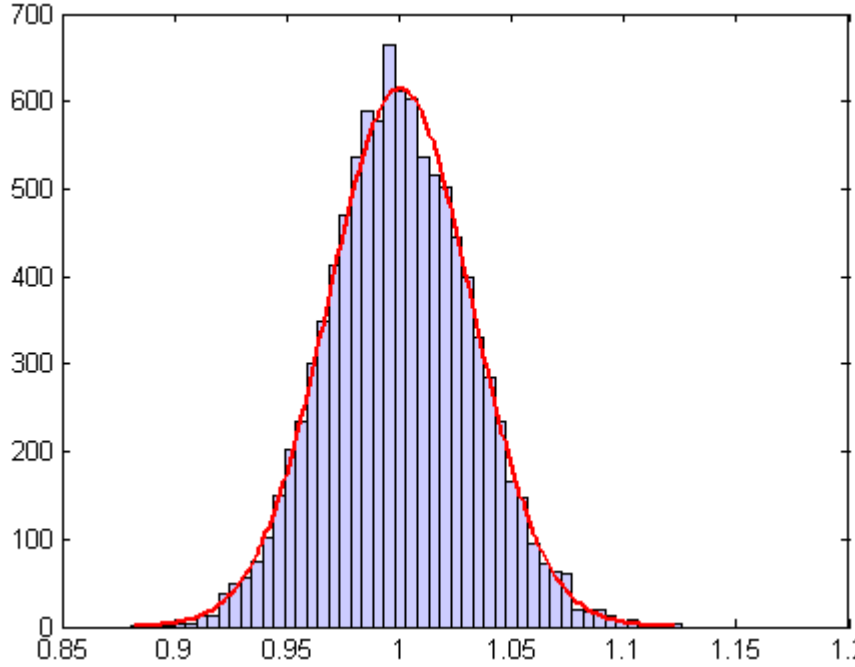
The Central Limit Theorem says that the means will be approximately normally distributed, regardless of the distribution of the data in the samples. The `normfit` function can be used to find the normal distribution that best fits the means:

```
[muhat,sigmahat,muci,sigmaci] = normfit(means)
muhat =
    1.0003
sigmahat =
    0.0319
muci =
    0.9997
    1.0010
sigmaci =
    0.0314
    0.0323
```

The function returns MLEs for the mean and standard deviation and their 95% confidence intervals.

To visualize the distribution of sample means together with the fitted normal distribution, you must scale the fitted pdf, with area = 1, to the area of the histogram being used to display the means:

```
numbins = 50;
hist(means,numbins)
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
hold on
[bincounts,binpositions] = hist(means,numbins);
binwidth = binpositions(2) - binpositions(1);
histarea = binwidth*sum(bincounts);
x = binpositions(1):0.001:binpositions(end);
y = normpdf(x,muhat,sigmahat);
plot(x,histarea*y,'r','LineWidth',2)
```



Fitting Piecewise Distributions

The parametric methods discussed in "Fitting Regular Distributions" on page 5-70 fit data samples with smooth distributions that have a relatively low-dimensional set of parameters controlling their shape. These methods work well in many cases, but there is no guarantee that a given sample will be described accurately by any of the supported Statistics Toolbox distributions.

The empirical distributions computed by `ecdf` and discussed in "Estimating Empirical CDFs" on page 5-63 assign equal probability to each observation in a sample, providing an exact match of the sample distribution. However, the distributions are not smooth, especially in the tails where data may be sparse.

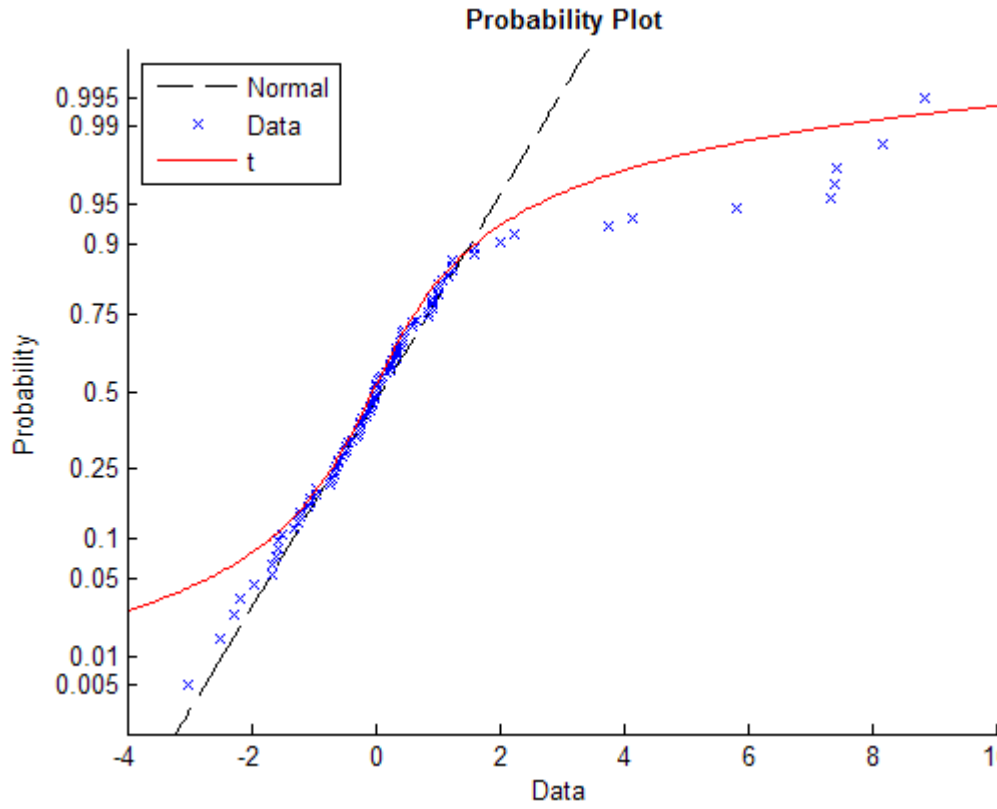
The `paretotails` function fits a distribution by piecing together the empirical distribution in the center of the sample with smooth generalized Pareto distributions (GPDs) in the tails. The output is an object of the `paretotails` class, with associated methods to evaluate the cdf, inverse cdf, and other functions of the fitted distribution.

As an example, consider the following data, with about 20% outliers:

```
left_tail = -exprnd(1,10,1);
right_tail = exprnd(5,10,1);
center = randn(80,1);
data = [left_tail;center;right_tail];
```

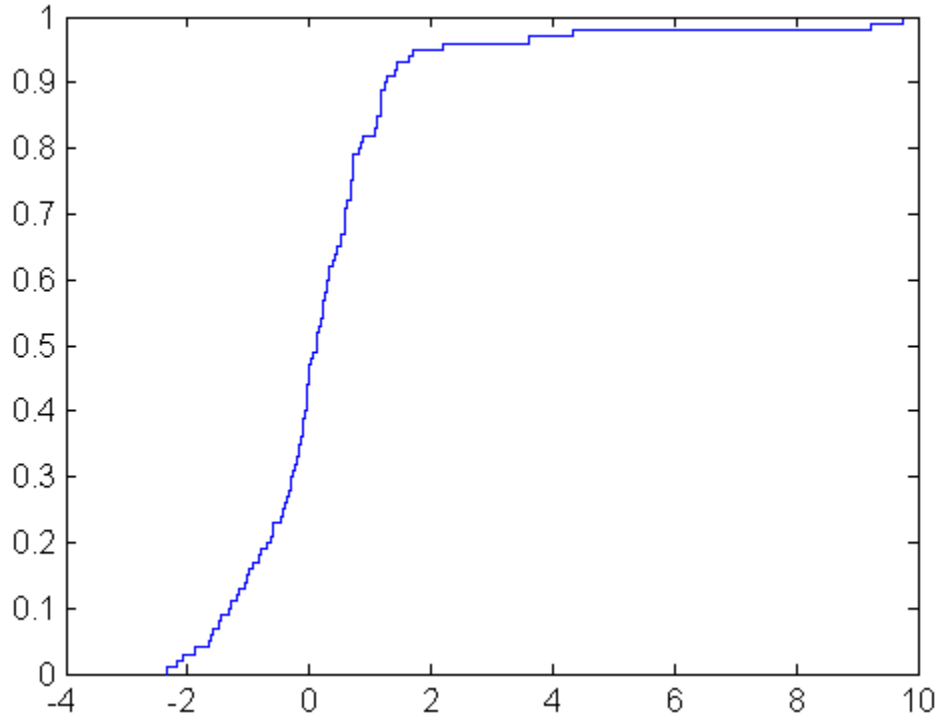
Neither a normal distribution nor a *t* distribution fits the tails very well:

```
probplot(data);
p = fitdist(data,'tlocationscale');
h = probplot(gca,p);
set(h,'color','r','linestyle','-')
title('{\bf Probability Plot}')
legend('Normal','Data','t','Location','NW')
```



On the other hand, the empirical distribution provides a perfect fit, but the outliers make the tails very discrete:

```
ecdf(data)
```

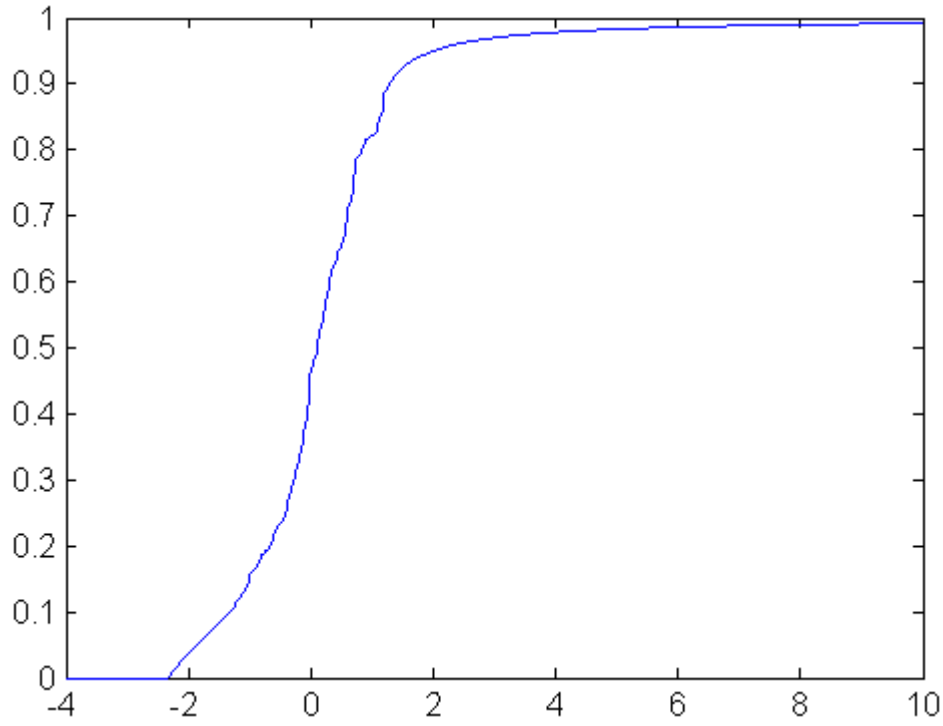


Random samples generated from this distribution by inversion might include, for example, values around 4.33 and 9.25, but nothing in-between.

The `paretotails` function provides a single, well-fit model for the entire sample. The following uses generalized Pareto distributions (GPDs) for the lower and upper 10% of the data:

```
pfit = paretotails(data,0.1,0.9)
pfit =
Piecewise distribution with 3 segments
 -Inf < x < -1.30726 (0 < p < 0.1)
        lower tail, GPD(-1.10167,1.12395)

 -1.30726 < x < 1.27213 (0.1 < p < 0.9)
        interpolated empirical cdf

  1.27213 < x < Inf (0.9 < p < 1)
```

```
        upper tail, GPD(1.03844,0.726038)

x = -4:0.01:10;
plot(x,cdf(pfit,x))
```



Access information about the fit using the methods of the `paretotails` class. Options allow for nonparametric estimation of the center of the cdf.

Negative Log-Likelihood Functions

Negative log-likelihood functions for supported Statistics Toolbox distributions all end with `like`, as in `explike`. Specific function names for specific distributions can be found in "Supported Distributions" on page 5-3.

Each function represents a parametric family of distributions. Input arguments are lists of parameter values specifying a particular member of the distribution family followed by an array of data. Functions return the negative log-likelihood of the parameters, given the data.

Negative log-likelihood functions are used as objective functions in search algorithms such as the one implemented by the MATLAB function `fminsearch`. Additional search algorithms are implemented by Optimization Toolbox™ functions and Global Optimization Toolbox functions.

When used to compute maximum likelihood estimates (MLEs), negative log-likelihood functions allow you to choose a search algorithm and exercise low-level control over algorithm execution. By contrast, the functions discussed in "Distribution Fitting Functions" on page 5-70 use preset algorithms with options limited to those set by the `statset` function.

Likelihoods are conditional probability densities. A parametric family of distributions is specified by its pdf $f(x,a)$, where x and a represent the variables and parameters, respectively. When a is fixed, the pdf is used to compute the density at x, $f(x \mid a)$. When x is fixed, the pdf is used to compute the *likelihood* of the parameters a, $f(a \mid x)$. The joint likelihood of the parameters over an independent random sample X is

$$L(a) = \prod_{x \in X} f(a \mid x)$$

Given X, MLEs maximize $L(a)$ over all possible a.

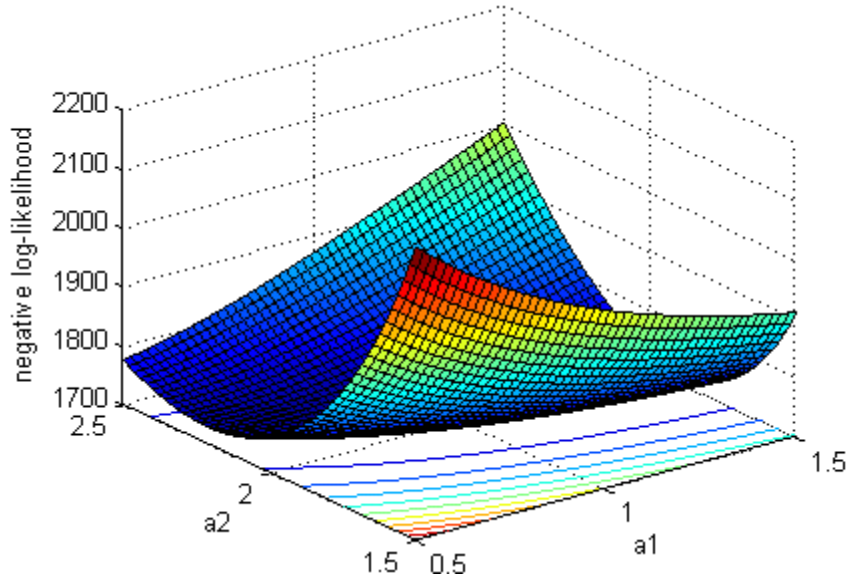
In numerical algorithms, the log-likelihood function, $\log(L(a))$, is (equivalently) optimized. The logarithm transforms the product of potentially small likelihoods into a sum of logs, which is easier to distinguish from 0 in computation. For convenience, Statistics Toolbox negative log-likelihood functions return the *negative* of this sum, since the optimization algorithms to which the values are passed typically search for minima rather than maxima.

For example, use `gamrnd` to generate a random sample from a specific gamma distribution:

```
a = [1,2];
X = gamrnd(a(1),a(2),1e3,1);
```

Given `X`, the `gamlike` function can be used to visualize the likelihood surface in the neighborhood of `a`:

```
mesh = 50;
delta = 0.5;
a1 = linspace(a(1)-delta,a(1)+delta,mesh);
a2 = linspace(a(2)-delta,a(2)+delta,mesh);
logL = zeros(mesh); % Preallocate memory
for i = 1:mesh
    for j = 1:mesh
        logL(i,j) = gamlike([a1(i),a2(j)],X);
    end
end

[A1,A2] = meshgrid(a1,a2);
surfc(A1,A2,logL)
```



The MATLAB function `fminsearch` is used to search for the minimum of the likelihood surface:

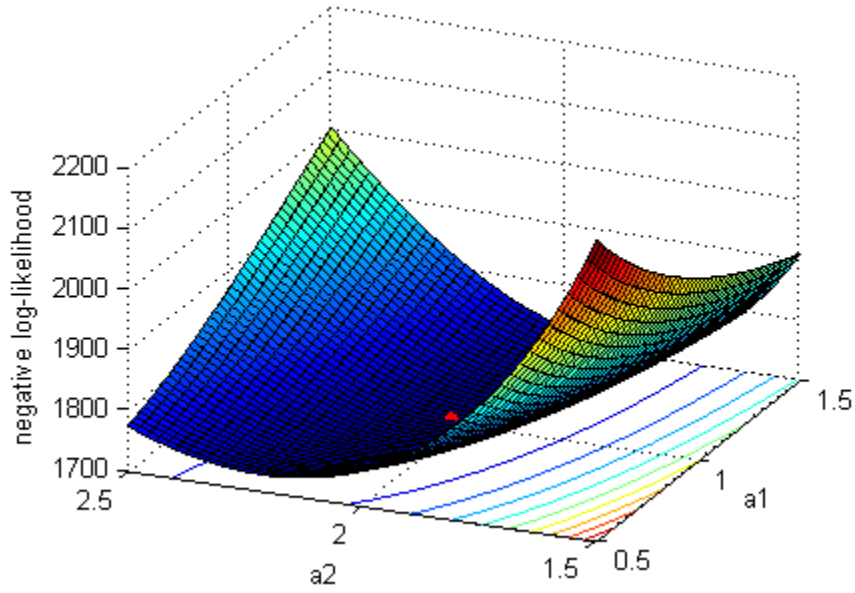
```
LL = @(u)gamlike([u(1),u(2)],X); % Likelihood given X
MLES = fminsearch(LL,[1,2])
MLES =
    1.0231    1.9729
```

These can be compared to the MLEs returned by the `gamfit` function, which uses a combination search and solve algorithm:

```
ahat = gamfit(X)
ahat =
    1.0231    1.9728
```

The MLEs can be added to the surface plot (rotated to show the minimum):

```
hold on
plot3(MLES(1),MLES(2),LL(MLES),...
      'ro','MarkerSize',5,...
      'MarkerFaceColor','r')
```



Random Number Generators

The Statistics Toolbox supports the generation of random numbers from various distributions. Each RNG represents a parametric family of distributions. RNGs return random numbers from the specified distribution in an array of the specified dimensions. Specific RNG names for specific distributions are in "Supported Distributions" on page 5-3.

Other random number generation functions which do not support specific distributions include:

- `cvpartition`
- `datasample`
- `hmmgenerate`
- `lhsdesign`
- `lhsnorm`
- `mhsample`
- `random`
- `randsample`
- `slicesample`

RNGs in Statistics Toolbox software depend on MATLAB's default random number stream via the `rand` and `randn` functions, each RNG uses one of the techniques discussed in "Common Generation Methods" on page 6-5 to generate random numbers from a given distribution.

By controlling the default random number stream and its state, you can control how the RNGs in Statistics Toolbox software generate random values. For example, to reproduce the same sequence of values from an RNG, you can save and restore the default stream's state, or reset the default stream. For details on managing the default random number stream, see "Managing the Global Stream".

MATLAB initializes the default random number stream to the same state each time it starts up. Thus, RNGs in Statistics Toolbox software will generate the same sequence of values for each MATLAB session unless you

modify that state at startup. One simple way to do that is to add commands to `startup.m` such as

```
rng('shuffle');
```

that initialize MATLAB's default random number stream to a different state for each session.

Dependencies of the Random Number Generators

The following table lists the dependencies of Statistics Toolbox RNGs on the MATLAB base RNGs `rand`, `randi`, and/or `randn`.

RNG	MATLAB Base RNG
`betarnd`	`rand, randn`
`binornd`	`rand`
`chi2rnd`	`rand, randn`
`evrnd`	`rand`
`exprnd`	`rand`
`datasample`	`rand, randi, randperm`
`frnd`	`rand, randn`
`gamrnd`	`rand, randn`
`geornd`	`rand`
`gevrnd`	`rand`
`gprnd`	`rand`
`hygernd`	`rand`
`iwishrnd`	`rand, randn`
`johnsrnd`	`randn`
`lhsdesign`	`rand`
`lhsnorm`	`rand`
`lognrnd`	`randn`
`mhsample`	`rand` or `randn`, depending on the RNG given for the proposal distribution
`mvnrnd`	`randn`
`mvtrnd`	`rand, randn`

RNG	MATLAB Base RNG
nbinrnd	rand, randn
ncfrnd	rand, randn
nctrnd	rand, randn
ncx2rnd	randn
normrnd	randn
pearsrnd	rand or randn, depending on the distribution type
poissrnd	rand, randn
random	rand or randn, depending on the specified distribution
randsample	rand
raylrnd	randn
slicesample	rand
trnd	rand, randn
unidrnd	rand
unifrnd	rand
wblrnd	rand
wishrnd	rand, randn

Using Probability Distribution Objects

In this section...

Using Distribution Objects

For many distributions supported by Statistics Toolbox software, objects are available for statistical analysis. This section gives a general overview of the uses of distribution objects, including sample work flows. For information on objects available for specific distributions, see "Object-Supported Distributions" on page 5-89.

Probability distribution objects allow you to easily fit, access, and store distribution information for a given data set. The following operations are easier to perform using distribution objects:

- Grouping a single dataset in a number of different ways using group names, and then fit a distribution to each group. For an example of how to fit distributions to grouped data, see "Example: Fitting Distributions to Grouped Data Within a Single Dataset" on page 5-91.
- Fitting different distributions to the same set of data. For an example of how objects make fitting multiple distribution types easier, see "Example: Fitting Multiple Distribution Types to a Single Dataset" on page 5-95.
- Sharing fitted distributions across workspaces. For an example of sharing information using probability distribution objects, see "Example: Saving and Sharing Distribution Fit Data" on page 5-97.

Deciding to Use Distribution Objects

If you know the type of distribution you would like to use, objects provide a less complex interface than functions and a more efficient functionality than the `dfittool` GUI.

If you are a novice statistician who would like to explore how various distributions look without having to manipulate data, see "Working with Distributions Through GUIs" on page 5-9.

If you have no data to fit, but want to calculate a `pdf`, `cdf`, etc for various parameters, see "Statistics Toolbox Distribution Functions" on page 5-52.

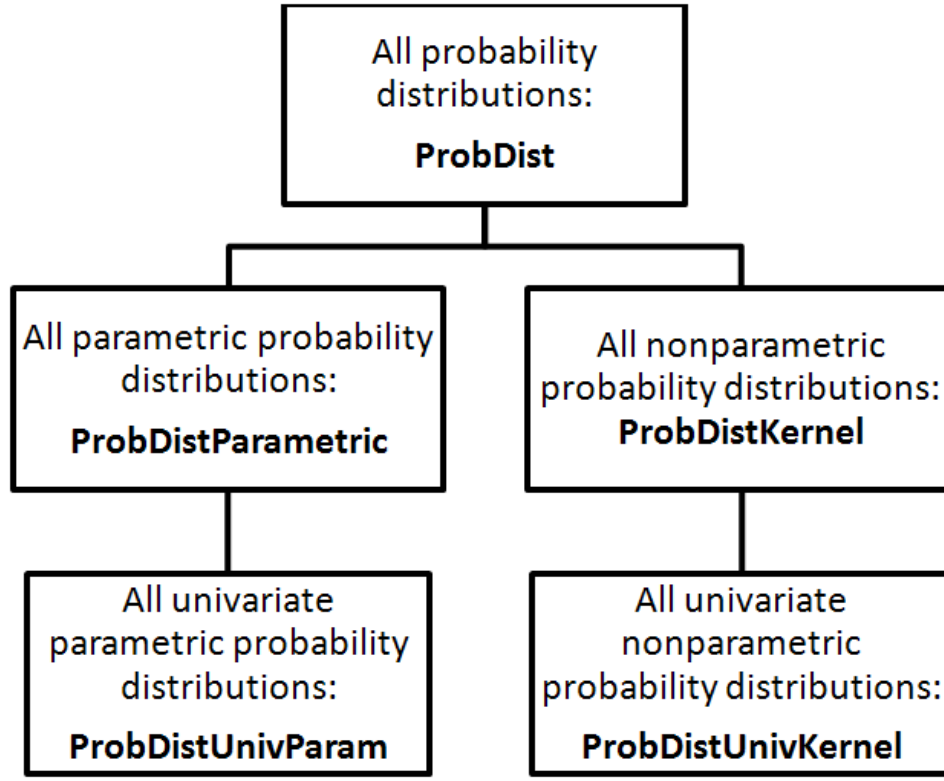
What are Objects?

Objects are, in short, a convenient way of storing data. They allow you to set rules for the types of data to store, while maintaining some flexibility for the actual values of the data. For example, in statistics groups of distributions have some general things in common:

- All distributions have a name (ex, Normal).
- Parametric distributions have parameters.
- Nonparametric distributions have kernel-smoothing functions.

Objects store all this information within properties. Classes of related objects (for example, all univariate parametric distributions) have the same properties with values and types relevant to a specified distribution. In addition to storing information within objects, you can perform certain actions (called *methods*) on objects.

Subclasses (for example, `ProbDistParametric` is a subclass of `ProbDist`) contain the same properties and methods as the original class, in addition to other properties relevant to that subclass. This concept is called *inheritance*. Inheritance means that subclasses of a class have all of its properties and methods. For example, parametric distributions, which are a subset (subclass) of probability distributions, have input data and a distribution name. The following diagram illustrates this point:



The left side of this diagram shows the inheritance line from all probability distributions down to univariate parametric probability distributions. The right side shows the lineage down to univariate kernel distributions. Here is how to interpret univariate parametric distribution lineage:

- `ProbDist` is a class of objects that includes all probability distributions. All probability distribution objects have at least these properties:
  - `DistName` — the name of the distribution (for example Normal or Weibull)
  - `InputData` — the data fit to the distribution

  In addition, you can perform the following actions on these objects, using the following methods:
  - `cdf` — Return the cumulative distribution function for a specified distribution.

  - `pdf` — Return the probability density function for a specified distribution.
  - `random` — Generate random numbers based on a specified distribution.

- `ProbDistParametric` is a class of objects that includes all parametric probability distributions. All parametric probability distribution objects have the properties and methods of a `ProbDist` object, in addition to at least the following properties:
  - `NLogL` — Negative log likelihood for input data
  - `NumParams` — Number of parameters for that distribution
  - `ParamCov` — Covariance matrix of parameter estimates
  - `ParamDescription` — Descriptions of parameters
  - `ParamNames` — Names of parameters
  - `Params` — Values of parameters

  No additional unique methods apply to `ProbDistParametric` objects.
- `ProbDistUnivParam` is a class of objects that includes only univariate parametric probability distributions. In addition to the properties and methods of `ProbDist` and `ProbDistParametric` objects, these objects also have at least the following methods:
  - `icdf` — Return the inverse cumulative distribution function for a specified distribution based on a given set of data.
  - `iqr` — Return the interquartile range for a specified distribution based on a given set of data.
  - `mean` — Return the mean for a specified distribution based on a given set of data.
  - `median` — Return the median for a specified distribution based on a given set of data.
  - `paramci` — Return the parameter confidence intervals for a specified distribution based on a given set of data.
  - `std` — Return the standard deviation for a specified distribution based on a given set of data.
  - `var` — Return the variance for a specified distribution based on a given set of data.

  No additional unique properties apply to `ProbDistUnivParam` objects.

The univariate nonparametric lineage reads in a similar manner, with different properties and methods. For more information on nonparametric objects and their methods and properties, see `ProbDistKernel` and `ProbDistUnivKernel`.

For more detailed information on object-oriented programming in MATLAB, see *Object-Oriented Programming*.

Creating Distribution Objects

There are two ways to create distribution objects:

- Use the `fitdist` function. See "Creating Distribution Objects Using fitdist" on page 5-88.
- Use the object constructor. See "Creating Distribution Objects Using Constructors" on page 5-88.

Creating Distribution Objects Using fitdist

Using the `fitdist` function is the simplest way of creating distribution objects. Like the `*fit` functions, `fitdist` fits your data to a specified distribution and returns relevant distribution information. `fitdist` creates an object relevant to the type of distribution you specify: if you specify a parametric distribution, it returns a `ProbDistUnivParam` object. For examples of how to use `fitdist` to fit your data, see "Performing Calculations Using Distribution Objects" on page 5-90.

Creating Distribution Objects Using Constructors

If you know the distribution you would like to use and would like to create a univariate parametric distribution with known parameters, you can use the `ProbDistUnivParam` constructor. For example, create a normal distribution with mean 100 and standard deviation 10:

```
pd = ProbDistUnivParam('normal',[100 10])
```

For nonparametric distributions, you must have a dataset. Using `fitdist` is a simpler way to fit nonparametric data, but you can use the `ProbDistUnivKernel` constructor as well. For example, create a nonparametric distribution of the MPG data from `carsmall.mat`:

```
load carsmall
pd = ProbDistUnivKernel(MPG)
```

Object-Supported Distributions

Object-oriented programming in the Statistics Toolbox supports the following distributions.

Parametric Distributions

Use the following distribution to create `ProbDistUnivParam` objects using `fitdist`. For more information on the cumulative distribution function (`cdf`) and probability density function (`pdf`) methods, as well as other available methods, see the `ProbDistUnivParam` class reference page.

Supported Distribution	Input to fitdist
"Beta Distribution" on page B-4	`'beta'`
"Binomial Distribution" on page B-7	`'binomial'`
"Birnbaum-Saunders Distribution" on page B-10	`'birnbaumsaunders'`
"Exponential Distribution" on page B-16	`'exponential'`
"Extreme Value Distribution" on page B-19	`'extreme value'` or `'ev'`
"Gamma Distribution" on page B-27	`'gamma'`
"Generalized Extreme Value Distribution" on page B-32	`'generalized extreme value'` or `'gev'`
"Generalized Pareto Distribution" on page B-37	`'generalized pareto'` or `'gp'`
"Inverse Gaussian Distribution" on page B-45	`'inversegaussian'`
"Logistic Distribution" on page B-49	`'logistic'`
"Loglogistic Distribution" on page B-50	`'loglogistic'`

Supported Distribution	Input to fitdist
"Lognormal Distribution" on page B-51	`'lognormal'`
"Nakagami Distribution" on page B-70	`'nakagami'`
"Negative Binomial Distribution" on page B-72	`'negative binomial'` or `'nbin'`
"Normal Distribution" on page B-83	`'normal'`
"Poisson Distribution" on page B-89	`'poisson'`
"Rayleigh Distribution" on page B-91	`'rayleigh'`
"Rician Distribution" on page B-93	`'rician'`
"t Location-Scale Distribution" on page B-97	`'tlocationscale'`
"Weibull Distribution" on page B-103	`'weibull'` or `'wbl'`

Nonparametric Distributions

Use the following distributions to create `ProbDistUnivKernel` objects. For more information on the cumulative distribution function (`cdf`) and probability density function (`pdf`) methods, as well as other available methods, see the `ProbDistUnivKernel` class reference page.

Supported Distribution	Input to fitdist
"Nonparametric Distributions" on page B-82	`'kernel'`

Performing Calculations Using Distribution Objects

Distribution objects make it easier for you to perform calculations on complex datasets. The following sample workflows show some of the functionality of these objects.

- "Example: Fitting a Single Distribution to a Single Dataset" on page 5-91

- "Example: Fitting Distributions to Grouped Data Within a Single Dataset" on page 5-91
- "Example: Fitting Multiple Distribution Types to a Single Dataset" on page 5-95

Example: Fitting a Single Distribution to a Single Dataset

Fit a single Normal distribution to a dataset using `fitdist`:

```
load carsmall
NormDist = fitdist(MPG,'normal')

NormDist =


normal distribution

    mu = 23.7181
    sigma = 8.03573
```

The output MATLAB returns is a `ProbDistUnivParam` object with a `DistName` property of `'normal distribution'`. The `ParamNames` property contains the strings `mu` and `sigma`, while the `Params` property contains the parameter values.

Example: Fitting Distributions to Grouped Data Within a Single Dataset

Often, datasets are collections of data you can group in different ways. Using `fitdist` and the data from `carsmall.mat`, group the MPG data by country of origin, then fit a Weibull distribution each group:

```
load carsmall
[WeiByOrig, Country] = fitdist(MPG,'weibull','by',Origin)
Warning: Error while fitting group 'Italy':
Not enough data in X to fit this distribution.
> In fitdist at 171

WeiByOrig =
```

```
  Columns 1 through 4

    [1x1 ProbDistUnivParam]    [1x1 ProbDistUnivParam] ...
         [1x1 ProbDistUnivParam]    [1x1 ProbDistUnivParam]

  Columns 5 through 6

    [1x1 ProbDistUnivParam]     []


Country =

    'USA'
    'France'
    'Japan'
    'Germany'
    'Sweden'
    'Italy'
```

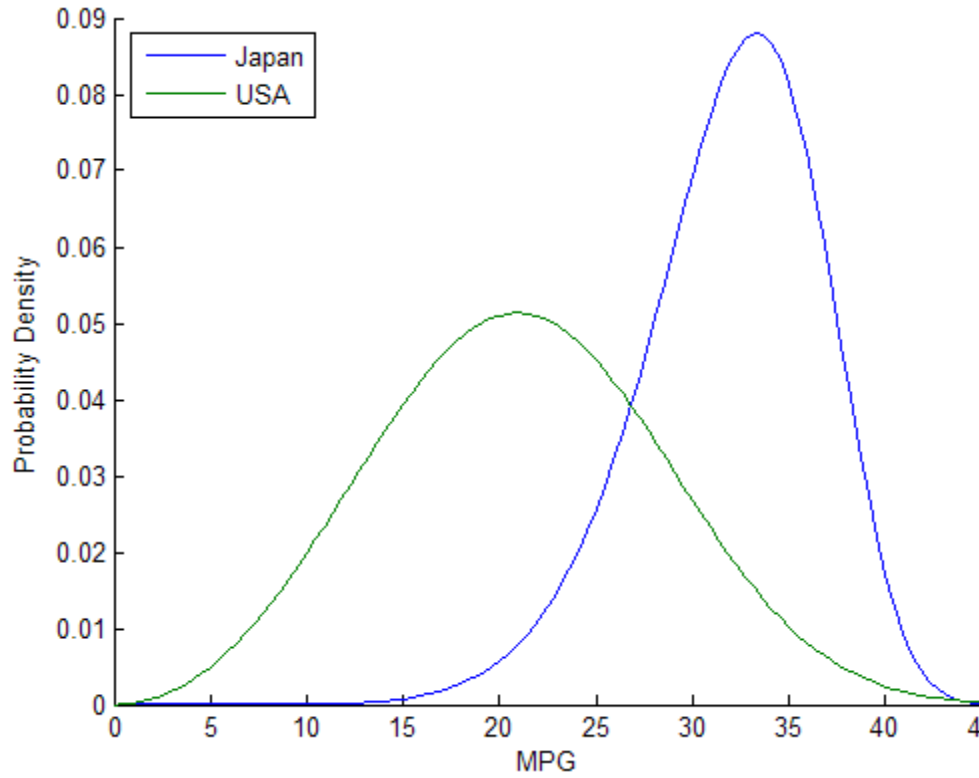
A warning appears informing you that, since the data only represents one Italian car, `fitdist` cannot fit a Weibull distribution to that group. Each one of the five other groups now has a distribution object associated with it, represented in the cell array `wd`. Each object contains properties that hold information about the data, the distribution, and the parameters. For more information on what properties exist and what information they contain, see `ProbDistUnivParam` or `ProbDistUnivKernel`.

Now access two of the objects and their properties:

```
% Get USA fit
distusa = WeiByOrig{1};
% Use the InputData property of ProbDistUnivParam objects to see
% the actual data used to fit the distribution:
dusa = distusa.InputData.data;

% Get Japan fit and data
distjapan = WeiByOrig{3};
djapan = distjapan.InputData.data;
```

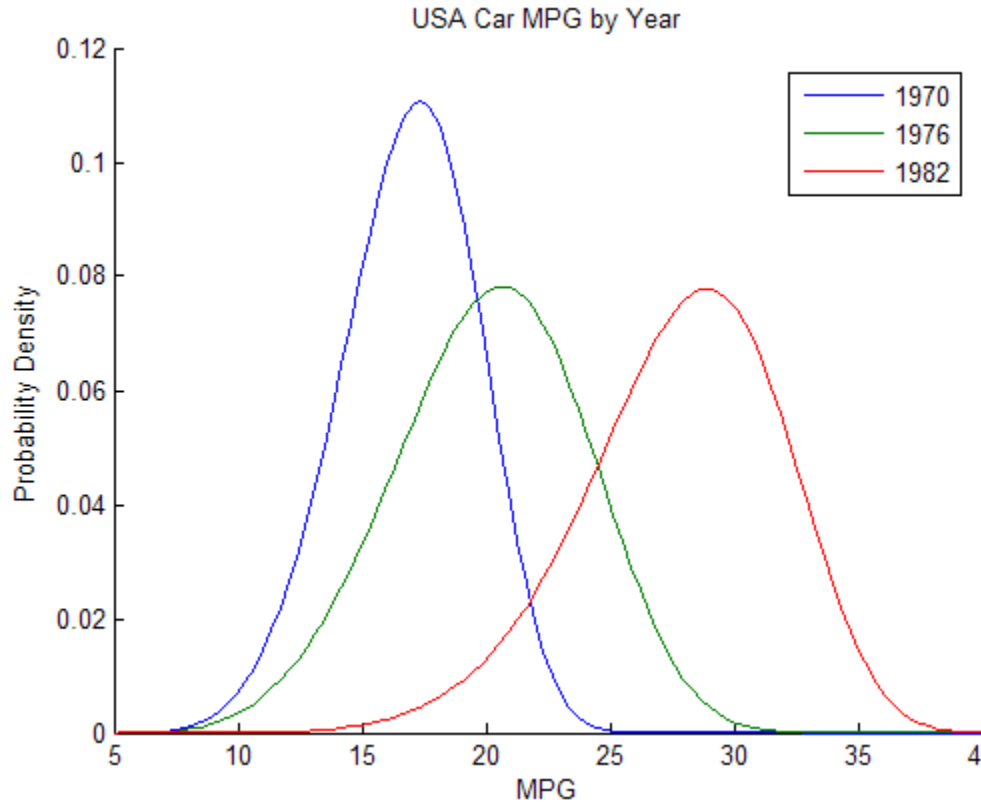
Now you can easily compare PDFs using the `pdf` method of the `ProbDistUnivParam` class:

```
time = linspace(0,45);
pdfjapan = pdf(distjapan,time);
pdfusa = pdf(distusa,time);
hold on
plot(time,[pdfjapan;pdfusa])
l = legend('Japan','USA')
set(l,'Location','Best')
xlabel('MPG')
ylabel('Probability Density')
```



You could then further group the data and compare, for example, MPG by year for American cars:

```
load carsmall
[WeiByYearOrig, Names] = fitdist(MPG,'weibull','by',...
    {Origin Model_Year});
USA70 = WeiByYearOrig{1};
USA76 = WeiByYearOrig{2};
USA82 = WeiByYearOrig{3};
time = linspace(0,45);
pdf70 = pdf(USA70,time);
pdf76 = pdf(USA76,time);
pdf82 = pdf(USA82,time);
line(t,[pdf70;pdf76;pdf82])
l = legend('1970','1976','1982')
set(l,'Location','Best')
title('USA Car MPG by Year')
xlabel('MPG')
ylabel('Probability Density')
```



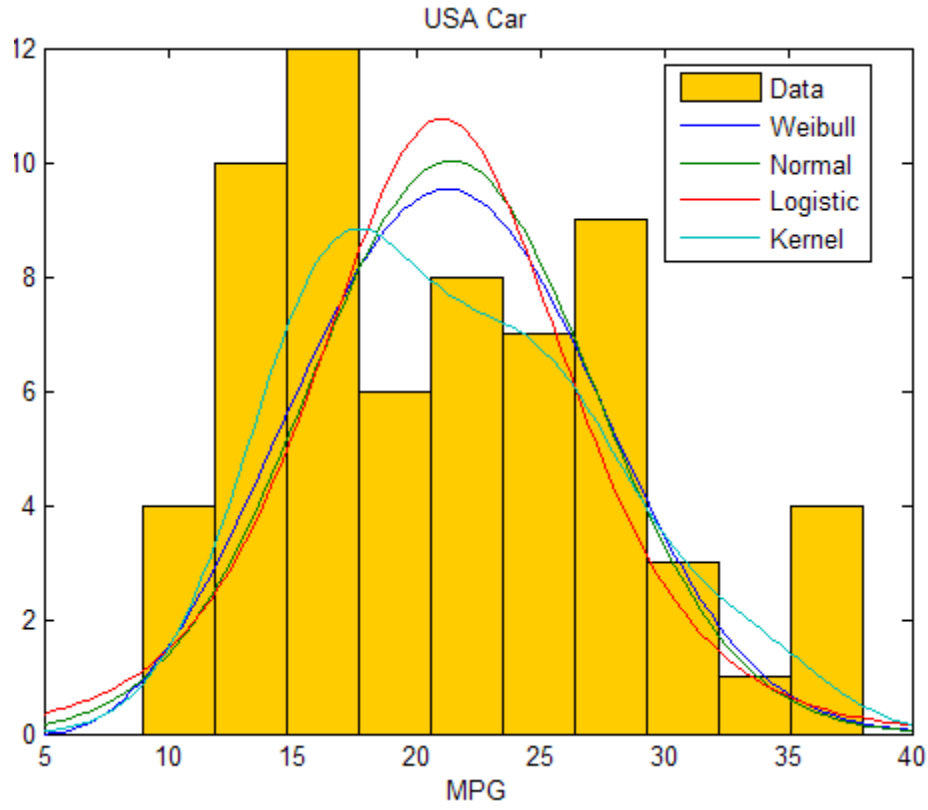
Example: Fitting Multiple Distribution Types to a Single Dataset

Distribution objects make it easy to fit multiple distributions to the same dataset, while minimizing workspace clutter. For example, use `fitdist` to group the MPG data by country of origin, then fit Weibull, Normal, Logistic, and nonparametric distributions for each group:

```
load carsmall;
[WeiByOrig, Country] = fitdist(MPG,'weibull','by',Origin);
[NormByOrig, Country] = fitdist(MPG,'normal','by',Origin);
[LogByOrig, Country] = fitdist(MPG,'logistic','by',Origin);
[KerByOrig, Country] = fitdist(MPG,'kernel','by',Origin);
```

Extract the fits for American cars and compare the fits visually against a histogram of the original data:

```
WeiUSA = WeiByOrig{1};
NormUSA = NormByOrig{1};
LogUSA = LogByOrig{1};
KerUSA = KerByOrig{1};

% Since all three distributions use the same set of data,
% you can extract the data from any of them:
data = WeiUSA.InputData.data;

% Create a histogram of the data:
[n,y] = hist(data,10);
b = bar(y,n,'hist');
set(b,'FaceColor',[1,0.8,0])

% Scale the density by the histogram area, for easier display:
area = sum(n) * (y(2)-y(1));
time = linspace(0,45);
pdfWei = pdf(WeiUSA,time);
pdfNorm = pdf(NormUSA,time);
pdfLog = pdf(LogUSA,time);
pdfKer = pdf(KerUSA,time);
allpdf = [pdfWei;pdfNorm;pdfLog;pdfKer];
line(t,area * allpdf)
l = legend('Data','Weibull','Normal','Logistic','Kernel')
set(l,'Location','Best')
title('USA Car')
xlabel('MPG')
```



You can see that only the nonparametric kernel distribution, `KerUSA`, comes close to revealing the two modes in the data.

Capturing Results Using Distribution Objects

Distribution objects allow you to share both your dataset and your analysis results simply by saving the information to a `.mat` file.

Example: Saving and Sharing Distribution Fit Data

Using the premise from the previous set of examples, group the MPG data in `carsmall.mat` by country of origin and fit four different distributions to each of the six sets of data:

```
load carsmall;
[WeiByOrig, Country] = fitdist(MPG,'weibull','by',Origin);
[NormByOrig, Country] = fitdist(MPG,'normal','by',Origin);
[LogByOrig, Country] = fitdist(MPG,'logistic','by',Origin);
[KerByOrig, Country] = fitdist(MPG,'kernel','by',Origin);
```

Combine all four fits and the country labels into a single cell array, including "headers" to indicate which distributions correspond to which objects. Then, save the array to a `.mat` file:

```
AllFits = cell(['Country' Country'; 'Weibull' WeiByOrig;...
     'Normal' NormByOrig; 'Logistic' LogByOrig; 'Kernel',...
     KerByOrig]);
save('CarSmallFits.mat','AllFits');
```

To show that the data is both safely saved and easily restored, clear your workspace of relevant variables. This command clears only those variables associated with this example:

```
clear('Weight','Acceleration','AllFits','Country',...
'Cylinders','Displacement','Horsepower','KerByOrig',...
'LogByOrig','MPG','Model','Model_Year','NormByOrig',...
'Origin','WeiByOrig')
```

Now, load the data:

```
load CarSmallFits
AllFits
```

You can now access the distributions objects as in the previous examples.

Probability Distributions Used for Multivariate Modeling

In this section...

Gaussian Mixture Models

Gaussian mixture models are formed by combining multivariate normal density components. For information on individual multivariate normal densities, see "Multivariate Normal Distribution" on page B-58 and related distribution functions listed under "Multivariate Distributions" on page 5-8.

In Statistics Toolbox software, use the `gmdistribution` class to fit data using an expectation maximization (EM) algorithm, which assigns posterior probabilities to each component density with respect to each observation. The fitting method uses an iterative algorithm that converges to a local optimum. Clustering using Gaussian mixture models is sometimes considered a soft clustering method. The posterior probabilities for each point indicate that each data point has some probability of belonging to each cluster.

For more information on clustering with Gaussian mixture models, see "Gaussian Mixture Models" on page 11-28. This section describes their creation.

Creating Gaussian Mixture Models

Specifying a Model. Use the `gmdistribution` constructor to create Gaussian mixture models with specified means, covariances, and mixture proportions. The following creates an object of the `gmdistribution` class defining a two-component mixture of bivariate Gaussian distributions:

```
MU = [1 2;-3 -5]; % Means
SIGMA = cat(3,[2 0;0 .5],[1 0;0 1]); % Covariances
p = ones(1,2)/2; % Mixing proportions

obj = gmdistribution(MU,SIGMA,p);
```

Display properties of the object with the MATLAB function `fieldnames`:

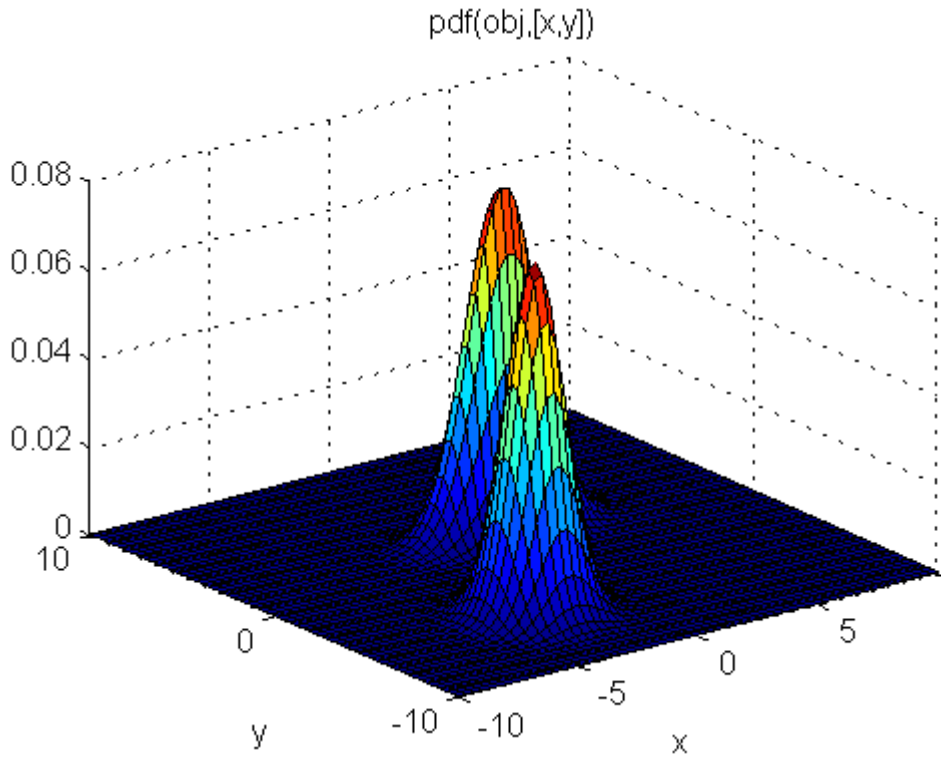
```
properties = fieldnames(obj)
properties =
    'NDimensions'
    'DistName'
    'NComponents'
    'PComponents'
    'mu'
    'Sigma'
    'NlogL'
    'AIC'
    'BIC'
    'Converged'
    'Iters'
    'SharedCov'
    'CovType'
    'RegV'
```

The `gmdistribution` reference page describes these properties. To access the value of a property, use dot indexing:

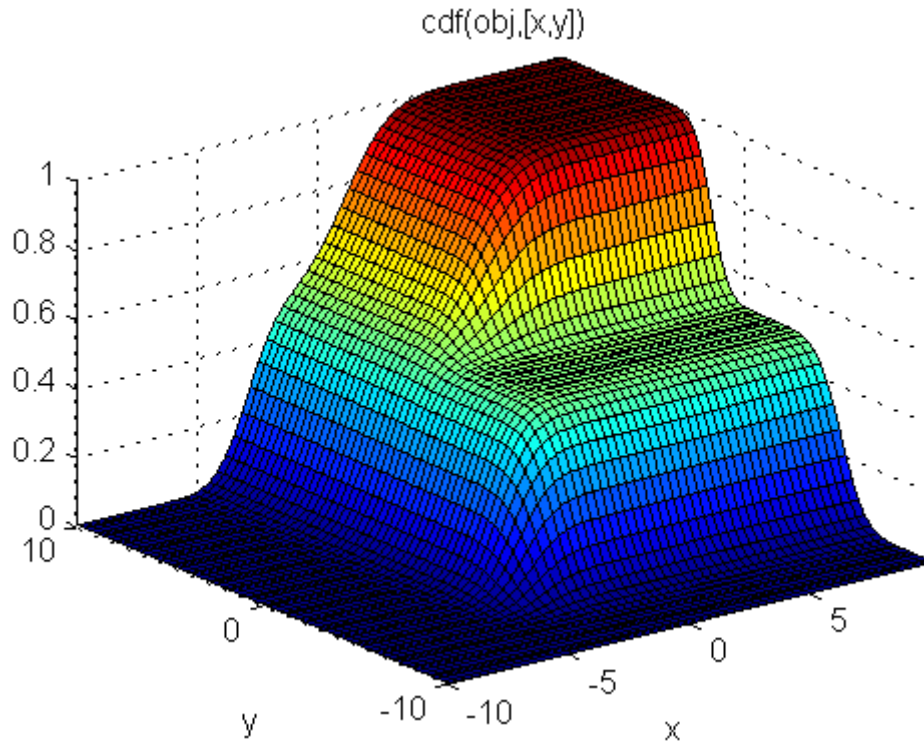
```
dimension = obj.NDimensions
dimension =
     2

name = obj.DistName
name =
gaussian mixture distribution
```

Use the methods `pdf` and `cdf` to compute values and visualize the object:

```
ezsurf(@(x,y)pdf(obj,[x y]),[-10 10],[-10 10])
```




```
ezsurf(@(x,y)cdf(obj,[x y]),[-10 10],[-10 10])
```



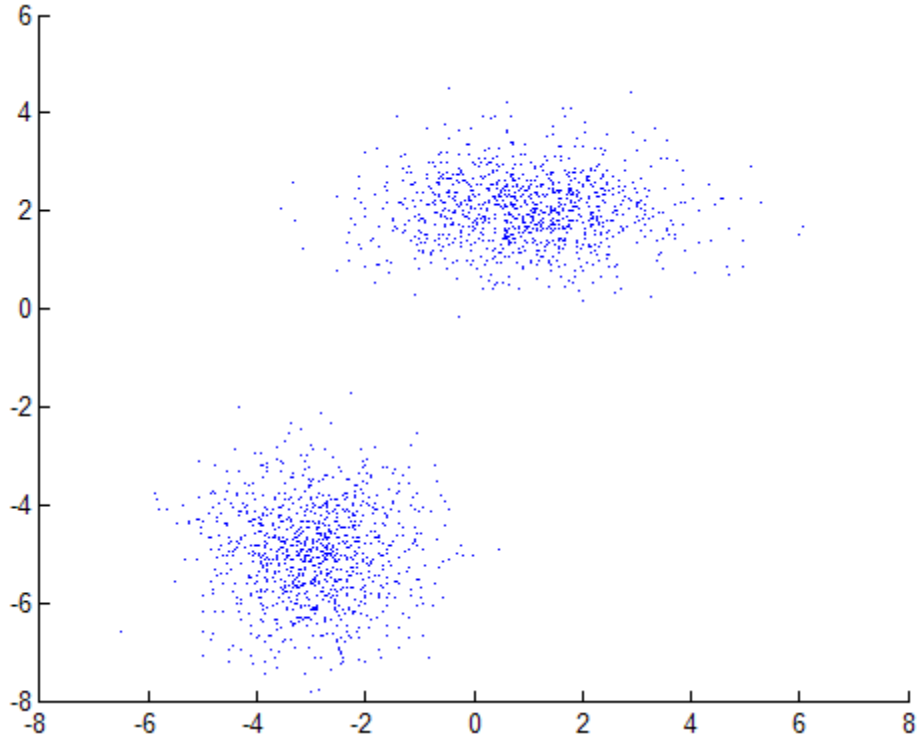
Fitting a Model to Data. You can also create Gaussian mixture models by fitting a parametric model with a specified number of components to data. The `fit` method of the `gmdistribution` class uses the syntax `obj = gmdistribution.fit(X,k)`, where `X` is a data matrix and `k` is the specified number of components. Choosing a suitable number of components `k` is essential for creating a useful model of the data—too few components fails to model the data accurately; too many components leads to an over-fit model with singular covariance matrices.

The following example illustrates this approach.

First, create some data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function:

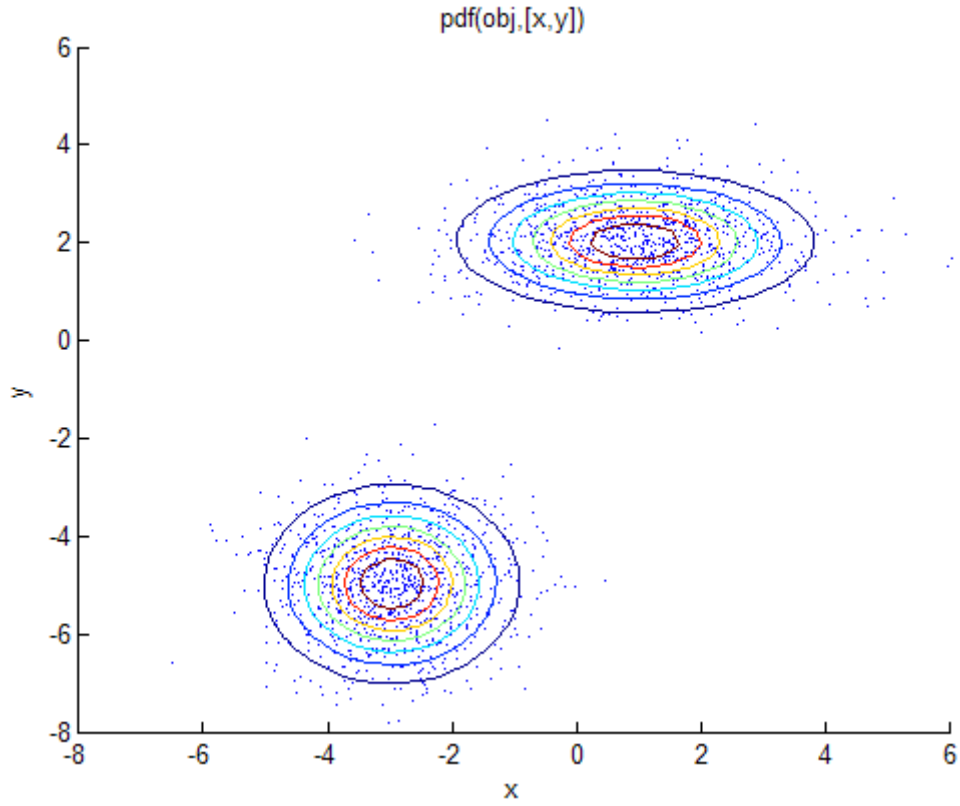
```
MU1 = [1 2];
SIGMA1 = [2 0; 0 .5];
```

```
MU2 = [-3 -5];
SIGMA2 = [1 0; 0 1];
X = [mvnrnd(MU1,SIGMA1,1000);
mvnrnd(MU2,SIGMA2,1000)];
scatter(X(:,1),X(:,2),10,'.')
```



Next, fit a two-component Gaussian mixture model:

```
options = statset('Display','final');
obj = gmdistribution.fit(X,2,'Options',options);
hold on
h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
hold off
```



Among the properties of the fit are the parameter estimates:

```
ComponentMeans = obj.mu
ComponentMeans =
    0.9391    2.0322
   -2.9823   -4.9737

ComponentCovariances = obj.Sigma
ComponentCovariances(:,:,1) =
    1.7786   -0.0528
   -0.0528    0.5312
ComponentCovariances(:,:,2) =
    1.0491   -0.0150
```

```
   -0.0150    0.9816

MixtureProportions = obj.PComponents
MixtureProportions =
    0.5000    0.5000
```

The two-component model minimizes the Akaike information:

```
AIC = zeros(1,4);
obj = cell(1,4);
for k = 1:4
    obj{k} = gmdistribution.fit(X,k);
    AIC(k)= obj{k}.AIC;
end

[minAIC,numComponents] = min(AIC);
numComponents
numComponents =
     2

model = obj{2}
model =
Gaussian mixture distribution
with 2 components in 2 dimensions
Component 1:
Mixing proportion: 0.500000
Mean:     0.9391    2.0322
Component 2:
Mixing proportion: 0.500000
Mean:    -2.9823   -4.9737
```

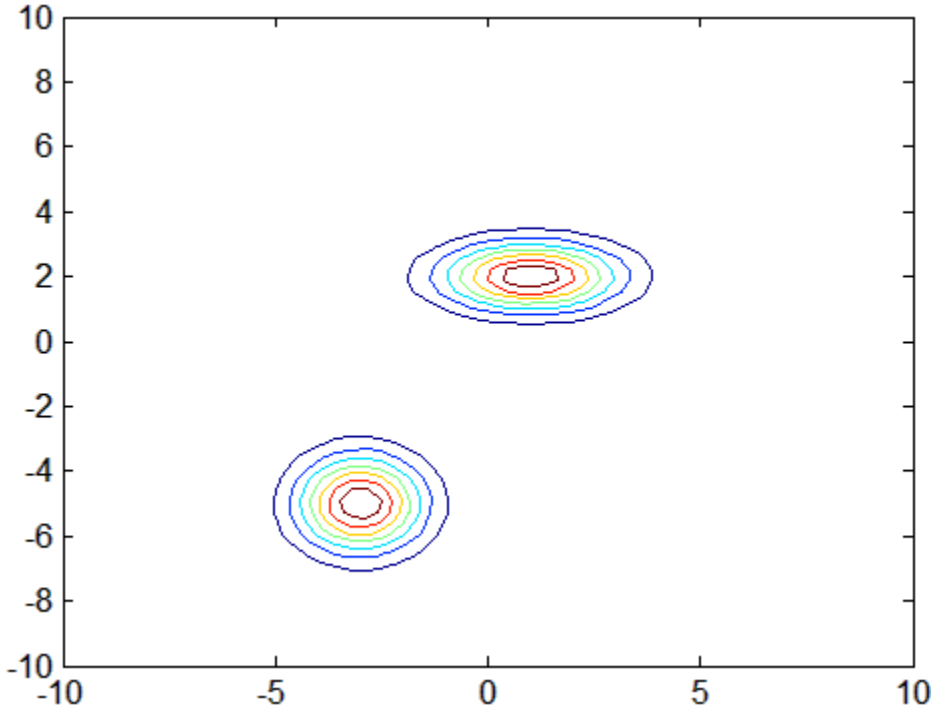
Both the Akaike and Bayes information are negative log-likelihoods for the data with penalty terms for the number of estimated parameters. You can use them to determine an appropriate number of components for a model when the number of components is unspecified.

Simulating Gaussian Mixtures

Use the method `random` of the `gmdistribution` class to generate random data from a Gaussian mixture model created with `gmdistribution` or `fit`.

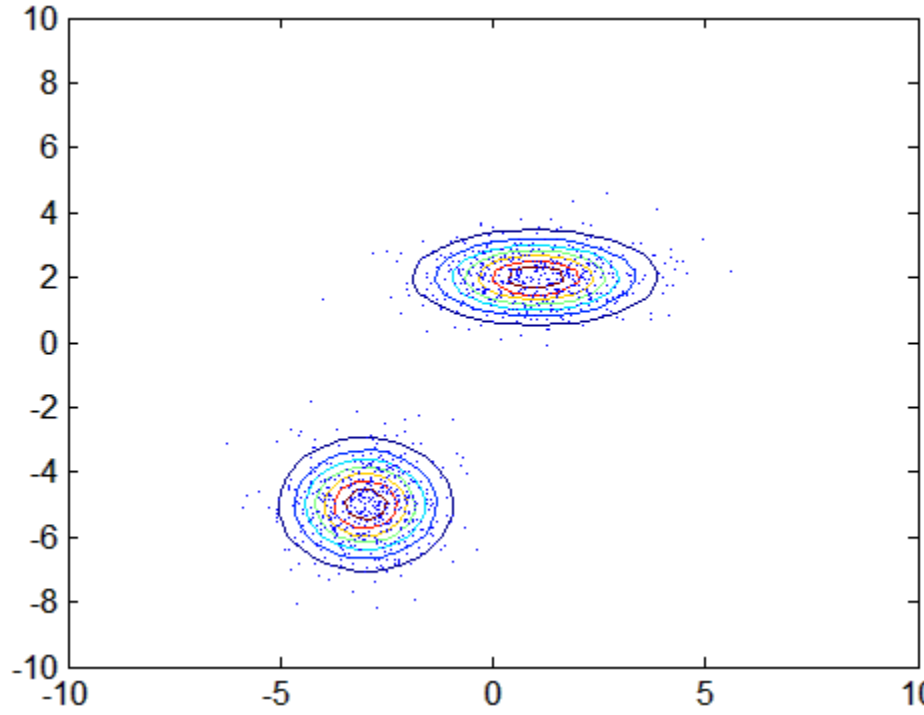
For example, the following specifies a `gmdistribution` object consisting of a two-component mixture of bivariate Gaussian distributions:

```
MU = [1 2;-3 -5];
SIGMA = cat(3,[2 0;0 .5],[1 0;0 1]);
p = ones(1,2)/2;
obj = gmdistribution(MU,SIGMA,p);

ezcontour(@(x,y)pdf(obj,[x y]),[-10 10],[-10 10])
hold on
```



Use `random (gmdistribution)` to generate 1000 random values:

```
Y = random(obj,1000);

scatter(Y(:,1),Y(:,2),10,'.')
```



Copulas

Copulas are functions that describe dependencies among variables, and provide a way to create distributions that model correlated multivariate data. Using a copula, you can construct a multivariate distribution by specifying marginal univariate distributions, and then choose a copula to provide a correlation structure between variables. Bivariate distributions, as well as distributions in higher dimensions, are possible.

Determining Dependence Between Simulation Inputs

One of the design decisions for a Monte Carlo simulation is a choice of probability distributions for the random inputs. Selecting a distribution for each individual variable is often straightforward, but deciding what dependencies should exist between the inputs may not be. Ideally, input data to a simulation should reflect what you know about dependence among the real quantities you are modeling. However, there may be little or no information on which to base any dependence in the simulation. In such cases, it is useful to experiment with different possibilities in order to determine the model's sensitivity.

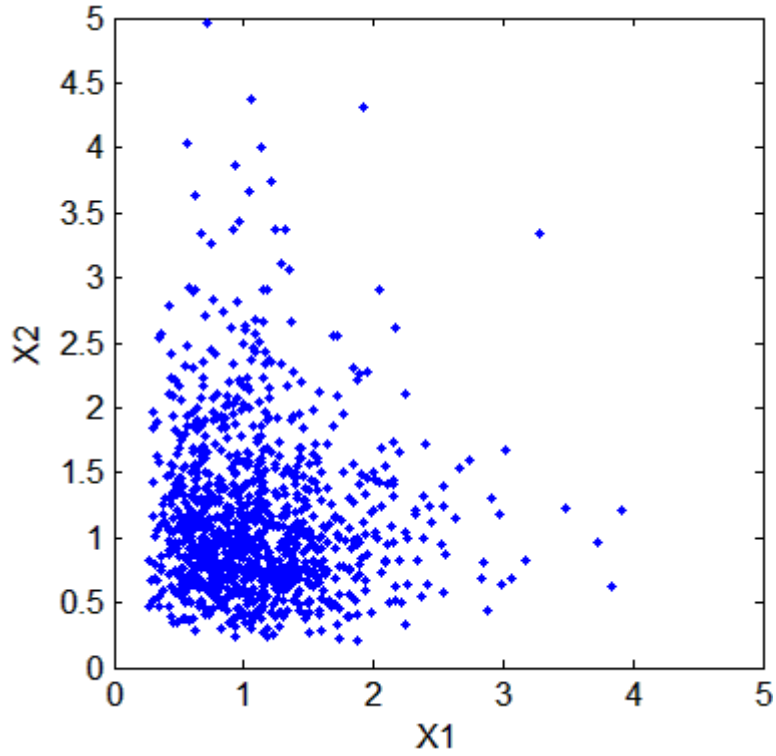
It can be difficult to generate random inputs with dependence when they have distributions that are not from a standard multivariate distribution. Further, some of the standard multivariate distributions can model only limited types of dependence. It is always possible to make the inputs independent, and while that is a simple choice, it is not always sensible and can lead to the wrong conclusions.

For example, a Monte-Carlo simulation of financial risk could have two random inputs that represent different sources of insurance losses. You could model these inputs as lognormal random variables. A reasonable question to ask is how dependence between these two inputs affects the results of the simulation. Indeed, you might know from real data that the same random conditions affect both sources; ignoring that in the simulation could lead to the wrong conclusions.

Example: Generate and Exponentiate Normal Random Variables.

The `lognrnd` function simulates independent lognormal random variables. In the following example, the `mvnrnd` function generates `n` pairs of independent normal random variables, and then exponentiates them. Notice that the covariance matrix used here is diagonal:

```
n = 1000;

sigma = .5;
SigmaInd = sigma.^2 .* [1 0; 0 1]
SigmaInd =
         0.25            0
            0         0.25
ZInd = mvnrnd([0 0],SigmaInd,n);
XInd = exp(ZInd);

plot(XInd(:,1),XInd(:,2),'.')
axis([0 5 0 5])
axis equal
xlabel('X1')
ylabel('X2')
```

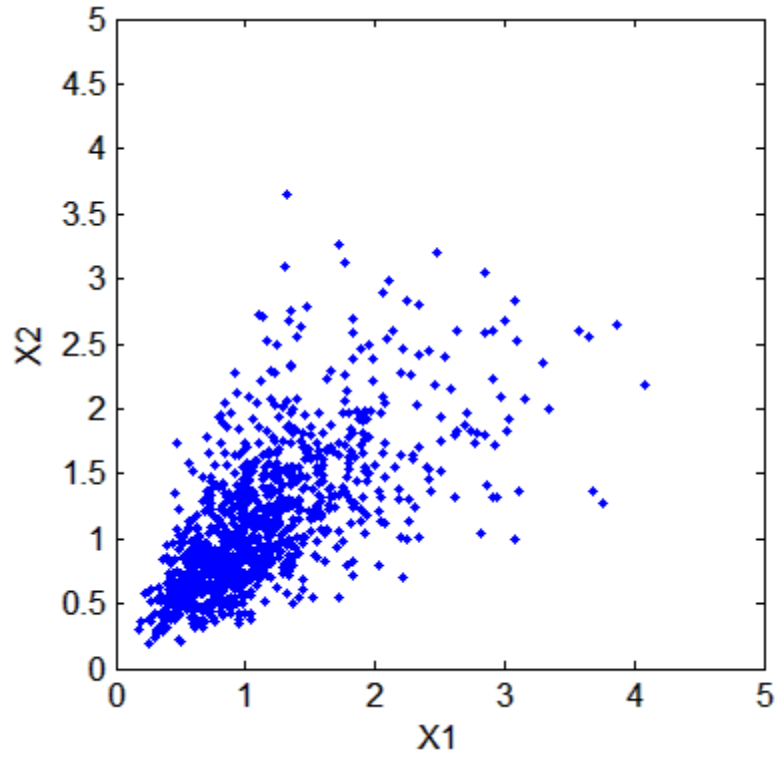


Dependent bivariate lognormal random variables are also easy to generate using a covariance matrix with nonzero off-diagonal terms:

```
rho = .7;

SigmaDep = sigma.^2 .* [1 rho; rho 1]
SigmaDep =
          0.25        0.175
         0.175         0.25

ZDep = mvnrnd([0 0],SigmaDep,n);
XDep = exp(ZDep);
```

A second scatter plot demonstrates the difference between these two bivariate distributions:

```
plot(XDep(:,1),XDep(:,2),'.')
axis([0 5 0 5])
axis equal
xlabel('X1')
ylabel('X2')
```



It is clear that there is a tendency in the second data set for large values of `X1` to be associated with large values of `X2`, and similarly for small values. The correlation parameter, ρ, of the underlying bivariate normal determines this dependence. The conclusions drawn from the simulation could well depend on whether you generate `X1` and `X2` with dependence. The bivariate lognormal distribution is a simple solution in this case; it easily generalizes to higher dimensions in cases where the marginal distributions are different lognormals.

Other multivariate distributions also exist. For example, the multivariate t and the Dirichlet distributions simulate dependent t and beta random variables, respectively. But the list of simple multivariate distributions is not long, and they only apply in cases where the marginals are all in the same family (or even the exact same distributions). This can be a serious limitation in many situations.

Constructing Dependent Bivariate Distributions

Although the construction discussed in the previous section creates a bivariate lognormal that is simple, it serves to illustrate a method that is more generally applicable.

1. Generate pairs of values from a bivariate normal distribution. There is statistical dependence between these two variables, and each has a normal marginal distribution.

2. Apply a transformation (the exponential function) separately to each variable, changing the marginal distributions into lognormals. The transformed variables still have a statistical dependence.

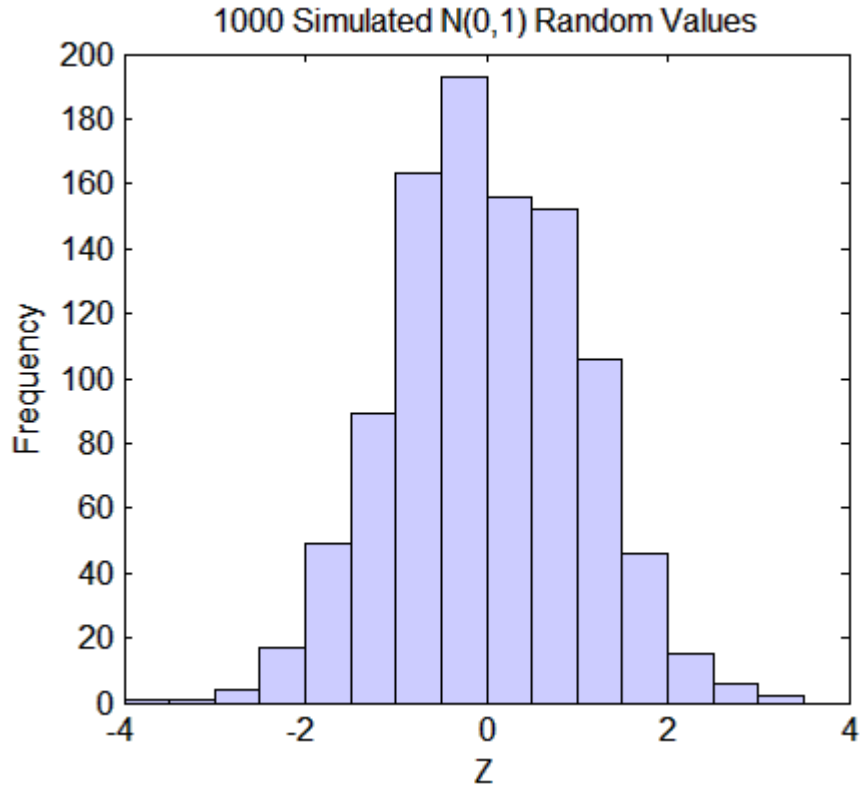
If a suitable transformation can be found, this method can be generalized to create dependent bivariate random vectors with other marginal distributions. In fact, a general method of constructing such a transformation does exist, although it is not as simple as exponentiation alone.

By definition, applying the normal cumulative distribution function (cdf), denoted here by Φ, to a standard normal random variable results in a random variable that is uniform on the interval [0,1]. To see this, if Z has a standard normal distribution, then the cdf of $U = \Phi(Z)$ is

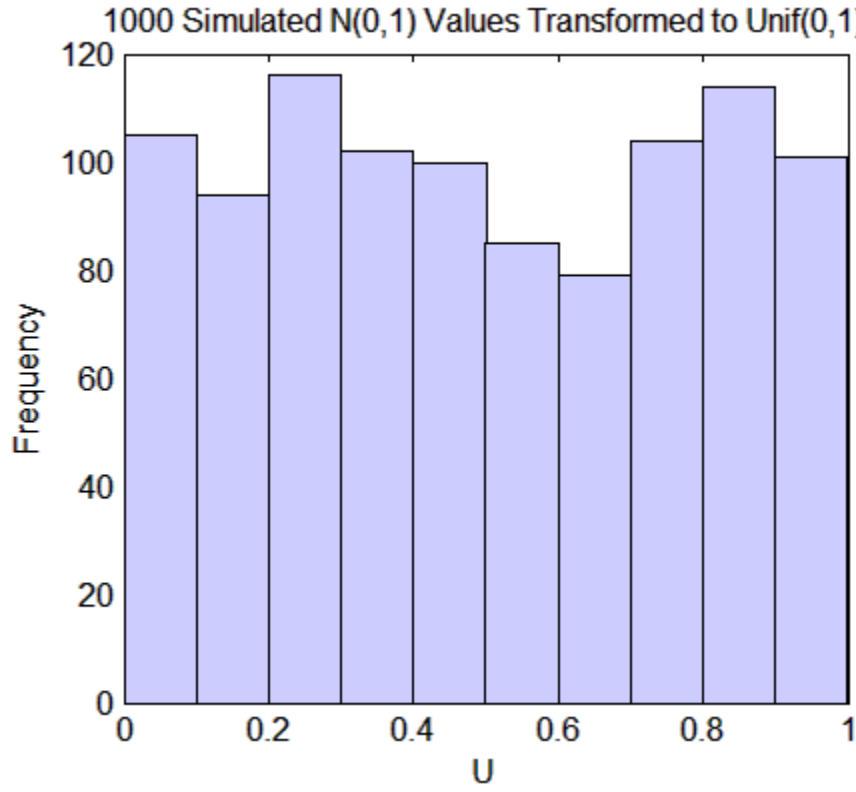
$$\Pr\{U \le u\} = \Pr\{\Phi(Z) \le u\} = \Pr(Z \le \Phi^{-1}(u)\} = u$$

and that is the cdf of a Unif(0,1) random variable. Histograms of some simulated normal and transformed values demonstrate that fact:

```
n = 1000;
z = normrnd(0,1,n,1);

hist(z,-3.75:.5:3.75)
xlim([-4 4])
title('1000 Simulated N(0,1) Random Values')
xlabel('Z')
ylabel('Frequency')
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
```

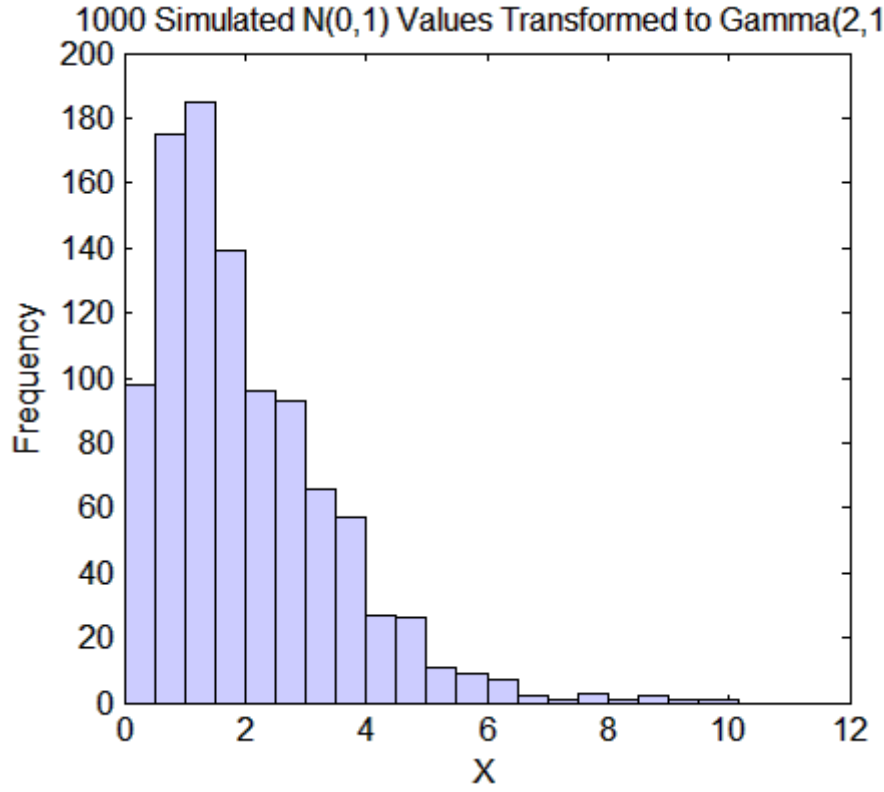



```
u = normcdf(z);

hist(u,.05:.1:.95)
title('1000 Simulated N(0,1) Values Transformed to Unif(0,1)')
xlabel('U')
ylabel('Frequency')
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
```



Borrowing from the theory of univariate random number generation, applying the inverse cdf of any distribution, *F*, to a Unif(0,1) random variable results in a random variable whose distribution is exactly *F* (see "Inversion Methods" on page 6-7). The proof is essentially the opposite of the preceding proof for the forward case. Another histogram illustrates the transformation to a gamma distribution:

```
x = gaminv(u,2,1);

hist(x,.25:.5:9.75)
title('1000 Simulated N(0,1) Values Transformed to Gamma(2,1)')
xlabel('X')
ylabel('Frequency')
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
```



You can apply this two-step transformation to each variable of a standard bivariate normal, creating dependent random variables with arbitrary marginal distributions. Because the transformation works on each component separately, the two resulting random variables need not even have the same marginal distributions. The transformation is defined as:

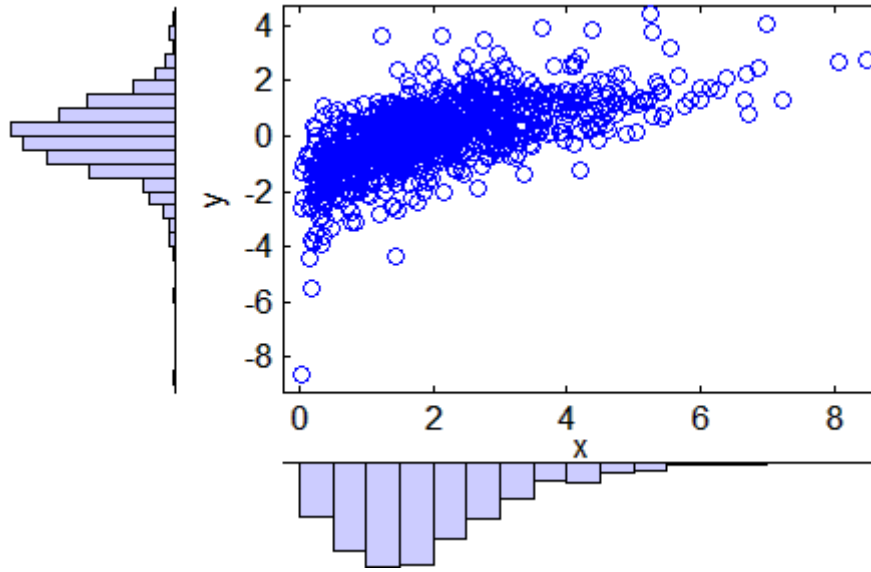
$$Z = [Z_1, Z_2] \sim N\left([0,0], \begin{bmatrix} 1 & \rho \\ \rho & 1 \end{bmatrix}\right)$$

$$U = \left[\Phi(Z_1), \Phi(Z_2)\right]$$

$$X = \left[G_1(U_1), G_2(U_2)\right]$$

where G_1 and G_2 are inverse cdfs of two possibly different distributions. For example, the following generates random vectors from a bivariate distribution with t_5 and Gamma(2,1) marginals:

```
n = 1000; rho = .7;
Z = mvnrnd([0 0],[1 rho; rho 1],n);
U = normcdf(Z);
X = [gaminv(U(:,1),2,1) tinv(U(:,2),5)];

scatterhist(X(:,1),X(:,2),'Direction','out')
```



This plot has histograms alongside a scatter plot to show both the marginal distributions, and the dependence.

Using Rank Correlation Coefficients

The correlation parameter, ρ, of the underlying bivariate normal determines the dependence between `X1` and `X2` in this construction. However, the linear correlation of `X1` and `X2` is not ρ. For example, in the original lognormal case, a closed form for that correlation is:

$$cor(X1, X2) = \frac{e^{\rho\sigma^2} - 1}{e^{\sigma^2} - 1}$$

which is strictly less than ρ, unless ρ is exactly 1. In more general cases such as the Gamma/t construction, the linear correlation between `X1` and `X2` is difficult or impossible to express in terms of ρ, but simulations show that the same effect happens.

That is because the linear correlation coefficient expresses the linear dependence between random variables, and when nonlinear transformations are applied to those random variables, linear correlation is not preserved. Instead, a rank correlation coefficient, such as Kendall's τ or Spearman's ρ, is more appropriate.

Roughly speaking, these rank correlations measure the degree to which large or small values of one random variable associate with large or small values of another. However, unlike the linear correlation coefficient, they measure the association only in terms of ranks. As a consequence, the rank correlation is preserved under any monotonic transformation. In particular, the transformation method just described preserves the rank correlation. Therefore, knowing the rank correlation of the bivariate normal Z exactly determines the rank correlation of the final transformed random variables, X. While the linear correlation coefficient, ρ, is still needed to parameterize the underlying bivariate normal, Kendall's τ or Spearman's ρ are more useful in describing the dependence between random variables, because they are invariant to the choice of marginal distribution.

For the bivariate normal, there is a simple one-to-one mapping between Kendall's τ or Spearman's ρ, and the linear correlation coefficient ρ:

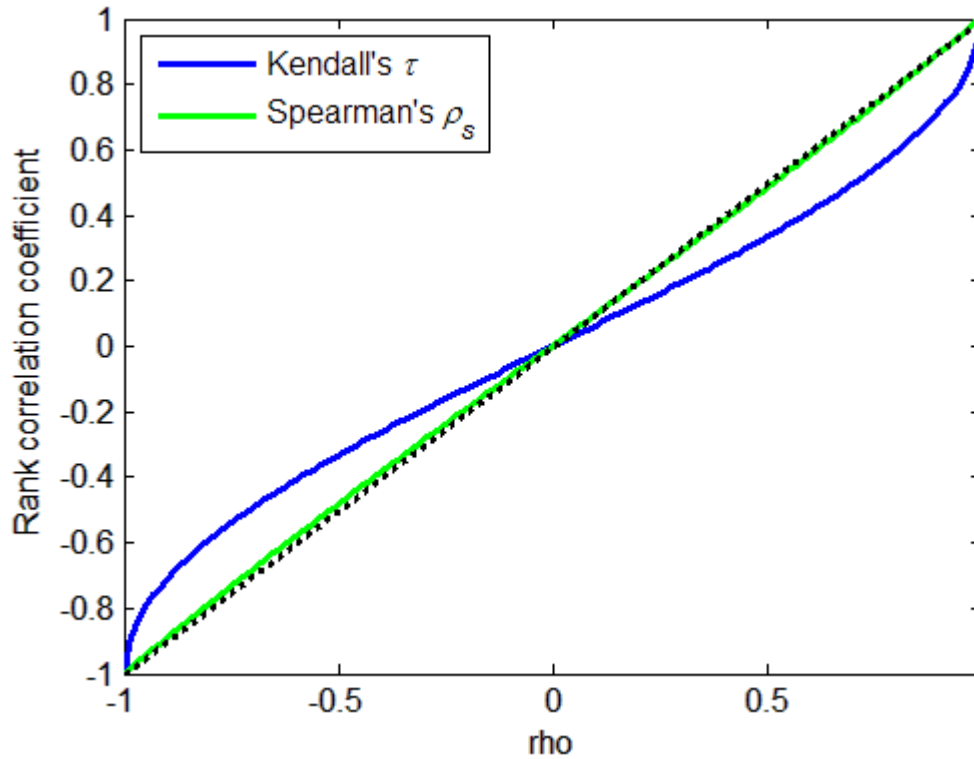
$$\tau = \frac{2}{\pi}\arcsin(\rho) \quad \text{or} \quad \rho = \sin\left(\tau\frac{\pi}{2}\right)$$

$$\rho_s = \frac{6}{\pi}\arcsin\left(\frac{\rho}{2}\right) \text{ or } \quad \rho = 2\sin\left(\rho_s\frac{\pi}{6}\right)$$

The following plot shows the relationship:

```
rho = -1:.01:1;
```

```
tau = 2.*asin(rho)./pi;
rho_s = 6.*asin(rho./2)./pi;

plot(rho,tau,'b-','LineWidth',2)
hold on
plot(rho,rho_s,'g-','LineWidth',2)
plot([-1 1],[-1 1],'k:','LineWidth',2)
axis([-1 1 -1 1])
xlabel('rho')
ylabel('Rank correlation coefficient')
legend('Kendall''s {\it\tau}', ...
       'Spearman''s {\it\rho_s}', ...
       'location','NW')
```



Thus, it is easy to create the desired rank correlation between `X1` and `X2`, regardless of their marginal distributions, by choosing the correct ρ parameter value for the linear correlation between `Z1` and `Z2`.

For the multivariate normal distribution, Spearman's rank correlation is almost identical to the linear correlation. However, this is not true once you transform to the final random variables.

Using Bivariate Copulas

The first step of the construction described in the previous section defines what is known as a bivariate Gaussian copula. A copula is a multivariate probability distribution, where each random variable has a uniform marginal distribution on the unit interval [0,1]. These variables may be completely independent, deterministically related (e.g., `U2 = U1`), or anything in between. Because of the possibility for dependence among variables, you can use a copula to construct a new multivariate distribution for dependent variables. By transforming each of the variables in the copula separately using the inversion method, possibly using different cdfs, the resulting distribution can have arbitrary marginal distributions. Such multivariate distributions are often useful in simulations, when you know that the different random inputs are not independent of each other.

Statistics Toolbox functions compute:

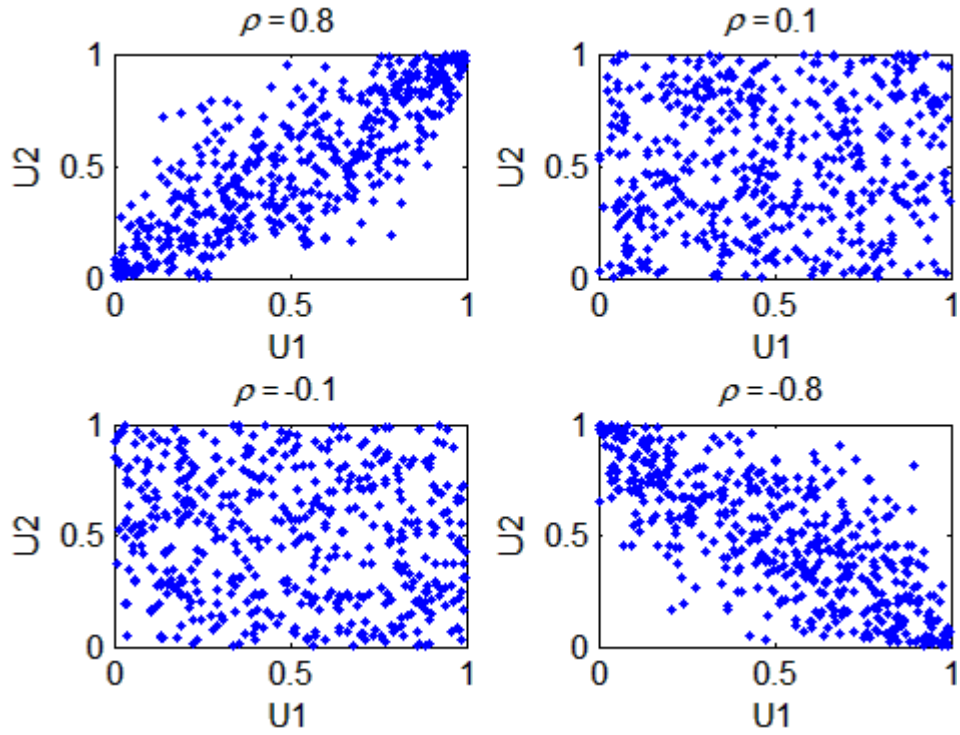
- Probability density functions (`copulapdf`) and the cumulative distribution functions (`copulacdf`) for Gaussian copulas
- Rank correlations from linear correlations (`copulastat`) and vice versa (`copulaparam`)
- Random vectors (`copularnd`)
- Parameters for copulas fit to data (`copulafit`)

For example, use the `copularnd` function to create scatter plots of random values from a bivariate Gaussian copula for various levels of ρ, to illustrate the range of different dependence structures. The family of bivariate Gaussian copulas is parameterized by the linear correlation matrix:

$$P = \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix}$$

`U1` and `U2` approach linear dependence as ρ approaches ±1, and approach complete independence as ρ approaches zero:

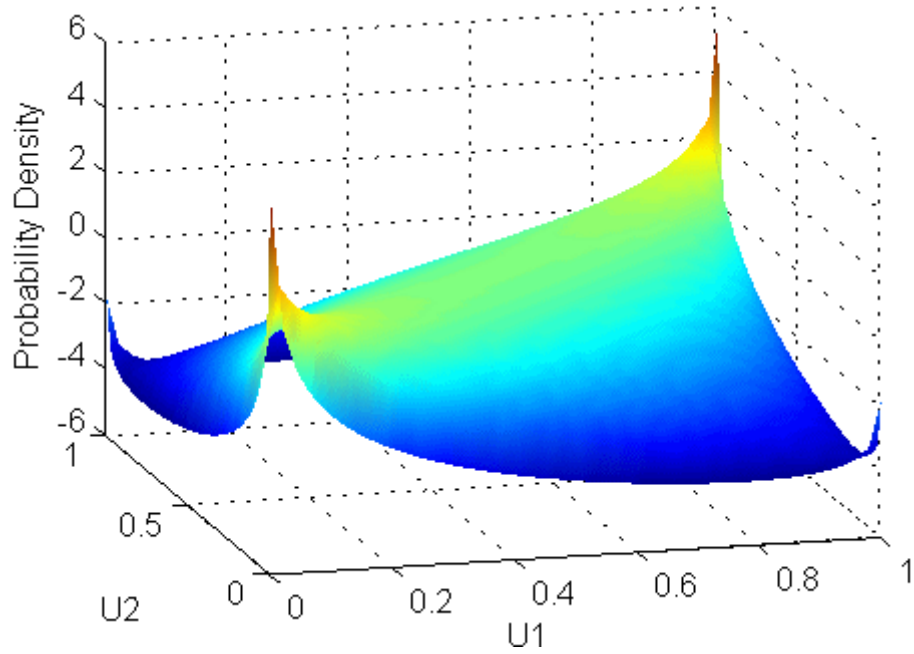
```
n = 500;

U = copularnd('Gaussian',[1 .8; .8 1],n);
subplot(2,2,1)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = 0.8')
xlabel('U1')
ylabel('U2')

U = copularnd('Gaussian',[1 .1; .1 1],n);
subplot(2,2,2)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = 0.1')
xlabel('U1')
ylabel('U2')

U = copularnd('Gaussian',[1 -.1; -.1 1],n);
subplot(2,2,3)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = -0.1')
xlabel('U1')
ylabel('U2')

U = copularnd('Gaussian',[1 -.8; -.8 1],n);
subplot(2,2,4)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = -0.8')
xlabel('U1')
ylabel('U2')
```



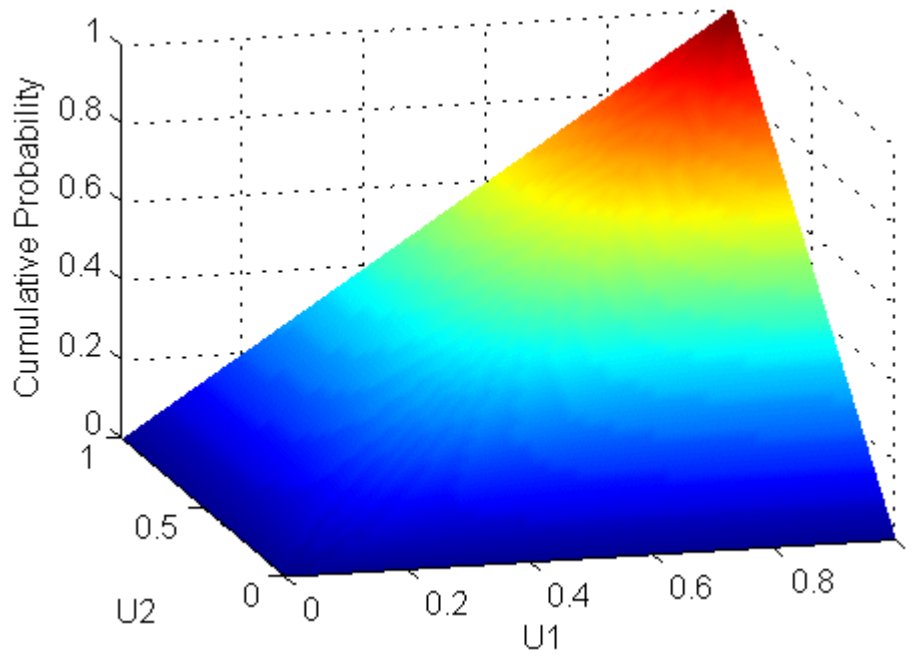
The dependence between `U1` and `U2` is completely separate from the marginal distributions of `X1 = G(U1)` and `X2 = G(U2)`. `X1` and `X2` can be given any marginal distributions, and still have the same rank correlation. This is one of the main appeals of copulas—they allow this separate specification of dependence and marginal distribution. You can also compute the pdf (`copulapdf`) and the cdf (`copulacdf`) for a copula. For example, these plots show the pdf and cdf for ρ = .8:

```
u1 = linspace(1e-3,1-1e-3,50);
u2 = linspace(1e-3,1-1e-3,50);
[U1,U2] = meshgrid(u1,u2);
Rho = [1 .8; .8 1];
f = copulapdf('t',[U1(:) U2(:)],Rho,5);
f = reshape(f,size(U1));

surf(u1,u2,log(f),'FaceColor','interp','EdgeColor','none')
```

```
view([-15,20])
xlabel('U1')
ylabel('U2')
zlabel('Probability Density')
```




```
u1 = linspace(1e-3,1-1e-3,50);
u2 = linspace(1e-3,1-1e-3,50);
[U1,U2] = meshgrid(u1,u2);
F = copulacdf('t',[U1(:) U2(:)],Rho,5);
F = reshape(F,size(U1));

surf(u1,u2,F,'FaceColor','interp','EdgeColor','none')
view([-15,20])
xlabel('U1')
ylabel('U2')
zlabel('Cumulative Probability')
```



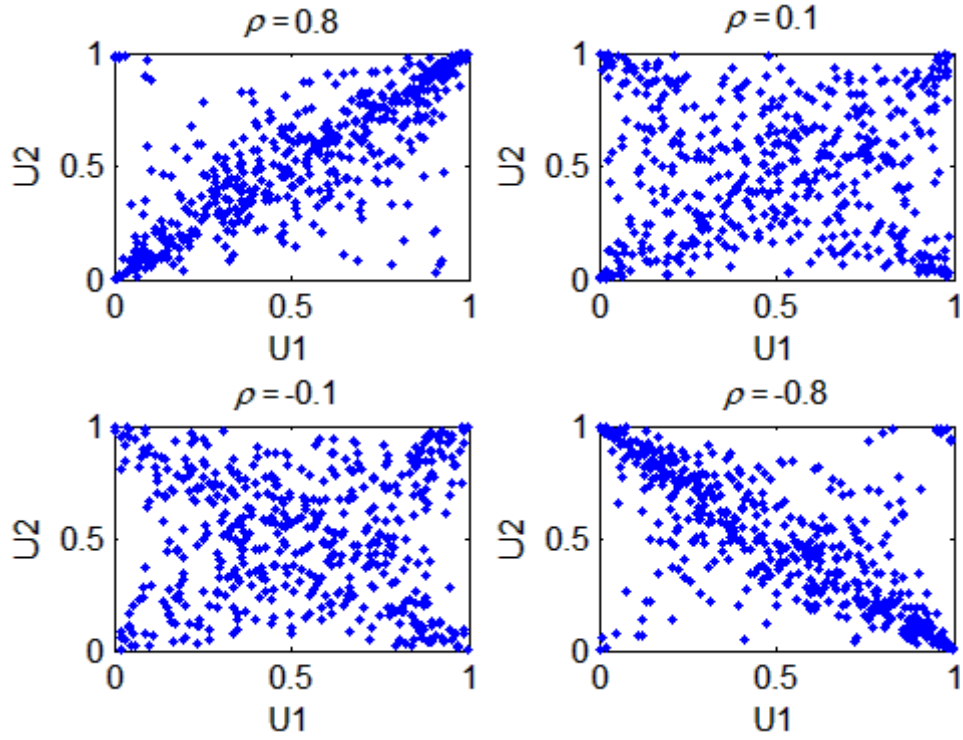
A different family of copulas can be constructed by starting from a bivariate t distribution and transforming using the corresponding t cdf. The bivariate t distribution is parameterized with P, the linear correlation matrix, and ν, the degrees of freedom. Thus, for example, you can speak of a t_1 or a t_5 copula, based on the multivariate t with one and five degrees of freedom, respectively.

Just as for Gaussian copulas, Statistics Toolbox functions for t copulas compute:

- Probability density functions (`copulapdf`) and the cumulative distribution functions (`copulacdf`) for Gaussian copulas
- Rank correlations from linear correlations (`copulastat`) and vice versa (`copulaparam`)
- Random vectors (`copularnd`)
- Parameters for copulas fit to data (`copulafit`)

For example, use the `copularnd` function to create scatter plots of random values from a bivariate t_1 copula for various levels of ρ, to illustrate the range of different dependence structures:

```
n = 500;
nu = 1;

U = copularnd('t',[1 .8; .8 1],nu,n);
subplot(2,2,1)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = 0.8')
xlabel('U1')
ylabel('U2')

U = copularnd('t',[1 .1; .1 1],nu,n);
subplot(2,2,2)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = 0.1')
xlabel('U1')
ylabel('U2')

U = copularnd('t',[1 -.1; -.1 1],nu,n);
subplot(2,2,3)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = -0.1')
xlabel('U1')
ylabel('U2')

U = copularnd('t',[1 -.8; -.8 1],nu, n);
subplot(2,2,4)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = -0.8')
xlabel('U1')
ylabel('U2')
```

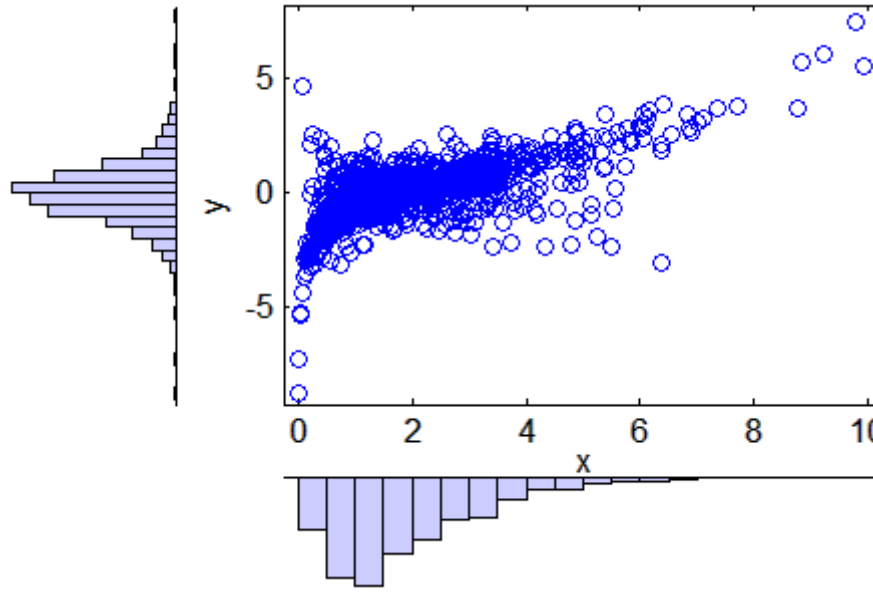


A t copula has uniform marginal distributions for `U1` and `U2`, just as a Gaussian copula does. The rank correlation τ or ρ_s between components in a t copula is also the same function of ρ as for a Gaussian. However, as these plots demonstrate, a t_1 copula differs quite a bit from a Gaussian copula, even when their components have the same rank correlation. The difference is in their dependence structure. Not surprisingly, as the degrees of freedom parameter ν is made larger, a t_ν copula approaches the corresponding Gaussian copula.

As with a Gaussian copula, any marginal distributions can be imposed over a t copula. For example, using a t copula with 1 degree of freedom, you can again generate random vectors from a bivariate distribution with Gamma(2,1) and t_5 marginals using `copularnd`:

```
n = 1000;
rho = .7;
nu = 1;
```

```
U = copularnd('t',[1 rho; rho 1],nu,n);
X = [gaminv(U(:,1),2,1) tinv(U(:,2),5)];

scatterhist(X(:,1),X(:,2),'Direction','out')
```

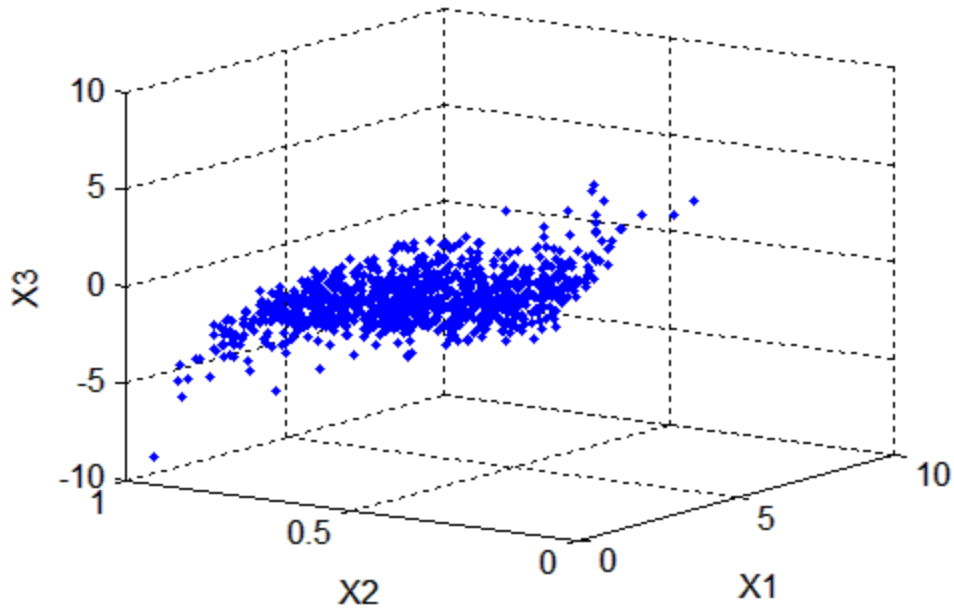


Compared to the bivariate Gamma/*t* distribution constructed earlier, which was based on a Gaussian copula, the distribution constructed here, based on a t_1 copula, has the same marginal distributions and the same rank correlation between variables but a very different dependence structure. This illustrates the fact that multivariate distributions are not uniquely defined by their marginal distributions, or by their correlations. The choice of a particular copula in an application may be based on actual observed data, or different copulas may be used as a way of determining the sensitivity of simulation results to the input distribution.

Higher Dimension Copulas

The Gaussian and *t* copulas are known as elliptical copulas. It is easy to generalize elliptical copulas to a higher number of dimensions. For example, simulate data from a trivariate distribution with Gamma(2,1), Beta(2,2), and t_5 marginals using a Gaussian copula and `copularnd`, as follows:

```
n = 1000;
Rho = [1 .4 .2; .4 1 -.8; .2 -.8 1];
U = copularnd('Gaussian',Rho,n);
X = [gaminv(U(:,1),2,1) betainv(U(:,2),2,2) tinv(U(:,3),5)];

subplot(1,1,1)
plot3(X(:,1),X(:,2),X(:,3),'.')
grid on
view([-55, 15])
xlabel('X1')
ylabel('X2')
zlabel('X3')
```



Notice that the relationship between the linear correlation parameter ρ and, for example, Kendall's τ, holds for each entry in the correlation matrix P used here. You can verify that the sample rank correlations of the data are approximately equal to the theoretical values:

```
tauTheoretical = 2.*asin(Rho)./pi
tauTheoretical =
```

```
            1      0.26198      0.12819
      0.26198            1     -0.59033
      0.12819     -0.59033            1

tauSample = corr(X,'type','Kendall')
tauSample =
            1      0.27254      0.12701
      0.27254            1     -0.58182
      0.12701     -0.58182            1
```

Archimedean Copulas

Statistics Toolbox functions are available for three bivariate Archimedean copula families:

- Clayton copulas
- Frank copulas
- Gumbel copulas

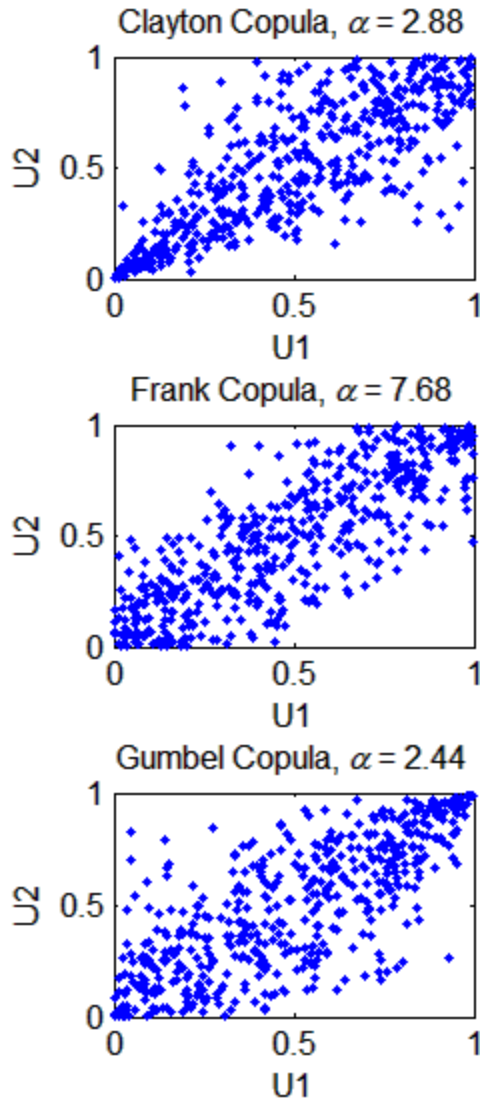
These are one-parameter families that are defined directly in terms of their cdfs, rather than being defined constructively using a standard multivariate distribution.

To compare these three Archimedean copulas to the Gaussian and *t* bivariate copulas, first use the `copulastat` function to find the rank correlation for a Gaussian or *t* copula with linear correlation parameter of 0.8, and then use the `copulaparam` function to find the Clayton copula parameter that corresponds to that rank correlation:

```
tau = copulastat('Gaussian',.8 ,'type','kendall')
tau =
      0.59033

alpha = copulaparam('Clayton',tau,'type','kendall')
alpha =
        2.882
```

Finally, plot a random sample from the Clayton copula with `copularnd`. Repeat the same procedure for the Frank and Gumbel copulas:

```
n = 500;

U = copularnd('Clayton',alpha,n);
subplot(3,1,1)
plot(U(:,1),U(:,2),'.');
title(['Clayton Copula, {\it\alpha} = ',sprintf('%0.2f',alpha)])
xlabel('U1')
ylabel('U2')

alpha = copulaparam('Frank',tau,'type','kendall');
U = copularnd('Frank',alpha,n);
subplot(3,1,2)
plot(U(:,1),U(:,2),'.')
title(['Frank Copula, {\it\alpha} = ',sprintf('%0.2f',alpha)])
xlabel('U1')
ylabel('U2')

alpha = copulaparam('Gumbel',tau,'type','kendall');
U = copularnd('Gumbel',alpha,n);
subplot(3,1,3)
plot(U(:,1),U(:,2),'.')
title(['Gumbel Copula, {\it\alpha} = ',sprintf('%0.2f',alpha)])
xlabel('U1')
ylabel('U2')
```



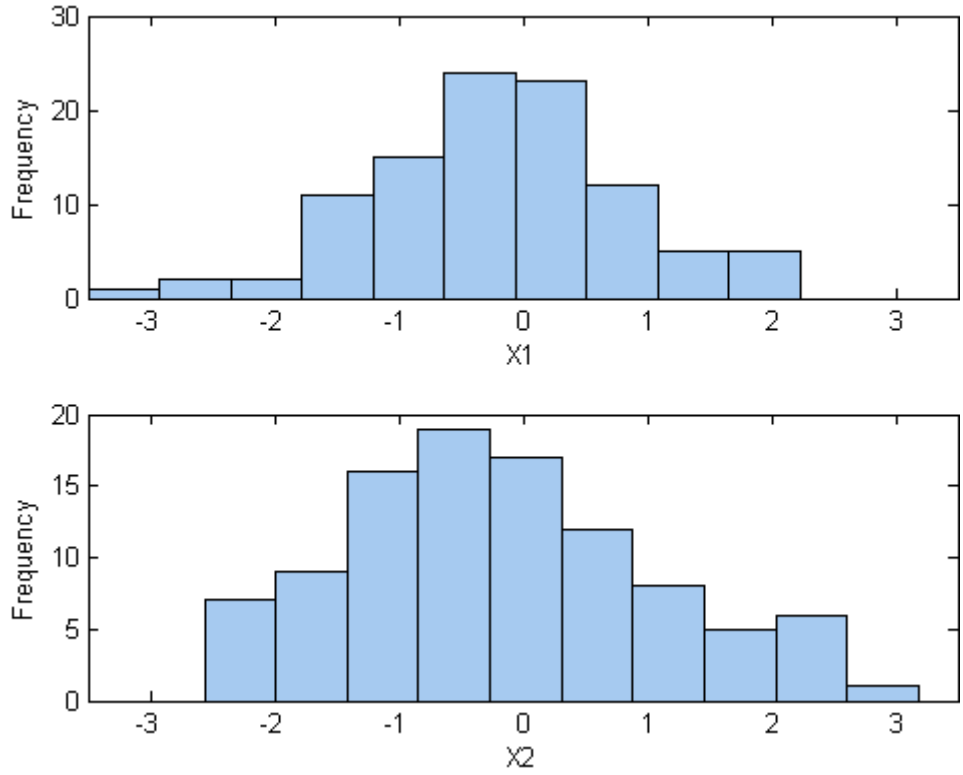
Simulating Dependent Multivariate Data Using Copulas

To simulate dependent multivariate data using a copula, you must specify each of the following:

- The copula family (and any shape parameters)
- The rank correlations among variables
- Marginal distributions for each variable

Suppose you have return data for two stocks and want to run a Monte Carlo simulation with inputs that follow the same distributions as the data:

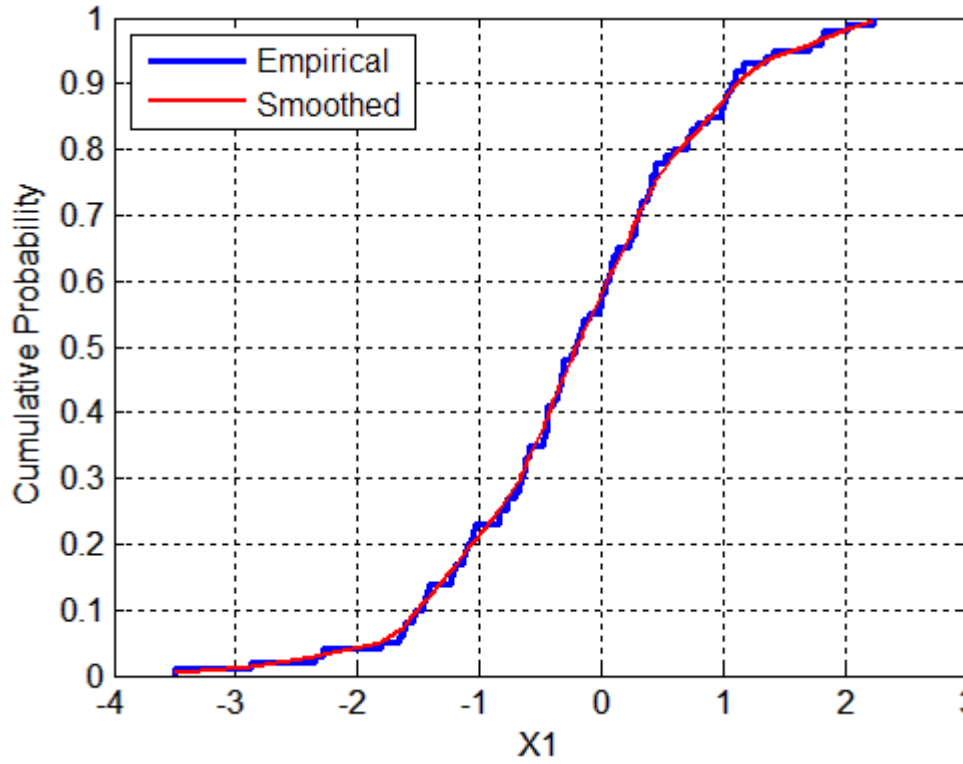
```
load stockreturns
nobs = size(stocks,1);

subplot(2,1,1)
hist(stocks(:,1),10)
xlim([-3.5 3.5])
xlabel('X1')
ylabel('Frequency')
set(get(gca,'Children'),'FaceColor',[.8 .8 1])

subplot(2,1,2)
hist(stocks(:,2),10)
xlim([-3.5 3.5])
xlabel('X2')
ylabel('Frequency')
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
```



You could fit a parametric model separately to each dataset, and use those estimates as the marginal distributions. However, a parametric model may not be sufficiently flexible. Instead, you can use a nonparametric model to transform to the marginal distributions. All that is needed is a way to compute the inverse cdf for the nonparametric model.

The simplest nonparametric model is the empirical cdf, as computed by the `ecdf` function. For a discrete marginal distribution, this is appropriate. However, for a continuous distribution, use a model that is smoother than the step function computed by `ecdf`. One way to do that is to estimate the empirical cdf and interpolate between the midpoints of the steps with a piecewise linear function. Another way is to use kernel smoothing with `ksdensity`. For example, compare the empirical cdf to a kernel smoothed cdf estimate for the first variable:

```
[Fi,xi] = ecdf(stocks(:,1));

stairs(xi,Fi,'b','LineWidth',2)
hold on

Fi_sm = ksdensity(stocks(:,1),xi,'function','cdf','width',.15);

plot(xi,Fi_sm,'r-','LineWidth',1.5)
xlabel('X1')
ylabel('Cumulative Probability')
legend('Empirical','Smoothed','Location','NW')
grid on
```



For the simulation, experiment with different copulas and correlations. Here, you will use a bivariate *t* copula with a fairly small degrees of freedom

parameter. For the correlation parameter, you can compute the rank correlation of the data, and then find the corresponding linear correlation parameter for the *t* copula using `copulaparam`:

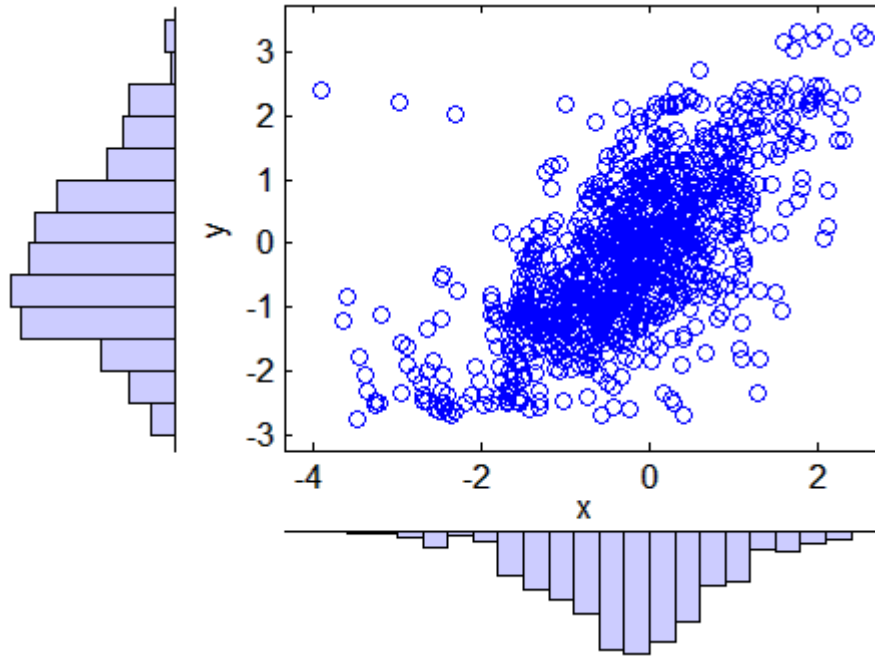
```
nu = 5;

tau = corr(stocks(:,1),stocks(:,2),'type','kendall')
tau =
      0.51798

rho = copulaparam('t', tau, nu, 'type','kendall')
rho =
      0.72679
```

Next, use `copularnd` to generate random values from the *t* copula and transform using the nonparametric inverse cdfs. The `ksdensity` function allows you to make a kernel estimate of distribution and evaluate the inverse cdf at the copula points all in one step:

```
n = 1000;

U = copularnd('t',[1 rho; rho 1],nu,n);
X1 = ksdensity(stocks(:,1),U(:,1),...
               'function','icdf','width',.15);
X2 = ksdensity(stocks(:,2),U(:,2),...
               'function','icdf','width',.15);
```

Alternatively, when you have a large amount of data or need to simulate more than one set of values, it may be more efficient to compute the inverse cdf over a grid of values in the interval (0,1) and use interpolation to evaluate it at the copula points:

```
p = linspace(0.00001,0.99999,1000);
G1 = ksdensity(stocks(:,1),p,'function','icdf','width',0.15);
X1 = interp1(p,G1,U(:,1),'spline');
G2 = ksdensity(stocks(:,2),p,'function','icdf','width',0.15);
X2 = interp1(p,G2,U(:,2),'spline');

scatterhist(X1,X2,'Direction','out')
```



The marginal histograms of the simulated data are a smoothed version of the histograms for the original data. The amount of smoothing is controlled by the bandwidth input to `ksdensity`.

Example: Fitting Copulas to Data

The `copulafit` function is used to calibrate copulas with data. To generate data `Xsim` with a distribution "just like" (in terms of marginal distributions and correlations) the distribution of data in the matrix `X`:

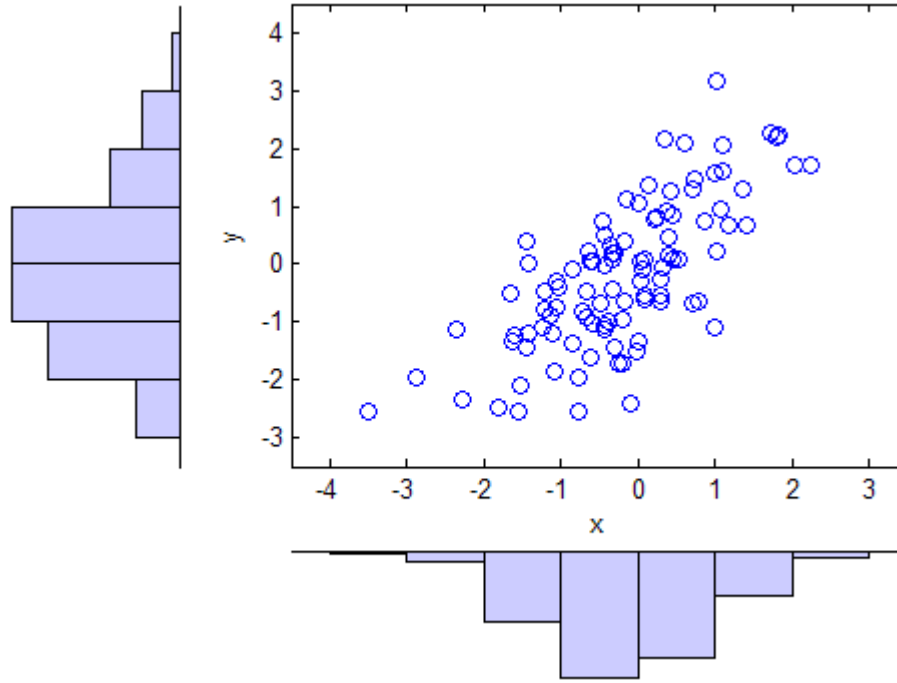
1. Fit marginal distributions to the columns of `X`.
2. Use appropriate cdf functions to transform `X` to `U`, so that `U` has values between `0` and `1`.
3. Use `copulafit` to fit a copula to `U`.
4. Generate new data `Usim` from the copula.

5 Use appropriate inverse cdf functions to transform `Usim` to `Xsim`.

The following example illustrates the procedure.

Load and plot simulated stock return data:

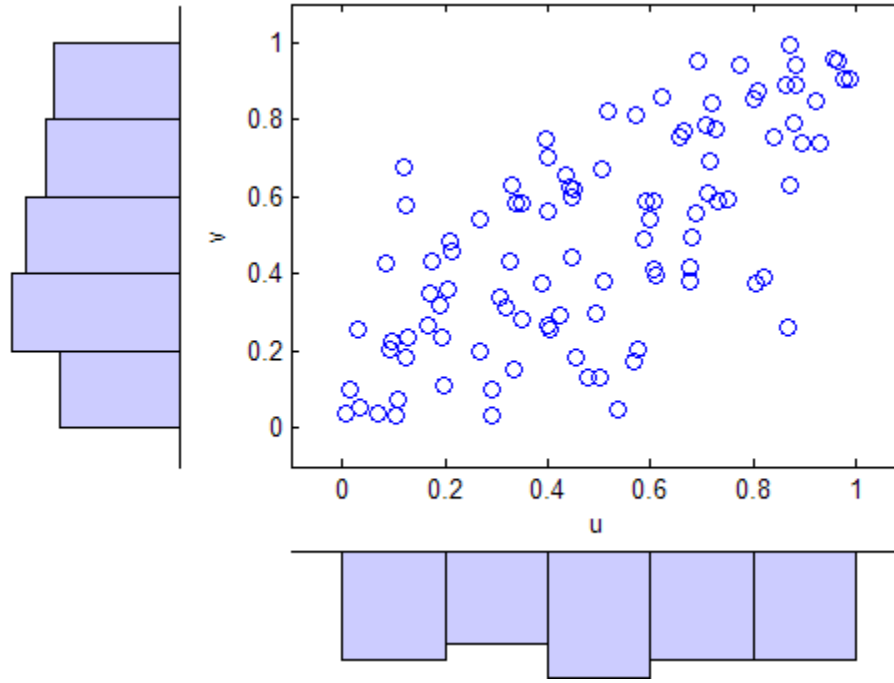
```
load stockreturns
x = stocks(:,1);
y = stocks(:,2);

scatterhist(x,y,'Direction','out')
```



Transform the data to the copula scale (unit square) using a kernel estimator of the cumulative distribution function:

```
u = ksdensity(x,x,'function','cdf');
v = ksdensity(y,y,'function','cdf');
```

```
scatterhist(u,v,'Direction','out')
xlabel('u')
ylabel('v')
```



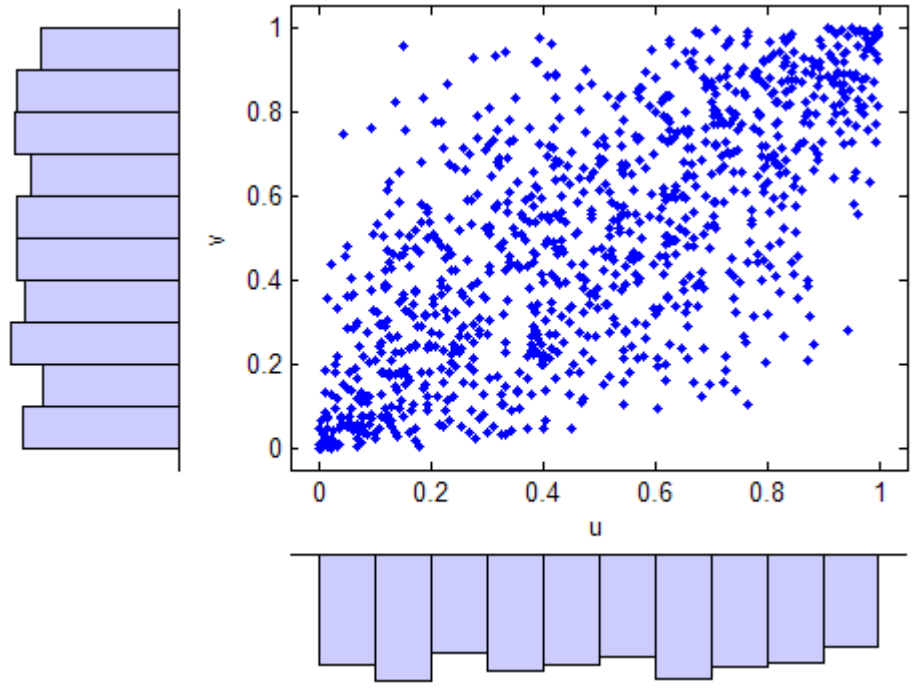
Fit a *t* copula:

```
[Rho,nu] = copulafit('t',[u v],'Method','ApproximateML')
Rho =
    1.0000    0.7220
    0.7220    1.0000
nu =
  3.2017e+006
```

Generate a random sample from the *t* copula:

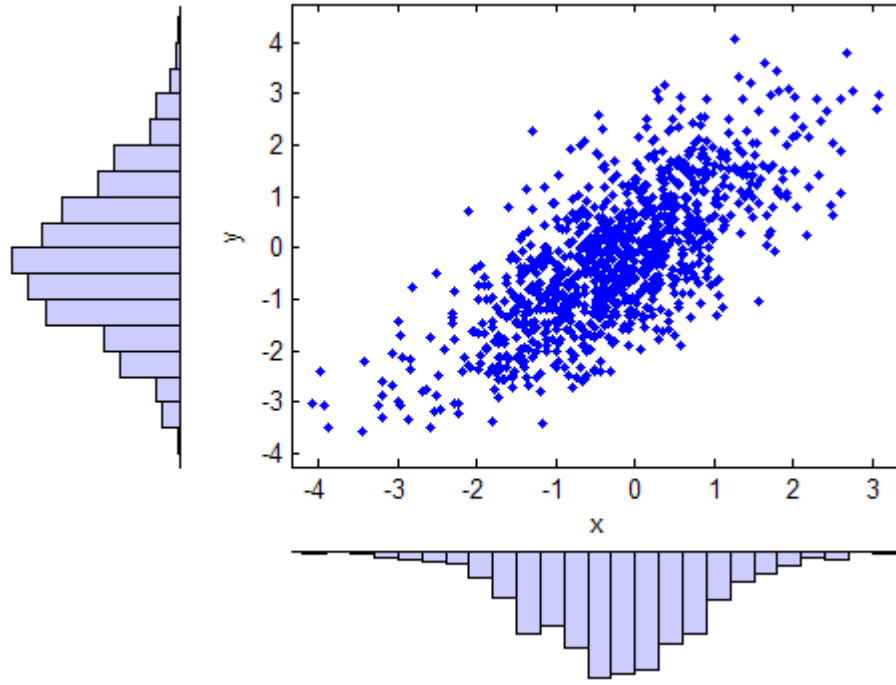
```
r = copularnd('t',Rho,nu,1000);
u1 = r(:,1);
v1 = r(:,2);
```

```
scatterhist(u1,v1,'Direction','out')
xlabel('u')
ylabel('v')
set(get(gca,'children'),'marker','.')
```



Transform the random sample back to the original scale of the data:

```
x1 = ksdensity(x,u1,'function','icdf');
y1 = ksdensity(y,v1,'function','icdf');

scatterhist(x1,y1,'Direction','out')
set(get(gca,'children'),'marker','.')
```



As the example illustrates, copulas integrate naturally with other distribution fitting functions.

6

Random Number Generation

Generating Random Data

Pseudorandom numbers are generated by deterministic algorithms. They are "random" in the sense that, on average, they pass statistical tests regarding their distribution and correlation. They differ from true random numbers in that they are generated by an algorithm, rather than a truly random process.

Random number generators (RNGs) like those in MATLAB are algorithms for generating pseudorandom numbers with a specified distribution.

For more information on random number generators for supported distributions, see “Random Number Generators” on page 5-80.

For more information on the GUI for generating random numbers from supported distributions, see “Visually Exploring Random Number Generation” on page 5-49.

Random Number Generation Functions

The following table lists the supported distributions and their respective random number generation functions. For more information on other functions for each distribution, see "Supported Distributions" on page 5-3. For more information on random number generators, see "Random Number Generators" on page 5-80.

Distribution	Random Number Generation Function
Beta	`betarnd`, `random`, `randtool`
Binomial	`binornd`, `random`, `randtool`
Chi-square	`chi2rnd`, `random`, `randtool`
Clayton copula	`copularnd`
Exponential	`exprnd`, `random`, `randtool`
Extreme value	`evrnd`, `random`, `randtool`
F	`frnd`, `random`, `randtool`
Frank copula	`copularnd`
Gamma	`gamrnd`, `randg`, `random`, `randtool`
Gaussian copula	`copularnd`
Gaussian mixture	`random`
Generalized extreme value	`gevrnd`, `random`, `randtool`
Generalized Pareto	`gprnd`, `random`, `randtool`
Geometric	`geornd`, `random`, `randtool`
Gumbel copula	`copularnd`
Hypergeometric	`hygernd`, `random`
Inverse Wishart	`iwishrnd`
Johnson system	`johnsrnd`
Lognormal	`lognrnd`, `random`, `randtool`
Multinomial	`mnrnd`

Distribution	Random Number Generation Function
Multivariate normal	`mvnrnd`
Multivariate t	`mvtrnd`
Negative binomial	`nbinrnd`, `random`, `randtool`
Noncentral chi-square	`ncx2rnd`, `random`, `randtool`
Noncentral F	`ncfrnd`, `random`, `randtool`
Noncentral t	`nctrnd`, `random`, `randtool`
Normal (Gaussian)	`normrnd`, `randn`, `random`, `randtool`
Pearson system	`pearsrnd`
Piecewise	`random`
Poisson	`poissrnd`, `random`, `randtool`
Rayleigh	`raylrnd`, `random`, `randtool`
Student's t	`trnd`, `random`, `randtool`
t copula	`copularnd`
Uniform (continuous)	`unifrnd`, `rand`, `random`
Uniform (discrete)	`unidrnd`, `random`, `randtool`
Weibull	`wblrnd`, `random`
Wishart	`wishrnd`

Common Generation Methods

In this section...

Methods for generating pseudorandom numbers usually start with uniform random numbers, like the MATLAB `rand` function produces. The methods described in this section detail how to produce random numbers from other distributions.

Direct Methods

Direct methods directly use the definition of the distribution.

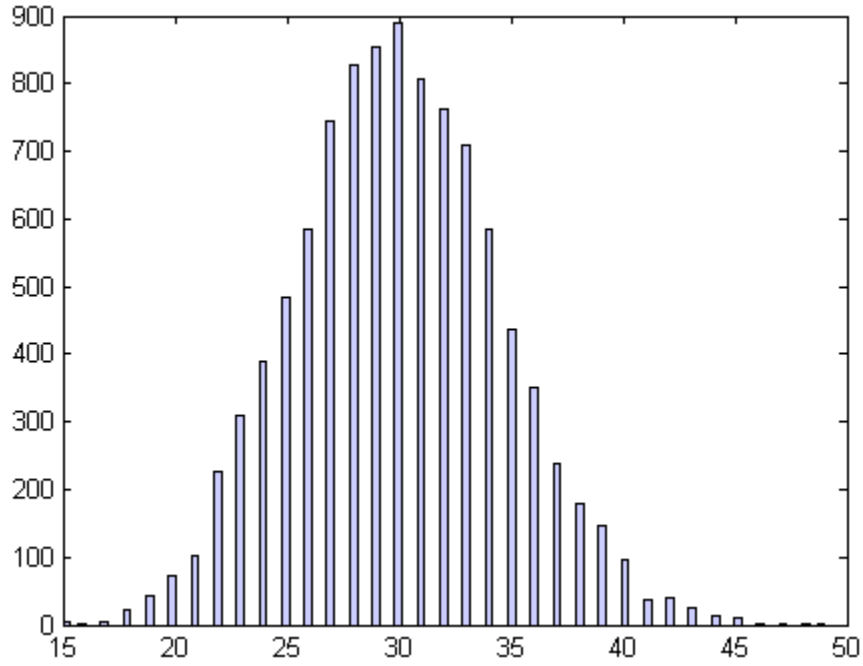
For example, consider binomial random numbers. A binomial random number is the number of heads in N tosses of a coin with probability p of a heads on any single toss. If you generate N uniform random numbers on the interval (0,1) and count the number less than p, then the count is a binomial random number with parameters N and p.

This function is a simple implementation of a binomial RNG using the direct approach:

```
function X = directbinornd(N,p,m,n)

X = zeros(m,n); % Preallocate memory
for i = 1:m*n
    u = rand(N,1);
    X(i) = sum(u < p);
end
```

For example:

```
X = directbinornd(100,0.3,1e4,1);
hist(X,101)
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
```



The Statistics Toolbox function `binornd` uses a modified direct method, based on the definition of a binomial random variable as the sum of Bernoulli random variables.

You can easily convert the previous method to a random number generator for the Poisson distribution with parameter λ. The Poisson distribution is the limiting case of the binomial distribution as N approaches infinity, p approaches zero, and Np is held fixed at λ. To generate Poisson random numbers, create a version of the previous generator that inputs λ rather than N and p, and internally sets N to some large number and p to λ/N.

The Statistics Toolbox function `poissrnd` actually uses two direct methods:

- A waiting time method for small values of λ
- A method due to Ahrens and Dieter for larger values of λ

Inversion Methods

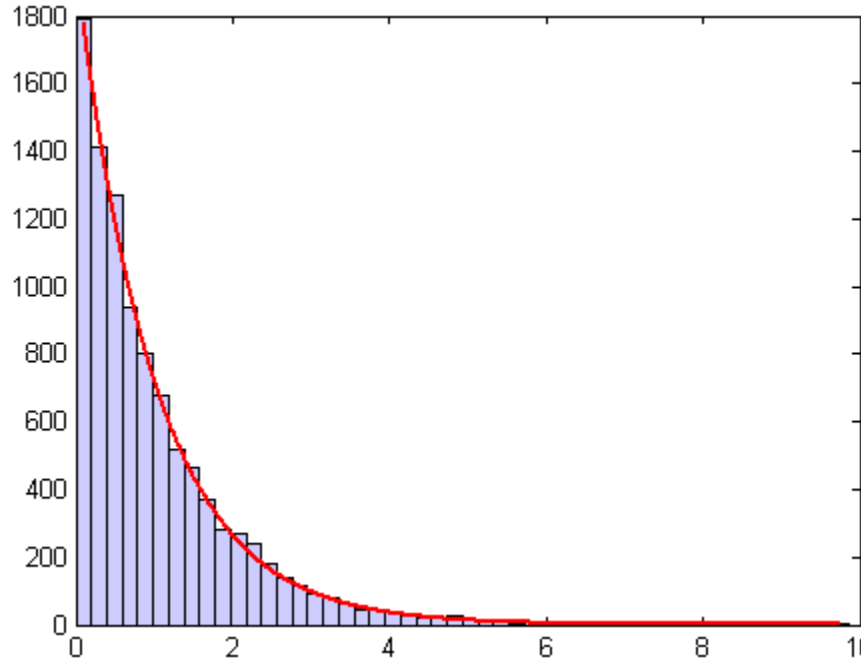
Inversion methods are based on the observation that continuous cumulative distribution functions (cdfs) range uniformly over the interval (0,1). If u is a uniform random number on (0,1), then using $X = F^{-1}(U)$ generates a random number X from a continuous distribution with specified cdf F.

For example, the following code generates random numbers from a specific exponential distribution using the inverse cdf and the MATLAB uniform random number generator `rand`:

```
mu = 1;
X = expinv(rand(1e4,1),mu);
```

Compare the distribution of the generated random numbers to the pdf of the specified exponential by scaling the pdf to the area of the histogram used to display the distribution:

```
numbins = 50;
hist(X,numbins)
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
hold on

[bincounts,binpositions] = hist(X,numbins);
binwidth = binpositions(2) - binpositions(1);
histarea = binwidth*sum(bincounts);

x = binpositions(1):0.001:binpositions(end);
y = exppdf(x,mu);
plot(x,histarea*y,'r','LineWidth',2)
```



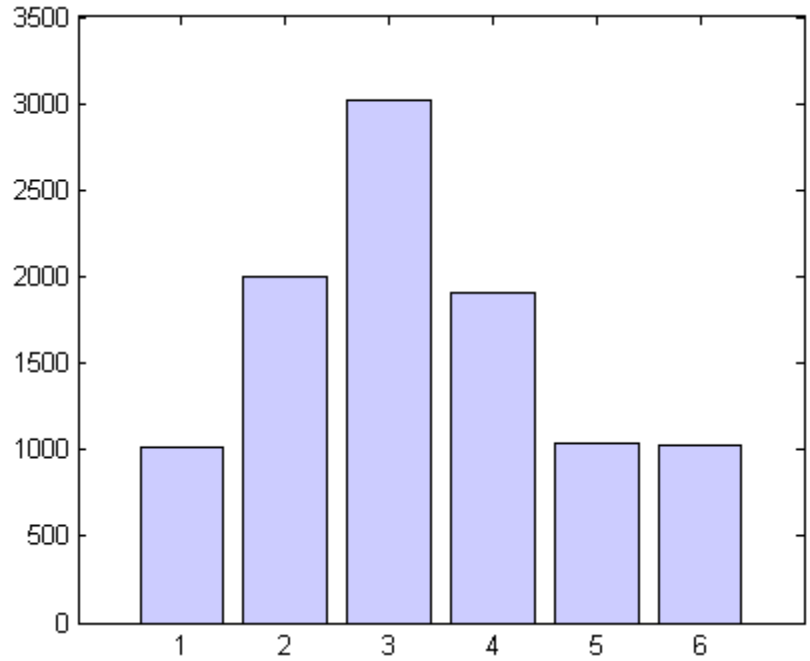
Inversion methods also work for discrete distributions. To generate a random number X from a discrete distribution with probability mass vector $P(X=x_i) = p_i$ where $x_0<x_1< x_2<...$, generate a uniform random number u on (0,1) and then set $X = x_i$ if $F(x_{i-1})<u<F(x_i)$.

For example, the following function implements an inversion method for a discrete distribution with probability mass vector p:

```
function X = discreteinvrnd(p,m,n)

X = zeros(m,n); % Preallocate memory
for i = 1:m*n
    u = rand;
    I = find(u < cumsum(p));
    X(i) = min(I);
end
```

Use the function to generate random numbers from any discrete distribution:

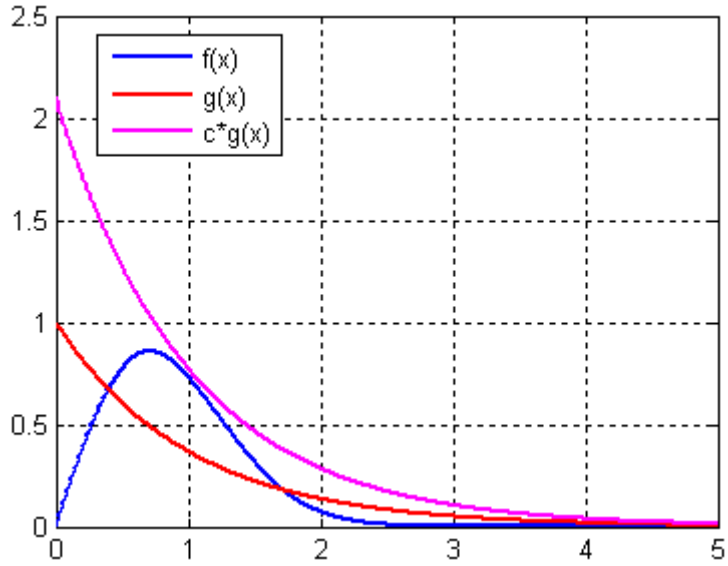
```
p = [0.1 0.2 0.3 0.2 0.1 0.1]; % Probability mass vector
X = discreteinvrnd(p,1e4,1);
[n,x] = hist(X,length(p));
bar(1:length(p),n)
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
```



Acceptance-Rejection Methods

The functional form of some distributions makes it difficult or time-consuming to generate random numbers using direct or inversion methods. Acceptance-rejection methods provide an alternative in these cases.

Acceptance-rejection methods begin with uniform random numbers, but require an additional random number generator. If your goal is to generate a random number from a continuous distribution with pdf f, acceptance-rejection methods first generate a random number from a continuous distribution with pdf g satisfying $f(x) \le cg(x)$ for some c and all x.



A continuous acceptance-rejection RNG proceeds as follows:

1. Chooses a density g.
2. Finds a constant c such that $f(x)/g(x) \le c$ for all x.
3. Generates a uniform random number u.
4. Generates a random number v from g.
5. If $cu \le f(v)/g(v)$, accepts and returns v.
6. Otherwise, rejects v and goes to step 3.

For efficiency, a "cheap" method is necessary for generating random numbers from g, and the scalar c should be small. The expected number of iterations to produce a single random number is c.

The following function implements an acceptance-rejection method for generating random numbers from pdf f, given f, g, the RNG `grnd` for g, and the constant c:

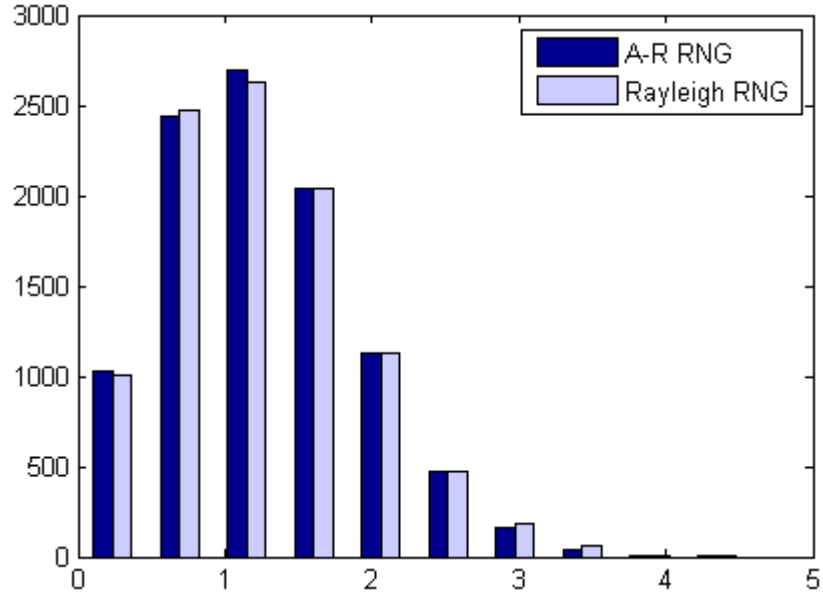
```
function X = accrejrnd(f,g,grnd,c,m,n)

X = zeros(m,n); % Preallocate memory
for i = 1:m*n
    accept = false;
    while accept == false
        u = rand();
        v = grnd();
        if c*u <= f(v)/g(v)
           X(i) = v;
           accept = true;
        end
    end
end
```

For example, the function $f(x) = xe^{-x^2/2}$ satisfies the conditions for a pdf on $[0,\infty)$ (nonnegative and integrates to 1). The exponential pdf with mean 1, $f(x) = e^{-x}$, dominates g for c greater than about 2.2. Thus, you can use `rand` and `exprnd` to generate random numbers from f:

```
f = @(x)x.*exp(-(x.^2)/2);
g = @(x)exp(-x);
grnd = @()exprnd(1);
X = accrejrnd(f,g,grnd,2.2,1e4,1);
```

The pdf f is actually a Rayleigh distribution with shape parameter 1. This example compares the distribution of random numbers generated by the acceptance-rejection method with those generated by `raylrnd`:

```
Y = raylrnd(1,1e4,1);
hist([X Y])
h = get(gca,'Children');
set(h(1),'FaceColor',[.8 .8 1])
legend('A-R RNG','Rayleigh RNG')
```



The Statistics Toolbox function `raylrnd` uses a transformation method, expressing a Rayleigh random variable in terms of a chi-square random variable, which you compute using `randn`.

Acceptance-rejection methods also work for discrete distributions. In this case, the goal is to generate random numbers from a distribution with probability mass $P_p(X = i) = p_i$, assuming that you have a method for generating random numbers from a distribution with probability mass $P_q(X = i) = q_i$. The RNG proceeds as follows:

1 Chooses a density P_q.

2 Finds a constant c such that $p_i/q_i \le c$ for all i .

3 Generates a uniform random number u.

4 Generates a random number v from P_q.

5 If $cu \le p_v/q_v$, accepts and returns v.

6 Otherwise, rejects v and goes to step 3.

Representing Sampling Distributions Using Markov Chain Samplers

In this section...

The methods in "Common Generation Methods" on page 6-5 might be inadequate when sampling distributions are difficult to represent in computations. Such distributions arise, for example, in Bayesian data analysis and in the large combinatorial problems of Markov chain Monte Carlo (MCMC) simulations. An alternative is to construct a Markov chain with a stationary distribution equal to the target sampling distribution, using the states of the chain to generate random numbers after an initial burn-in period in which the state distribution converges to the target.

Using the Metropolis-Hastings Algorithm

The Metropolis-Hastings algorithm draws samples from a distribution that is only known up to a constant. Random numbers are generated from a distribution with a probability density function that is equal to or proportional to a proposal function.

To generate random numbers:

1. Assume an initial value $x(t)$.
2. Draw a sample, $y(t)$, from a proposal distribution $q(y \mid x(t))$.
3. Accept $y(t)$ as the next sample $x(t + 1)$ with probability $r(x(t),y(t))$, and keep $x(t)$ as the next sample $x(t + 1)$ with probability $1 - r(x(t),y(t))$, where:

$$r(x,y) = min\left\{\frac{f(y)}{f(x)}\frac{q(x \mid y)}{q(y \mid x)}, 1\right\}$$

4. Increment $t \rightarrow t+1$, and repeat steps 2 and 3 until you get the desired number of samples.

Generate random numbers using the Metropolis-Hastings method with the `mhsample` function. To produce quality samples efficiently with the Metropolis-Hastings algorithm, it is crucial to select a good proposal distribution. If it is difficult to find an efficient proposal distribution, use the slice sampling algorithm (`slicesample`) without explicitly specifying a proposal distribution.

Using Slice Sampling

In instances where it is difficult to find an efficient Metropolis-Hastings proposal distribution, the slice sampling algorithm does not require an explicit specification. The slice sampling algorithm draws samples from the region under the density function using a sequence of vertical and horizontal steps. First, it selects a height at random from 0 to the density function $f(x)$. Then, it selects a new x value at random by sampling from the horizontal "slice" of the density above the selected height. A similar slice sampling algorithm is used for a multivariate distribution.

If a function $f(x)$ proportional to the density function is given, then do the following to generate random numbers:

1. Assume an initial value $x(t)$ within the domain of $f(x)$.
2. Draw a real value y uniformly from $(0, f(x(t)))$, thereby defining a horizontal "slice" as $S = \{x: y < f(x)\}$.
3. Find an interval $I = (L, R)$ around $x(t)$ that contains all, or much of the "slice" S.
4. Draw the new point $x(t+1)$ within this interval.
5. Increment $t \rightarrow t+1$ and repeat steps 2 through 4 until you get the desired number of samples.

Slice sampling can generate random numbers from a distribution with an arbitrary form of the density function, provided that an efficient numerical procedure is available to find the interval $I = (L,R)$, which is the "slice" of the density.

Generate random numbers using the slice sampling method with the `slicesample` function.

Generating Quasi-Random Numbers

In this section...

Quasi-Random Sequences

Quasi-random number generators (QRNGs) produce highly uniform samples of the unit hypercube. QRNGs minimize the *discrepancy* between the distribution of generated points and a distribution with equal proportions of points in each sub-cube of a uniform partition of the hypercube. As a result, QRNGs systematically fill the "holes" in any initial segment of the generated quasi-random sequence.

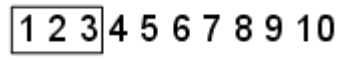
Unlike the pseudorandom sequences described in "Common Generation Methods" on page 6-5, quasi-random sequences fail many statistical tests for randomness. Approximating true randomness, however, is not their goal. Quasi-random sequences seek to fill space uniformly, and to do so in such a way that initial segments approximate this behavior up to a specified density.

QRNG applications include:

- **Quasi-Monte Carlo (QMC) integration.** Monte Carlo techniques are often used to evaluate difficult, multi-dimensional integrals without a closed-form solution. QMC uses quasi-random sequences to improve the convergence properties of these techniques.
- **Space-filling experimental designs.** In many experimental settings, taking measurements at every factor setting is expensive or infeasible. Quasi-random sequences provide efficient, uniform sampling of the design space.
- **Global optimization.** Optimization algorithms typically find a local optimum in the neighborhood of an initial value. By using a quasi-random sequence of initial values, searches for global optima uniformly sample the basins of attraction of all local minima.

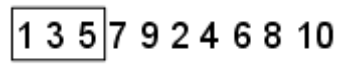
Example: Using Scramble, Leap, and Skip

Imagine a simple 1-D sequence that produces the integers from 1 to 10. This is the basic sequence and the first three points are `[1,2,3]`:

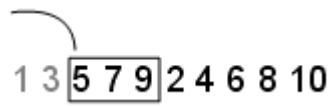


Now look at how `Scramble`, `Leap`, and `Skip` work together:

- `Scramble` — Scrambling shuffles the points in one of several different ways. In this example, assume a scramble turns the sequence into `1,3,5,7,9,2,4,6,8,10`. The first three points are now `[1,3,5]`:



- `Skip` — A `Skip` value specifies the number of initial points to ignore. In this example, set the `Skip` value to 2. The sequence is now `5,7,9,2,4,6,8,10` and the first three points are `[5,7,9]`:



- `Leap` — A `Leap` value specifies the number of points to ignore for each one you take. Continuing the example with the `Skip` set to 2, if you set the `Leap` to 1, the sequence uses every other point. In this example, the sequence is now `5,9,4,8` and the first three points are `[5,9,4]`:

Quasi-Random Point Sets

Statistics Toolbox functions support these quasi-random sequences:

- **Halton sequences.** Produced by the `haltonset` function. These sequences use different prime bases to form successively finer uniform partitions of the unit interval in each dimension.

- **Sobol sequences.** Produced by the `sobolset` function. These sequences use a base of 2 to form successively finer uniform partitions of the unit interval, and then reorder the coordinates in each dimension.
- **Latin hypercube sequences.** Produced by the `lhsdesign` function. Though not quasi-random in the sense of minimizing discrepancy, these sequences nevertheless produce sparse uniform samples useful in experimental designs.

Quasi-random sequences are functions from the positive integers to the unit hypercube. To be useful in application, an initial *point set* of a sequence must be generated. Point sets are matrices of size n-by-d, where n is the number of points and d is the dimension of the hypercube being sampled. The functions `haltonset` and `sobolset` construct point sets with properties of a specified quasi-random sequence. Initial segments of the point sets are generated by the `net` method of the `qrandset` class (parent class of the `haltonset` class and `sobolset` class), but points can be generated and accessed more generally using parenthesis indexing.

Because of the way in which quasi-random sequences are generated, they may contain undesirable correlations, especially in their initial segments, and especially in higher dimensions. To address this issue, quasi-random point sets often *skip*, *leap* over, or *scramble* values in a sequence. The `haltonset` and `sobolset` functions allow you to specify both a `Skip` and a `Leap` property of a quasi-random sequence, and the `scramble` method of the `qrandset` class allows you apply a variety of scrambling techniques. Scrambling reduces correlations while also improving uniformity.

Example: Generate a Quasi-Random Point Set

This example uses `haltonset` to construct a 2-D Halton point set—an object, `p`, of the `haltonset` class—that skips the first 1000 values of the sequence and then retains every 101st point:

```
p = haltonset(2,'Skip',1e3,'Leap',1e2)
p =
    Halton point set in 2 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none
```

The object `p` encapsulates properties of the specified quasi-random sequence. The point set is finite, with a length determined by the `Skip` and `Leap` properties and by limits on the size of point set indices (maximum value of 2^{53}).

Use `scramble` to apply reverse-radix scrambling:

```
p = scramble(p,'RR2')
p =
    Halton point set in 2 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : RR2
```

Use `net` to generate the first 500 points:

```
X0 = net(p,500);
```

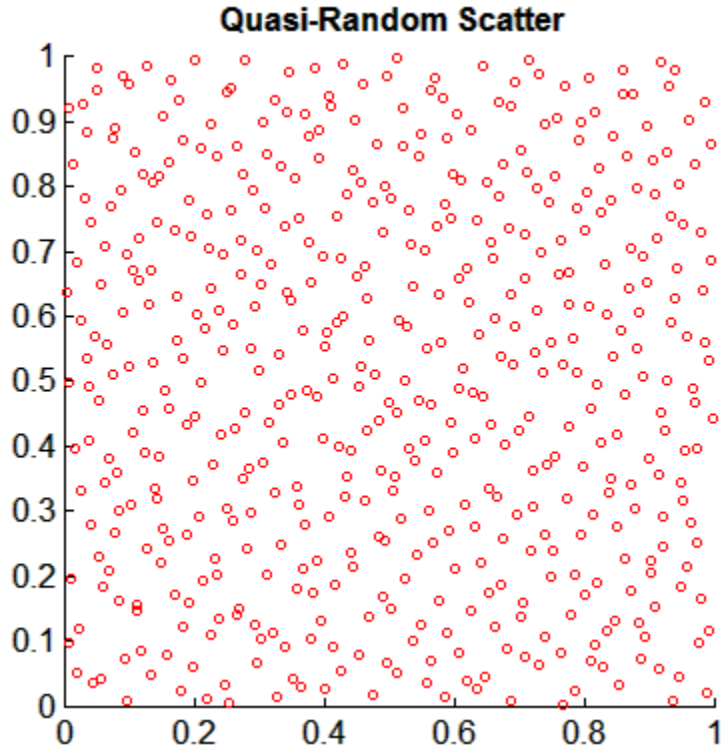
This is equivalent to:

```
X0 = p(1:500,:);
```

Values of the point set `X0` are not generated and stored in memory until you access `p` using `net` or parenthesis indexing.

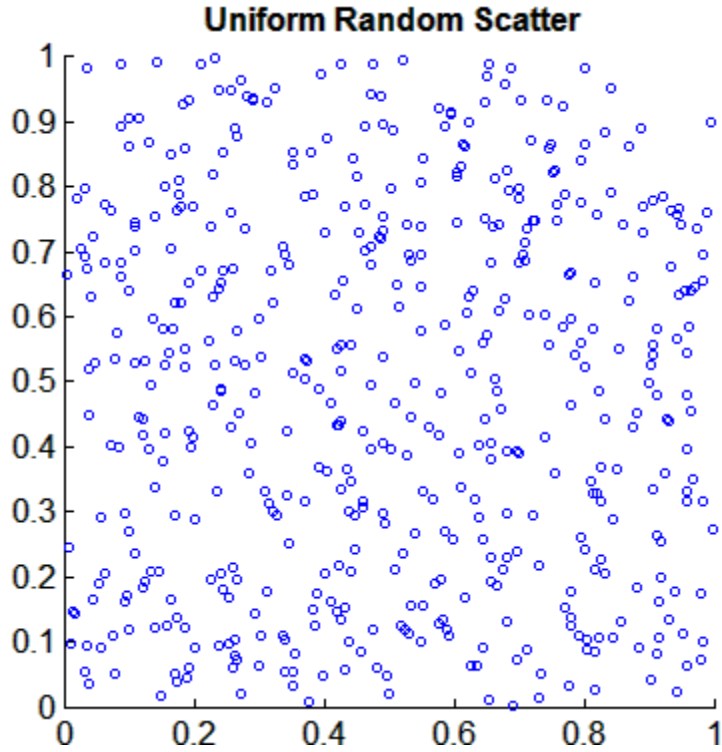
To appreciate the nature of quasi-random numbers, create a scatter of the two dimensions in `X0`:

```
scatter(X0(:,1),X0(:,2),5,'r')
axis square
title('{\bf Quasi-Random Scatter}')
```



Compare this to a scatter of uniform pseudorandom numbers generated by the MATLAB `rand` function:

```
X = rand(500,2);

scatter(X(:,1),X(:,2),5,'b')
axis square
title('{\bf Uniform Random Scatter}')
```

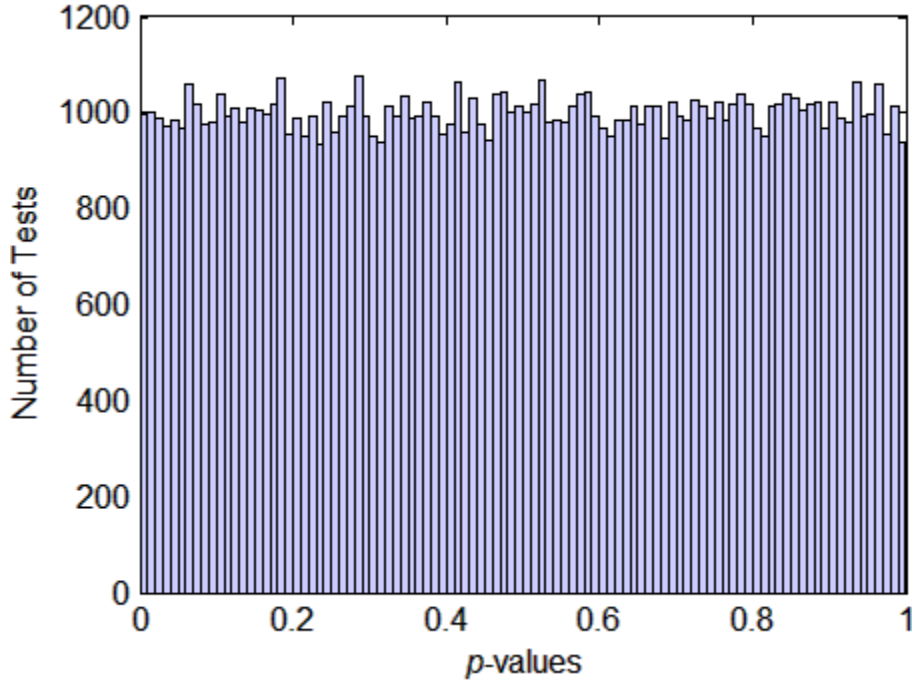


The quasi-random scatter appears more uniform, avoiding the clumping in the pseudorandom scatter.

In a statistical sense, quasi-random numbers are too uniform to pass traditional tests of randomness. For example, a Kolmogorov-Smirnov test, performed by `kstest`, is used to assess whether or not a point set has a uniform random distribution. When performed repeatedly on uniform pseudorandom samples, such as those generated by `rand`, the test produces a uniform distribution of *p*-values:

```
nTests = 1e5;
sampSize = 50;
PVALS = zeros(nTests,1);
for test = 1:nTests
    x = rand(sampSize,1);
    [h,pval] = kstest(x,[x,x]);
```

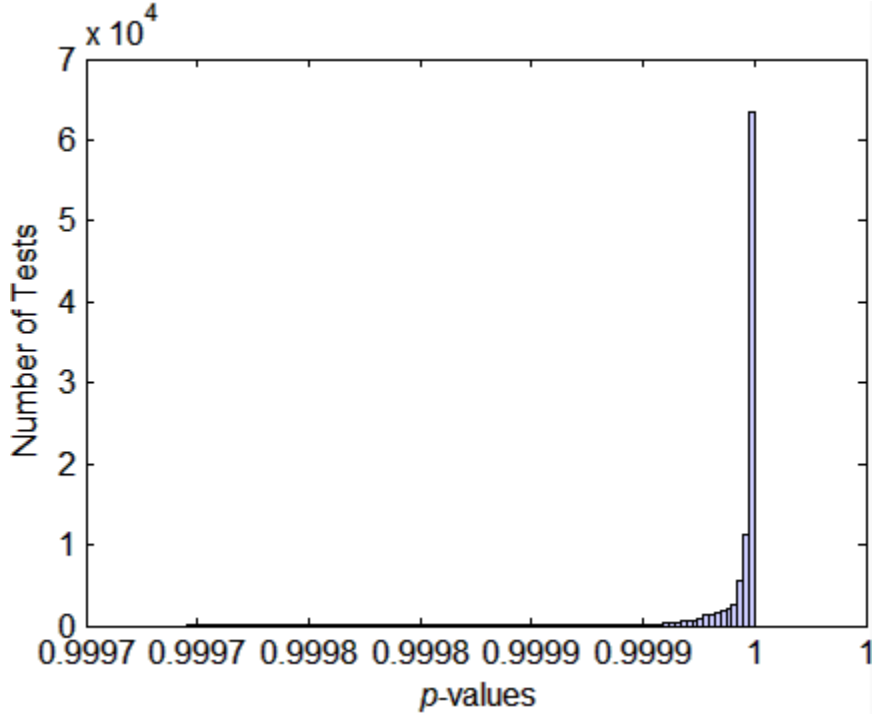
```
    PVALS(test) = pval;
end

hist(PVALS,100)
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
xlabel('{\it p}-values')
ylabel('Number of Tests')
```



The results are quite different when the test is performed repeatedly on uniform quasi-random samples:

```
p = haltonset(1,'Skip',1e3,'Leap',1e2);
p = scramble(p,'RR2');

nTests = 1e5;
sampSize = 50;
PVALS = zeros(nTests,1);
for test = 1:nTests
```

```
    x = p(test:test+(sampSize-1),:);
    [h,pval] = kstest(x,[x,x]);
    PVALS(test) = pval;
end

hist(PVALS,100)
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
xlabel('{\it p}-values')
ylabel('Number of Tests')
```



Small *p*-values call into question the null hypothesis that the data are uniformly distributed. If the hypothesis is true, about 5% of the *p*-values are expected to fall below 0.05. The results are remarkably consistent in their failure to challenge the hypothesis.

Quasi-Random Streams

Quasi-random *streams*, produced by the `qrandstream` function, are used to generate sequential quasi-random outputs, rather than point sets of a specific size. Streams are used like pseudoRNGS, such as `rand`, when client applications require a source of quasi-random numbers of indefinite size that can be accessed intermittently. Properties of a quasi-random stream, such as its type (Halton or Sobol), dimension, skip, leap, and scramble, are set when the stream is constructed.

In implementation, quasi-random streams are essentially very large quasi-random point sets, though they are accessed differently. The *state* of a quasi-random stream is the scalar index of the next point to be taken from the stream. Use the `qrand` method of the `qrandstream` class to generate points from the stream, starting from the current state. Use the `reset` method to reset the state to `1`. Unlike point sets, streams do not support parenthesis indexing.

Example: Generate a Quasi-Random Stream

For example, the following code, taken from the example at the end of "Quasi-Random Point Sets" on page 6-16, uses `haltonset` to create a quasi-random point set `p`, and then repeatedly increments the index into the point set, `test`, to generate different samples:

```
p = haltonset(1,'Skip',1e3,'Leap',1e2);
p = scramble(p,'RR2');

nTests = 1e5;
sampSize = 50;
PVALS = zeros(nTests,1);
for test = 1:nTests
    x = p(test:test+(sampSize-1),:);
    [h,pval] = kstest(x,[x,x]);
    PVALS(test) = pval;
end
```

The same results are obtained by using `qrandstream` to construct a quasi-random stream `q` based on the point set `p` and letting the stream take care of increments to the index:

```
p = haltonset(1,'Skip',1e3,'Leap',1e2);
p = scramble(p,'RR2');
q = qrandstream(p)

nTests = 1e5;
sampSize = 50;
PVALS = zeros(nTests,1);
for test = 1:nTests
    X = qrand(q,sampSize);
    [h,pval] = kstest(X,[X,X]);
    PVALS(test) = pval;
end
```

Generating Data Using Flexible Families of Distributions

In this section...

Pearson and Johnson Systems

As described in "Using Probability Distributions" on page 5-2, choosing an appropriate parametric family of distributions to model your data can be based on *a priori* or *a posteriori* knowledge of the data-producing process, but the choice is often difficult. The *Pearson and Johnson systems* can make such a choice unnecessary. Each system is a flexible parametric family of distributions that includes a wide range of distribution shapes, and it is often possible to find a distribution within one of these two systems that provides a good match to your data.

Data Input

The following parameters define each member of the Pearson and Johnson systems

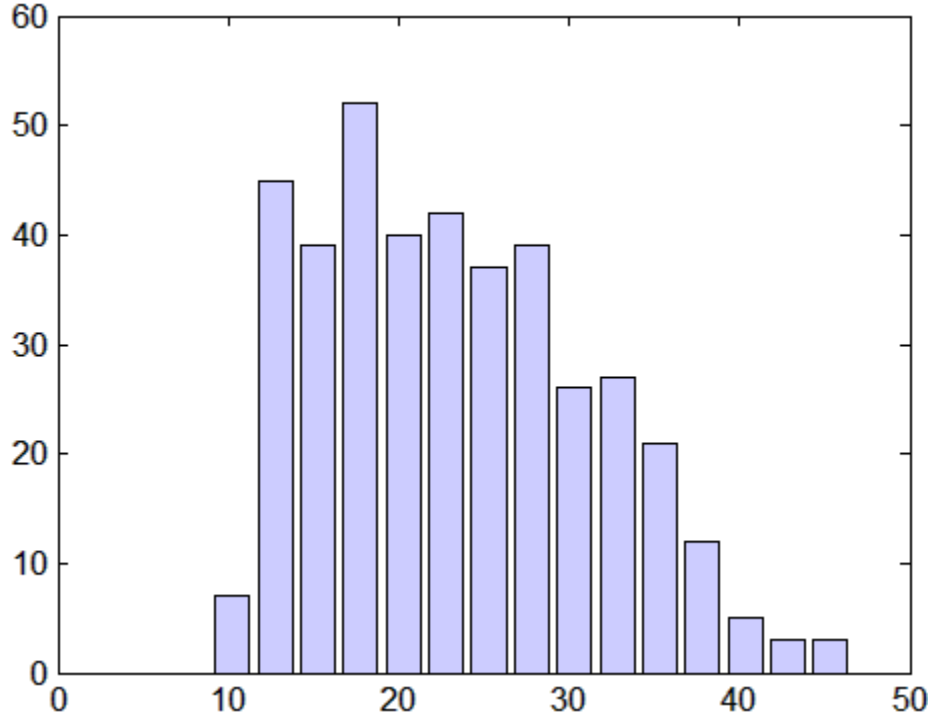
- Mean — Estimated by `mean`
- Standard deviation — Estimated by `std`
- Skewness — Estimated by `skewness`
- Kurtosis — Estimated by `kurtosis`

These statistics can also be computed with the `moment` function. The Johnson system, while based on these four parameters, is more naturally described using quantiles, estimated by the `quantile` function.

The Statistics Toolbox functions `pearsrnd` and `johnsrnd` take input arguments defining a distribution (parameters or quantiles, respectively) and return the type and the coefficients of the distribution in the corresponding system. Both functions also generate random numbers from the specified distribution.

As an example, load the data in `carbig.mat`, which includes a variable `MPG` containing measurements of the gas mileage for each car.

```
load carbig
MPG = MPG(~isnan(MPG));
[n,x] = hist(MPG,15);
bar(x,n)
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
```



The following two sections model the distribution with members of the Pearson and Johnson systems, respectively.

Generating Data Using the Pearson System

The statistician Karl Pearson devised a system, or family, of distributions that includes a unique distribution corresponding to every valid combination of mean, standard deviation, skewness, and kurtosis. If you compute sample

values for each of these moments from data, it is easy to find the distribution in the Pearson system that matches these four moments and to generate a random sample.

The Pearson system embeds seven basic types of distribution together in a single parametric framework. It includes common distributions such as the normal and *t* distributions, simple transformations of standard distributions such as a shifted and scaled beta distribution and the inverse gamma distribution, and one distribution—the Type IV—that is not a simple transformation of any standard distribution.

For a given set of moments, there are distributions that are not in the system that also have those same first four moments, and the distribution in the Pearson system may not be a good match to your data, particularly if the data are multimodal. But the system does cover a wide range of distribution shapes, including both symmetric and skewed distributions.

To generate a sample from the Pearson distribution that closely matches the `MPG` data, simply compute the four sample moments and treat those as distribution parameters.

```
moments = {mean(MPG),std(MPG),skewness(MPG),kurtosis(MPG)};
[r,type] = pearsrnd(moments{:},10000,1);
```

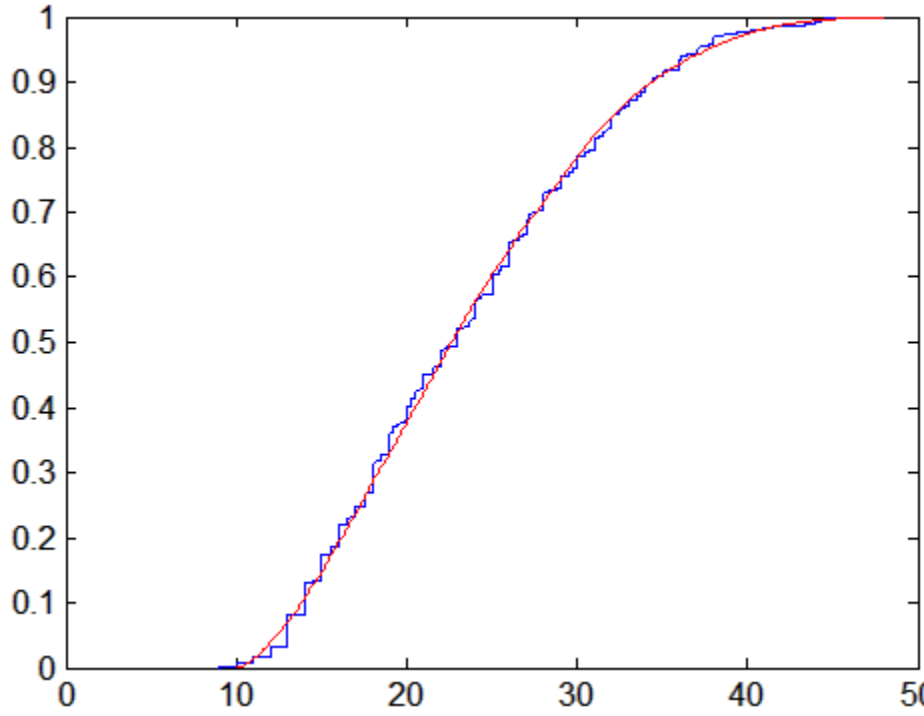
The optional second output from `pearsrnd` indicates which type of distribution within the Pearson system matches the combination of moments.

```
type
type =
     1
```

In this case, `pearsrnd` has determined that the data are best described with a Type I Pearson distribution, which is a shifted, scaled beta distribution.

Verify that the sample resembles the original data by overlaying the empirical cumulative distribution functions.

```
ecdf(MPG);
[Fi,xi] = ecdf(r);
hold on, stairs(xi,Fi,'r'); hold off
```



Generating Data Using the Johnson System

Statistician Norman Johnson devised a different system of distributions that also includes a unique distribution for every valid combination of mean, standard deviation, skewness, and kurtosis. However, since it is more natural to describe distributions in the Johnson system using quantiles, working with this system is different than working with the Pearson system.

The Johnson system is based on three possible transformations of a normal random variable, plus the identity transformation. The three nontrivial cases are known as `SL`, `SU`, and `SB`, corresponding to exponential, logistic, and hyperbolic sine transformations. All three can be written as

$$X = \gamma + \delta \cdot \Gamma\left(\frac{(Z-\xi)}{\lambda}\right)$$

where Z is a standard normal random variable, Γ is the transformation, and γ, δ, ξ, and λ are scale and location parameters. The fourth case, `SN`, is the identity transformation.

To generate a sample from the Johnson distribution that matches the `MPG` data, first define the four quantiles to which the four evenly spaced standard normal quantiles of -1.5, -0.5, 0.5, and 1.5 should be transformed. That is, you compute the sample quantiles of the data for the cumulative probabilities of 0.067, 0.309, 0.691, and 0.933.

```
probs = normcdf([-1.5 -0.5 0.5 1.5])
probs =
     0.066807      0.30854      0.69146      0.93319

quantiles = quantile(MPG,probs)
quantiles =
   13.0000   18.0000   27.2000   36.0000
```

Then treat those quantiles as distribution parameters.

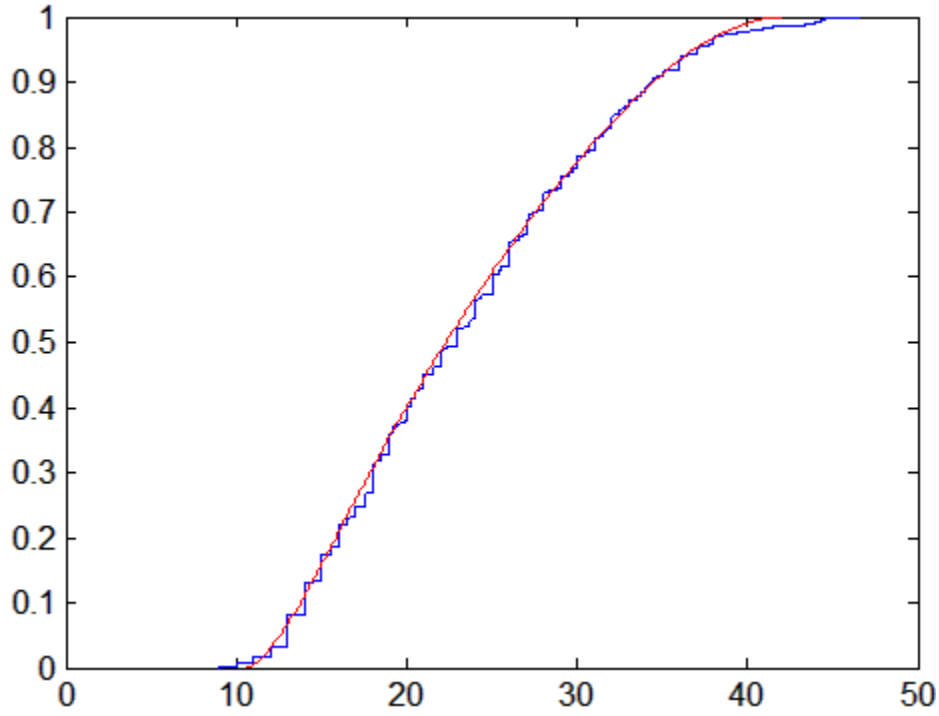
```
[r1,type] = johnsrnd(quantiles,10000,1);
```

The optional second output from `johnsrnd` indicates which type of distribution within the Johnson system matches the quantiles.

```
type
type =
SB
```

You can verify that the sample resembles the original data by overlaying the empirical cumulative distribution functions.

```
ecdf(MPG);
[Fi,xi] = ecdf(r1);
hold on, stairs(xi,Fi,'r'); hold off
```

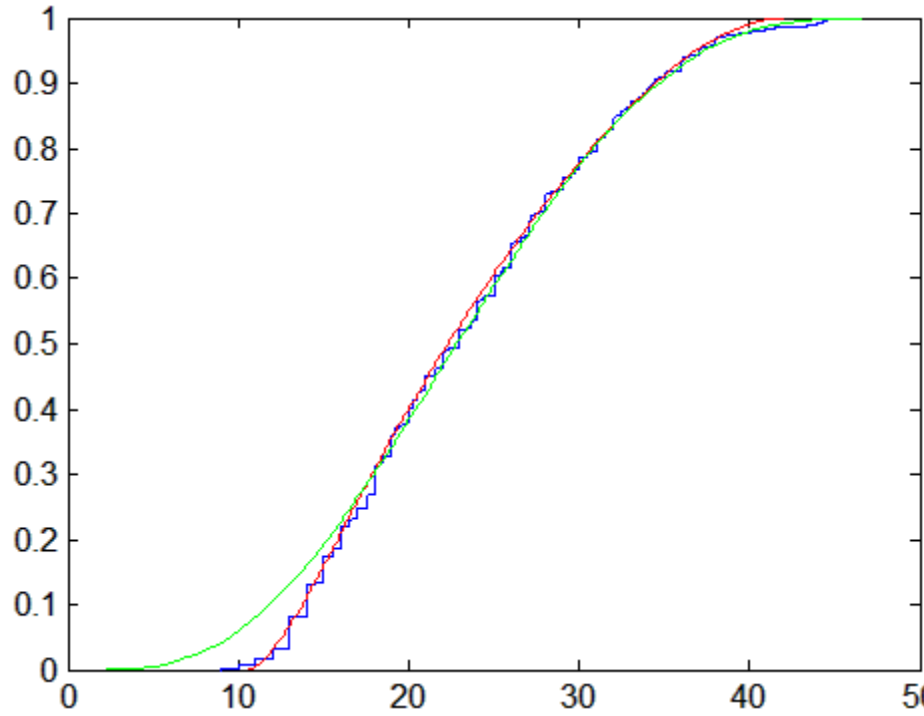


In some applications, it may be important to match the quantiles better in some regions of the data than in others. To do that, specify four evenly spaced standard normal quantiles at which you want to match the data, instead of the default -1.5, -0.5, 0.5, and 1.5. For example, you might care more about matching the data in the right tail than in the left, and so you specify standard normal quantiles that emphasizes the right tail.

```
qnorm = [-.5 .25 1 1.75];
probs = normcdf(qnorm);
qemp = quantile(MPG,probs);
r2 = johnsrnd([qnorm; qemp],10000,1);
```

However, while the new sample matches the original data better in the right tail, it matches much worse in the left tail.

```
[Fj,xj] = ecdf(r2);
hold on, stairs(xj,Fj,'g'); hold off
```


1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
10
20
30
40
50

7

Hypothesis Tests

Introduction to Hypothesis Tests

Hypothesis testing is a common method of drawing inferences about a population based on statistical evidence from a sample.

As an example, suppose someone says that at a certain time in the state of Massachusetts the average price of a gallon of regular unleaded gas was $1.15. How could you determine the truth of the statement? You could try to find prices at every gas station in the state at the time. That approach would be definitive, but it could be time-consuming, costly, or even impossible.

A simpler approach would be to find prices at a small number of randomly selected gas stations around the state, and then compute the sample average.

Sample averages differ from one another due to chance variability in the selection process. Suppose your sample average comes out to be $1.18. Is the $0.03 difference an artifact of random sampling or significant evidence that the average price of a gallon of gas was in fact greater than $1.15? Hypothesis testing is a statistical method for making such decisions.

Hypothesis Test Terminology

All hypothesis tests share the same basic terminology and structure.

- A *null hypothesis* is an assertion about a population that you would like to test. It is "null" in the sense that it often represents a status quo belief, such as the absence of a characteristic or the lack of an effect. It may be formalized by asserting that a population parameter, or a combination of population parameters, has a certain value. In the example given in the "Introduction to Hypothesis Tests" on page 7-2, the null hypothesis would be that the average price of gas across the state was \$1.15. This is written H_0: $\mu = 1.15$.
- An *alternative hypothesis* is a contrasting assertion about the population that can be tested against the null hypothesis. In the example given in the "Introduction to Hypothesis Tests" on page 7-2, possible alternative hypotheses are:

  H_1: $\mu \neq 1.15$ — State average was different from \$1.15 (two-tailed test)

  H_1: $\mu > 1.15$ — State average was greater than \$1.15 (right-tail test)

  H_1: $\mu < 1.15$ — State average was less than \$1.15 (left-tail test)
- To conduct a hypothesis test, a random sample from the population is collected and a relevant *test statistic* is computed to summarize the sample. This statistic varies with the type of test, but its distribution under the null hypothesis must be known (or assumed).
- The *p value* of a test is the probability, under the null hypothesis, of obtaining a value of the test statistic as extreme or more extreme than the value computed from the sample.
- The *significance level* of a test is a threshold of probability α agreed to before the test is conducted. A typical value of α is 0.05. If the p value of a test is less than α, the test rejects the null hypothesis. If the p value is greater than α, there is insufficient evidence to reject the null hypothesis. Note that lack of evidence for rejecting the null hypothesis is not evidence for accepting the null hypothesis. Also note that substantive "significance" of an alternative cannot be inferred from the statistical significance of a test.
- The significance level α can be interpreted as the probability of rejecting the null hypothesis when it is actually true—a *type I error*. The distribution of the test statistic under the null hypothesis determines the probability

α of a type I error. Even if the null hypothesis is not rejected, it may still be false—a *type II error*. The distribution of the test statistic under the alternative hypothesis determines the probability β of a type II error. Type II errors are often due to small sample sizes. The *power* of a test, $1 - \beta$, is the probability of correctly rejecting a false null hypothesis.

- Results of hypothesis tests are often communicated with a *confidence interval*. A confidence interval is an estimated range of values with a specified probability of containing the true population value of a parameter. Upper and lower bounds for confidence intervals are computed from the sample estimate of the parameter and the known (or assumed) sampling distribution of the estimator. A typical assumption is that estimates will be normally distributed with repeated sampling (as dictated by the Central Limit Theorem). Wider confidence intervals correspond to poor estimates (smaller samples); narrow intervals correspond to better estimates (larger samples). If the null hypothesis asserts the value of a population parameter, the test rejects the null hypothesis when the hypothesized value lies outside the computed confidence interval for the parameter.

Hypothesis Test Assumptions

Different hypothesis tests make different assumptions about the distribution of the random variable being sampled in the data. These assumptions must be considered when choosing a test and when interpreting the results.

For example, the *z*-test (`ztest`) and the *t*-test (`ttest`) both assume that the data are independently sampled from a normal distribution. Statistics Toolbox functions are available for testing this assumption, such as `chi2gof`, `jbtest`, `lillietest`, and `normplot`.

Both the *z*-test and the *t*-test are relatively robust with respect to departures from this assumption, so long as the sample size n is large enough. Both tests compute a sample mean $\bar{x}$, which, by the Central Limit Theorem, has an approximately normal sampling distribution with mean equal to the population mean μ, regardless of the population distribution being sampled.

The difference between the *z*-test and the *t*-test is in the assumption of the standard deviation σ of the underlying normal distribution. A *z*-test assumes that σ is known; a *t*-test does not. As a result, a *t*-test must compute an estimate s of the standard deviation from the sample.

Test statistics for the *z*-test and the *t*-test are, respectively,

$$z = \frac{\bar{x} - \mu}{\sigma / \sqrt{n}}$$

$$t = \frac{\bar{x} - \mu}{s / \sqrt{n}}$$

Under the null hypothesis that the population is distributed with mean μ, the *z*-statistic has a standard normal distribution, $N(0,1)$. Under the same null hypothesis, the *t*-statistic has Student's t distribution with $n - 1$ degrees of freedom. For small sample sizes, Student's t distribution is flatter and wider than $N(0,1)$, compensating for the decreased confidence in the estimate s. As sample size increases, however, Student's t distribution approaches the standard normal distribution, and the two tests become essentially equivalent.

Knowing the distribution of the test statistic under the null hypothesis allows for accurate calculation of p-values. Interpreting p-values in the context of the test assumptions allows for critical analysis of test results.

Assumptions underlying Statistics Toolbox hypothesis tests are given in the reference pages for implementing functions.

Example: Hypothesis Testing

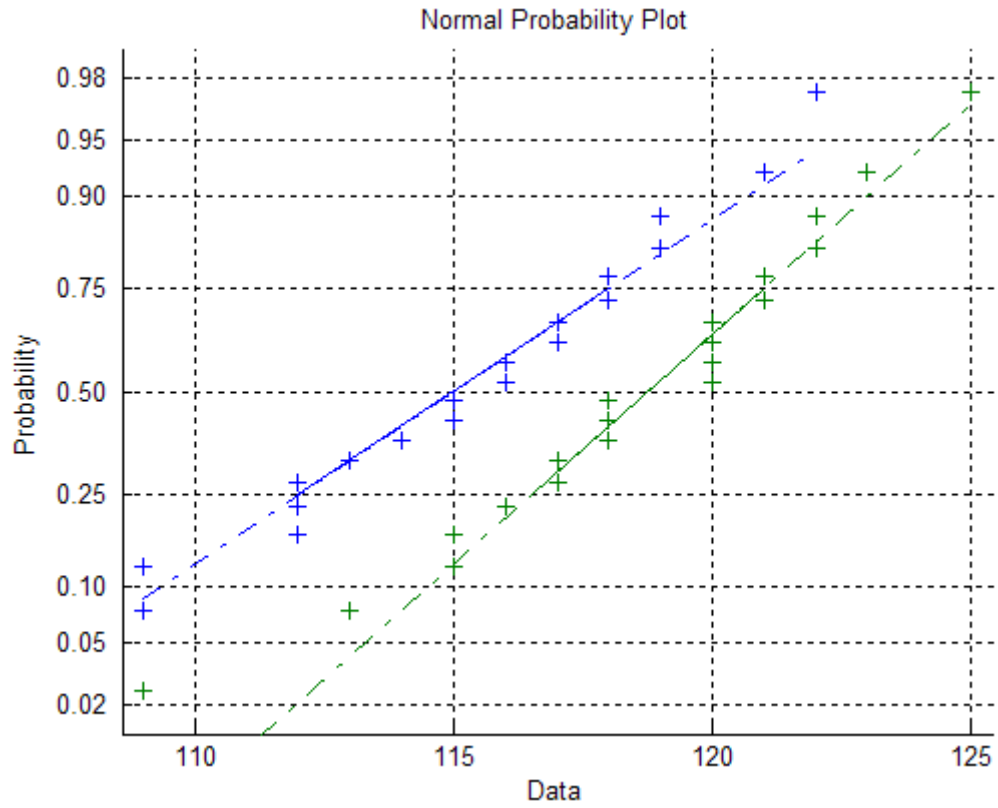
This example uses the gas price data in the file `gas.mat`. The file contains two random samples of prices for a gallon of gas around the state of Massachusetts in 1993. The first sample, `price1`, contains 20 random observations around the state on a single day in January. The second sample, `price2`, contains 20 random observations around the state one month later.

```
load gas
prices = [price1 price2];
```

As a first step, you might want to test the assumption that the samples come from normal distributions.

A normal probability plot gives a quick idea.

```
normplot(prices)
```



Both scatters approximately follow straight lines through the first and third quartiles of the samples, indicating approximate normal distributions. The February sample (the right-hand line) shows a slight departure from normality in the lower tail. A shift in the mean from January to February is evident.

A hypothesis test is used to quantify the test of normality. Since each sample is relatively small, a Lilliefors test is recommended.

```
lillietest(price1)
ans =
     0
lillietest(price2)
ans =
     0
```

The default significance level of `lillietest` is 5%. The logical 0 returned by each test indicates a failure to reject the null hypothesis that the samples are normally distributed. This failure may reflect normality in the population or it may reflect a lack of strong evidence against the null hypothesis due to the small sample size.

Now compute the sample means:

```
sample_means = mean(prices)
sample_means =
  115.1500  118.5000
```

You might want to test the null hypothesis that the mean price across the state on the day of the January sample was $1.15. If you know that the standard deviation in prices across the state has historically, and consistently, been $0.04, then a *z*-test is appropriate.

```
[h,pvalue,ci] = ztest(price1/100,1.15,0.04)
h =
     0
pvalue =
    0.8668
ci =
    1.1340
    1.1690
```

The logical output `h = 0` indicates a failure to reject the null hypothesis at the default significance level of 5%. This is a consequence of the high probability under the null hypothesis, indicated by the *p* value, of observing a value as extreme or more extreme of the *z*-statistic computed from the sample. The 95% confidence interval on the mean [1.1340 1.1690] includes the hypothesized population mean of $1.15.

Does the later sample offer stronger evidence for rejecting a null hypothesis of a state-wide average price of $1.15 in February? The shift shown in the probability plot and the difference in the computed sample means suggest this. The shift might indicate a significant fluctuation in the market, raising questions about the validity of using the historical standard deviation. If a known standard deviation cannot be assumed, a *t*-test is more appropriate.

```
[h,pvalue,ci] = ttest(price2/100,1.15)
h =
     1
pvalue =
  4.9517e-004
ci =
    1.1675
    1.2025
```

The logical output `h = 1` indicates a rejection of the null hypothesis at the default significance level of 5%. In this case, the 95% confidence interval on the mean does not include the hypothesized population mean of $1.15.

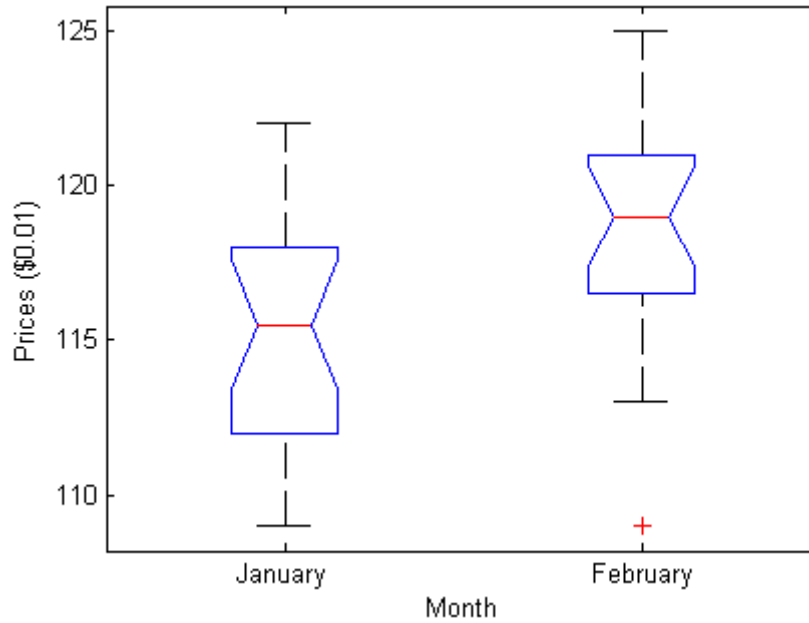
You might want to investigate the shift in prices a little more closely. The function `ttest2` tests if two independent samples come from normal distributions with equal but unknown standard deviations and the same mean, against the alternative that the means are unequal.

```
[h,sig,ci] = ttest2(price1,price2)
h =
     1
sig =
    0.0083
ci =
   -5.7845
   -0.9155
```

The null hypothesis is rejected at the default 5% significance level, and the confidence interval on the difference of means does not include the hypothesized value of 0.

A notched box plot is another way to visualize the shift.

```
boxplot(prices,1)
set(gca,'XTick',[1 2])
set(gca,'XtickLabel',{'January','February'})
xlabel('Month')
ylabel('Prices ($0.01)')
```



The plot displays the distribution of the samples around their medians. The heights of the notches in each box are computed so that the side-by-side boxes have nonoverlapping notches when their medians are different at a default 5% significance level. The computation is based on an assumption of normality in the data, but the comparison is reasonably robust for other distributions. The side-by-side plots provide a kind of visual hypothesis test, comparing medians rather than means. The plot above appears to barely reject the null hypothesis of equal medians.

The nonparametric Wilcoxon rank sum test, implemented by the function `ranksum`, can be used to quantify the test of equal medians. It tests if two independent samples come from identical continuous (not necessarily normal) distributions with equal medians, against the alternative that they do not have equal medians.

```
[p,h] = ranksum(price1,price2)
p =
    0.0095
h =
     1
```

The test rejects the null hypothesis of equal medians at the default 5% significance level.

Available Hypothesis Tests

Function	Description
`ansaribradley`	Ansari-Bradley test. Tests if two independent samples come from the same distribution, against the alternative that they come from distributions that have the same median and shape but different variances.
`chi2gof`	Chi-square goodness-of-fit test. Tests if a sample comes from a specified distribution, against the alternative that it does not come from that distribution.
`dwtest`	Durbin-Watson test. Tests if the residuals from a linear regression are uncorrelated, against the alternative that there is autocorrelation among them.
`jbtest`	Jarque-Bera test. Tests if a sample comes from a normal distribution with unknown mean and variance, against the alternative that it does not come from a normal distribution.
`kstest`	One-sample Kolmogorov-Smirnov test. Tests if a sample comes from a continuous distribution with specified parameters, against the alternative that it does not come from that distribution.
`kstest2`	Two-sample Kolmogorov-Smirnov test. Tests if two samples come from the same continuous distribution, against the alternative that they do not come from the same distribution.
`lillietest`	Lilliefors test. Tests if a sample comes from a distribution in the normal family, against the alternative that it does not come from a normal distribution.
`linhyptest`	Linear hypothesis test. Tests if `H*b = c` for parameter estimates `b` with estimated covariance `H` and specified `c`, against the alternative that `H*b  c`.

Function	Description
ranksum	Wilcoxon rank sum test. Tests if two independent samples come from identical continuous distributions with equal medians, against the alternative that they do not have equal medians.
runstest	Runs test. Tests if a sequence of values comes in random order, against the alternative that the ordering is not random.
signrank	One-sample or paired-sample Wilcoxon signed rank test. Tests if a sample comes from a continuous distribution symmetric about a specified median, against the alternative that it does not have that median.
signtest	One-sample or paired-sample sign test. Tests if a sample comes from an arbitrary continuous distribution with a specified median, against the alternative that it does not have that median.
ttest	One-sample or paired-sample *t*-test. Tests if a sample comes from a normal distribution with unknown variance and a specified mean, against the alternative that it does not have that mean.
ttest2	Two-sample *t*-test. Tests if two independent samples come from normal distributions with unknown but equal (or, optionally, unequal) variances and the same mean, against the alternative that the means are unequal.
vartest	One-sample chi-square variance test. Tests if a sample comes from a normal distribution with specified variance, against the alternative that it comes from a normal distribution with a different variance.
vartest2	Two-sample *F*-test for equal variances. Tests if two independent samples come from normal distributions with the same variance, against the alternative that they come from normal distributions with different variances.

Function	Description
`vartestn`	Bartlett multiple-sample test for equal variances. Tests if multiple samples come from normal distributions with the same variance, against the alternative that they come from normal distributions with different variances.
`ztest`	One-sample *z*-test. Tests if a sample comes from a normal distribution with known variance and specified mean, against the alternative that it does not have that mean.

Note In addition to the previous functions, Statistics Toolbox functions are available for analysis of variance (ANOVA), which perform hypothesis tests in the context of linear modeling. These functions are discussed in Chapter 8, "Analysis of Variance".

8

Analysis of Variance

Introduction to Analysis of Variance

Analysis of variance (ANOVA) is a procedure for assigning sample variance to different sources and deciding whether the variation arises within or among different population groups. Samples are described in terms of variation around group means and variation of group means around an overall mean. If variations within groups are small relative to variations between groups, a difference in group means may be inferred. Chapter 7, "Hypothesis Tests" are used to quantify decisions.

This chapter treats ANOVA among groups, that is, among categorical predictors. ANOVA for regression, with continuous predictors, is discussed in "Tabulating Diagnostic Statistics" on page 9-13.

Multivariate analysis of variance (MANOVA), for data with multiple measured responses, is also discussed in this chapter.

ANOVA

In this section...

One-Way ANOVA

Introduction to One-Way ANOVA

The purpose of one-way ANOVA is to find out whether data from several groups have a common mean. That is, to determine whether the groups are actually different in the measured characteristic.

One-way ANOVA is a simple special case of the linear model. The one-way ANOVA form of the model is

$$y_{ij} = \alpha_{.j} + \varepsilon_{ij}$$

where:

- y_{ij} is a matrix of observations in which each column represents a different group.

- $a_{\cdot j}$ is a matrix whose columns are the group means. (The "dot j" notation means that a applies to all rows of column j. That is, the value a_{ij} is the same for all i.)
- ε_{ij} is a matrix of random disturbances.

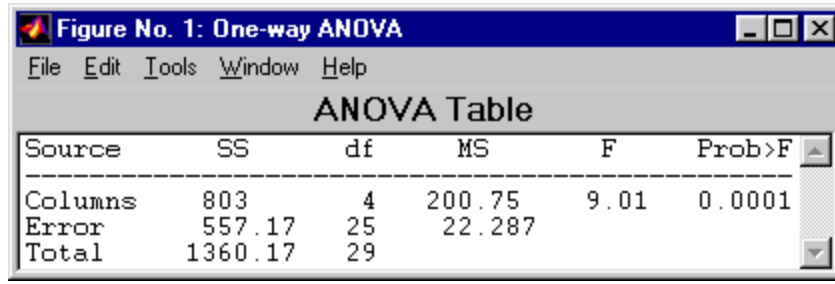
The model assumes that the columns of y are a constant plus a random disturbance. You want to know if the constants are all the same.

Example: One-Way ANOVA

The data below comes from a study by Hogg and Ledolter [48] of bacteria counts in shipments of milk. The columns of the matrix `hogg` represent different shipments. The rows are bacteria counts from cartons of milk chosen randomly from each shipment. Do some shipments have higher counts than others?

```
load hogg
hogg
hogg =

    24    14    11     7    19
    15     7     9     7    24
    21    12     7     4    19
    27    17    13     7    15
    33    14    12    12    10
    23    16    18    18    20

[p,tbl,stats] = anova1(hogg);
p
p =
   1.1971e-04
```

The standard ANOVA table has columns for the sums of squares, degrees of freedom, mean squares (SS/df), F statistic, and p value.

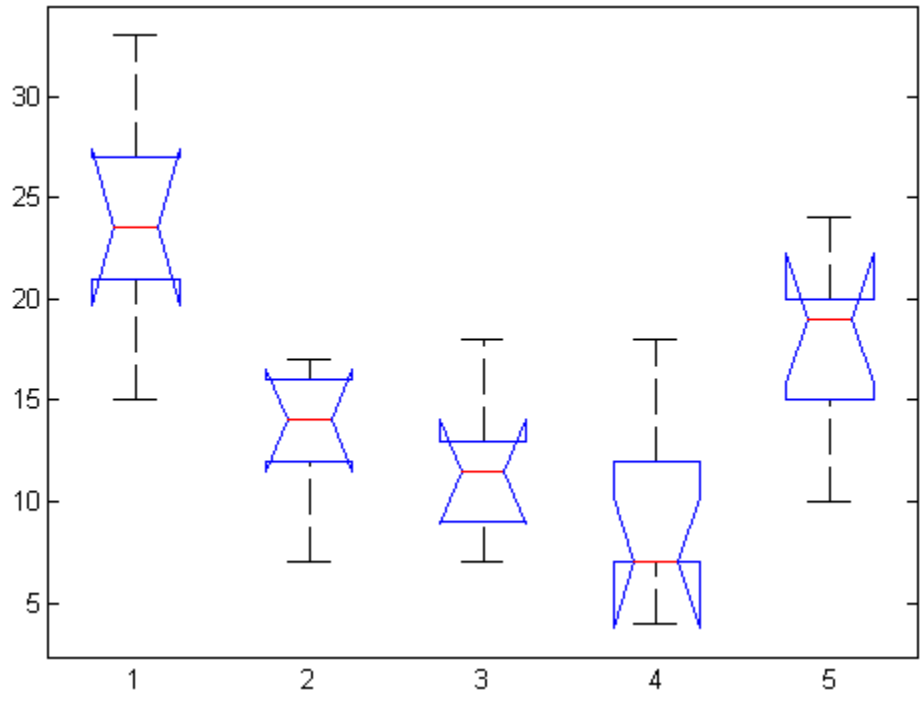


You can use the *F* statistic to do a hypothesis test to find out if the bacteria counts are the same. `anova1` returns the *p* value from this hypothesis test.

In this case the *p* value is about 0.0001, a very small value. This is a strong indication that the bacteria counts from the different shipments are not the same. An *F* statistic as extreme as the observed *F* would occur by chance only once in 10,000 times if the counts were truly equal.

The *p* value returned by `anova1` depends on assumptions about the random disturbances ε_{ij} in the model equation. For the *p* value to be correct, these disturbances need to be independent, normally distributed, and have constant variance.

You can get some graphical assurance that the means are different by looking at the box plots in the second figure window displayed by `anova1`. Note, however, that the notches are used for a comparison of medians, not a comparison of means. For more information on this display, see "Box Plots" on page 4-6.



Multiple Comparisons

Sometimes you need to determine not just whether there are any differences among the means, but specifically which pairs of means are significantly different. It is tempting to perform a series of *t* tests, one for each pair of means, but this procedure has a pitfall.

In a *t* test, you compute a *t* statistic and compare it to a critical value. The critical value is chosen so that when the means are really the same (any apparent difference is due to random chance), the probability that the *t* statistic will exceed the critical value is small, say 5%. When the means are different, the probability that the statistic will exceed the critical value is larger.

In this example there are five means, so there are 10 pairs of means to compare. It stands to reason that if all the means are the same, and if there is a 5% chance of incorrectly concluding that there is a difference in one pair,

then the probability of making at least one incorrect conclusion among all 10 pairs is much larger than 5%.

Fortunately, there are procedures known as *multiple comparison procedures* that are designed to compensate for multiple tests.

Example: Multiple Comparisons

You can perform a multiple comparison test using the `multcompare` function and supplying it with the `stats` output from `anova1`.

```
load hogg
[p,tbl,stats] = anova1(hogg);
[c,m] = multcompare(stats)
c =
    1.0000    2.0000    2.4953   10.5000   18.5047
    1.0000    3.0000    4.1619   12.1667   20.1714
    1.0000    4.0000    6.6619   14.6667   22.6714
    1.0000    5.0000   -2.0047    6.0000   14.0047
    2.0000    3.0000   -6.3381    1.6667    9.6714
    2.0000    4.0000   -3.8381    4.1667   12.1714
    2.0000    5.0000  -12.5047   -4.5000    3.5047
    3.0000    4.0000   -5.5047    2.5000   10.5047
    3.0000    5.0000  -14.1714   -6.1667    1.8381
    4.0000    5.0000  -16.6714   -8.6667   -0.6619
m =
   23.8333    1.9273
   13.3333    1.9273
   11.6667    1.9273
    9.1667    1.9273
   17.8333    1.9273
```

The first output from `multcompare` has one row for each pair of groups, with an estimate of the difference in group means and a confidence interval for that group. For example, the second row has the values

```
1.0000    3.0000    4.1619   12.1667   20.1714
```

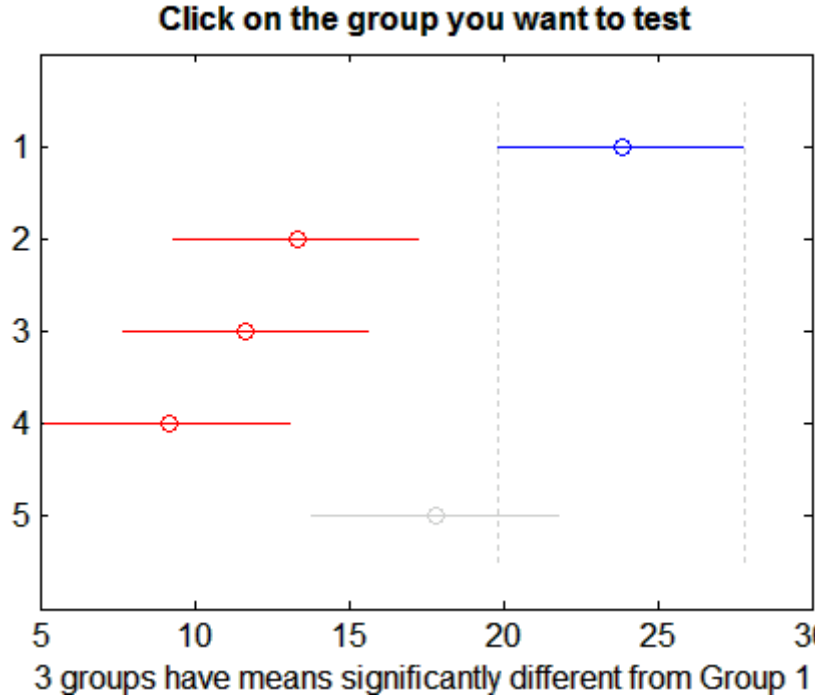
indicating that the mean of group 1 minus the mean of group 3 is estimated to be 12.1667, and a 95% confidence interval for this difference is

[4.1619, 20.1714]. This interval does not contain 0, so you can conclude that the means of groups 1 and 3 are different.

The second output contains the mean and its standard error for each group.

It is easier to visualize the difference between group means by looking at the graph that `multcompare` produces.

There are five groups. The graph instructs you to **Click on the group you want to test**. Three groups have slopes significantly different from group one.



The graph shows that group 1 is significantly different from groups 2, 3, and 4. By using the mouse to select group 4, you can determine that it is also significantly different from group 5. Other pairs are not significantly different.

Two-Way ANOVA

Introduction to Two-Way ANOVA

The purpose of two-way ANOVA is to find out whether data from several groups have a common mean. One-way ANOVA and two-way ANOVA differ in that the groups in two-way ANOVA have two categories of defining characteristics instead of one.

Suppose an automobile company has two factories, and each factory makes the same three models of car. It is reasonable to ask if the gas mileage in the cars varies from factory to factory as well as from model to model. There are two predictors, factory and model, to explain differences in mileage.

There could be an overall difference in mileage due to a difference in the production methods between factories. There is probably a difference in the mileage of the different models (irrespective of the factory) due to differences in design specifications. These effects are called *additive*.

Finally, a factory might make high mileage cars in one model (perhaps because of a superior production line), but not be different from the other factory for other models. This effect is called an *interaction*. It is impossible to detect an interaction unless there are duplicate observations for some combination of factory and car model.

Two-way ANOVA is a special case of the linear model. The two-way ANOVA form of the model is

$$y_{ijk} = \mu + \alpha_{.j} + \beta_{i.} + \gamma_{ij} + \varepsilon_{ijk}$$

where, with respect to the automobile example above:

- y_{ijk} is a matrix of gas mileage observations (with row index i, column index j, and repetition index k).
- μ is a constant matrix of the overall mean gas mileage.

- $a_{.j}$ is a matrix whose columns are the deviations of each car's gas mileage (from the mean gas mileage μ) that are attributable to the car's *model*. All values in a given column of $a_{.j}$ are identical, and the values in each row of $a_{.j}$ sum to 0.
- $\beta_{i.}$ is a matrix whose rows are the deviations of each car's gas mileage (from the mean gas mileage μ) that are attributable to the car's *factory*. All values in a given row of $\beta_{i.}$ are identical, and the values in each column of $\beta_{i.}$ sum to 0.
- γ_{ij} is a matrix of interactions. The values in each row of γ_{ij} sum to 0, and the values in each column of γ_{ij} sum to 0.
- ε_{ijk} is a matrix of random disturbances.

Example: Two-Way ANOVA

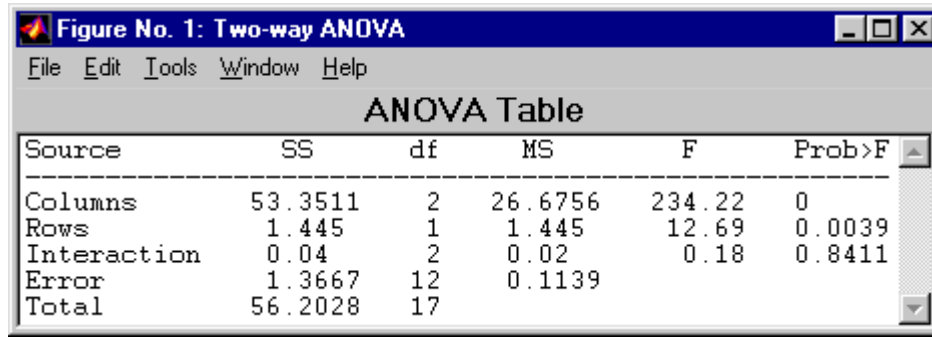
The purpose of the example is to determine the effect of car model and factory on the mileage rating of cars.

```
load mileage
mileage

mileage =

   33.3000   34.5000   37.4000
   33.4000   34.8000   36.8000
   32.9000   33.8000   37.6000
   32.6000   33.4000   36.6000
   32.5000   33.7000   37.0000
   33.0000   33.9000   36.7000

cars = 3;
[p,tbl,stats] = anova2(mileage,cars);
p

p =
    0.0000    0.0039    0.8411
```

There are three models of cars (columns) and two factories (rows). The reason there are six rows in `mileage` instead of two is that each factory provides

three cars of each model for the study. The data from the first factory is in the first three rows, and the data from the second factory is in the last three rows.

The standard ANOVA table has columns for the sums of squares, degrees-of-freedom, mean squares (SS/df), *F* statistics, and *p*-values.



Source	SS	df	MS	F	Prob>F
Columns	53.3511	2	26.6756	234.22	0
Rows	1.445	1	1.445	12.69	0.0039
Interaction	0.04	2	0.02	0.18	0.8411
Error	1.3667	12	0.1139		
Total	56.2028	17			

You can use the *F* statistics to do hypotheses tests to find out if the mileage is the same across models, factories, and model-factory pairs (after adjusting for the additive effects). `anova2` returns the *p* value from these tests.

The *p* value for the model effect is zero to four decimal places. This is a strong indication that the mileage varies from one model to another. An *F* statistic as extreme as the observed *F* would occur by chance less than once in 10,000 times if the gas mileage were truly equal from model to model. If you used the `multcompare` function to perform a multiple comparison test, you would find that each pair of the three models is significantly different.

The *p* value for the factory effect is 0.0039, which is also highly significant. This indicates that one factory is out-performing the other in the gas mileage of the cars it produces. The observed *p* value indicates that an *F* statistic as extreme as the observed *F* would occur by chance about four out of 1000 times if the gas mileage were truly equal from factory to factory.

There does not appear to be any interaction between factories and models. The *p* value, 0.8411, means that the observed result is quite likely (84 out 100 times) given that there is no interaction.

The p-values returned by `anova2` depend on assumptions about the random disturbances ε_{ijk} in the model equation. For the p-values to be correct these disturbances need to be independent, normally distributed, and have constant variance.

In addition, `anova2` requires that data be *balanced*, which in this case means there must be the same number of cars for each combination of model and factory. The next section discusses a function that supports unbalanced data with any number of predictors.

N-Way ANOVA

Introduction to N-Way ANOVA

You can use N-way ANOVA to determine if the means in a set of data differ when grouped by multiple factors. If they do differ, you can determine which factors or combinations of factors are associated with the difference.

N-way ANOVA is a generalization of two-way ANOVA. For three factors, the model can be written

$$y_{ijkl} = \mu + \alpha_{.j.} + \beta_{i..} + \gamma_{..k} + (\alpha\beta)_{ij.} + (\alpha\gamma)_{i.k} + (\beta\gamma)_{.jk} + (\alpha\beta\gamma)_{ijk} + \varepsilon_{ijkl}$$

In this notation parameters with two subscripts, such as $(\alpha\beta)_{ij.}$, represent the interaction effect of two factors. The parameter $(\alpha\beta\gamma)_{ijk}$ represents the three-way interaction. An ANOVA model can have the full set of parameters or any subset, but conventionally it does not include complex interaction terms unless it also includes all simpler terms for those factors. For example, one would generally not include the three-way interaction without also including all two-way interactions.

The anovan function performs N-way ANOVA. Unlike the anova1 and anova2 functions, anovan does not expect data in a tabular form. Instead, it expects a vector of response measurements and a separate vector (or text array) containing the values corresponding to each factor. This input data format is more convenient than matrices when there are more than two factors or when the number of measurements per factor combination is not constant.

N-Way ANOVA with a Small Data Set

Consider the following two-way example using anova2.

```
m = [23 15 20;27 17 63;43 3 55;41 9 90]
m =
    23    15    20
    27    17    63
    43     3    55
    41     9    90

anova2(m,2)

ans =
    0.0197    0.2234    0.2663
```

The factor information is implied by the shape of the matrix m and the number of measurements at each factor combination (2). Although anova2 does not actually require arrays of factor values, for illustrative purposes you could create them as follows.

```
cfactor = repmat(1:3,4,1)

cfactor =
     1     2     3
     1     2     3
     1     2     3
     1     2     3

rfactor = [ones(2,3); 2*ones(2,3)]

rfactor =

     1     1     1
```

```
     1     1     1
     2     2     2
     2     2     2
```

The `cfactor` matrix shows that each column of `m` represents a different level of the column factor. The `rfactor` matrix shows that the top two rows of `m` represent one level of the row factor, and bottom two rows of `m` represent a second level of the row factor. In other words, each value `m(i,j)` represents an observation at column factor level `cfactor(i,j)` and row factor level `rfactor(i,j)`.

To solve the above problem with `anovan`, you need to reshape the matrices `m`, `cfactor`, and `rfactor` to be vectors.

```
m = m(:);
cfactor = cfactor(:);
rfactor = rfactor(:);

[m cfactor rfactor]

ans =

    23     1     1
    27     1     1
    43     1     2
    41     1     2
    15     2     1
    17     2     1
     3     2     2
     9     2     2
    20     3     1
    63     3     1
    55     3     2
    90     3     2

anovan(m,{cfactor rfactor},2)

ans =

    0.0197
```

```
    0.2234
    0.2663
```

N-Way ANOVA with a Large Data Set

The previous example used `anova2` to study a small data set measuring car mileage. This example illustrates how to analyze a larger set of car data with mileage and other information on 406 cars made between 1970 and 1982. First, load the data set and look at the variable names.

```
load carbig
whos
```

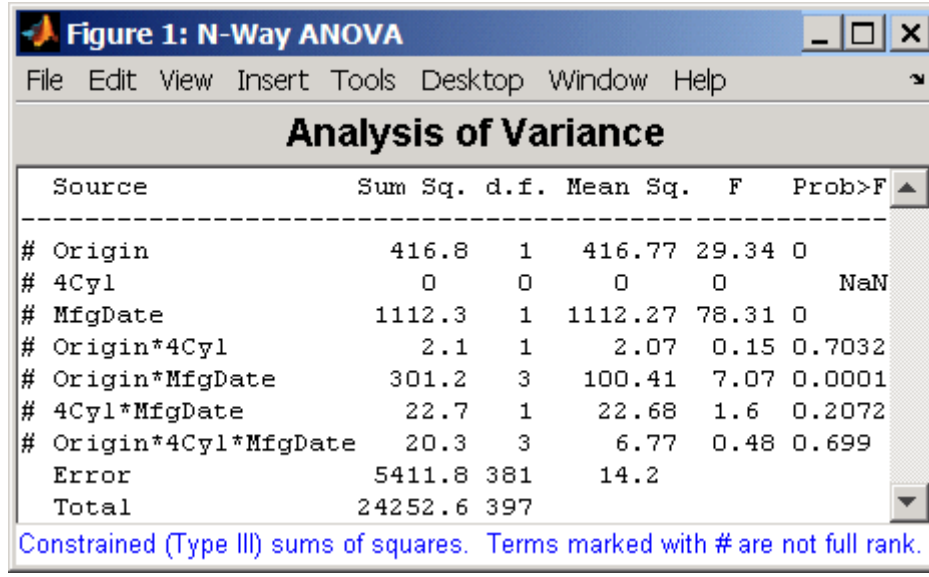
```
  Name               Size         Bytes  Class

  Acceleration     406x1           3248  double array
  Cylinders        406x1           3248  double array
  Displacement     406x1           3248  double array
  Horsepower       406x1           3248  double array
  MPG              406x1           3248  double array
  Model            406x36         29232  char array
  Model_Year       406x1           3248  double array
  Origin           406x7           5684  char array
  Weight           406x1           3248  double array
  cyl4             406x5           4060  char array
  org              406x7           5684  char array
  when             406x5           4060  char array
```

The example focusses on four variables. `MPG` is the number of miles per gallon for each of 406 cars (though some have missing values coded as `NaN`). The other three variables are factors: `cyl4` (four-cylinder car or not), `org` (car originated in Europe, Japan, or the USA), and `when` (car was built early in the period, in the middle of the period, or late in the period).

First, fit the full model, requesting up to three-way interactions and Type 3 sums-of-squares.

```
varnames = {'Origin';'4Cyl';'MfgDate'};
anovan(MPG,{org cyl4 when},3,3,varnames)
ans =
    0.0000
```

```
       NaN
         0
    0.7032
    0.0001
    0.2072
    0.6990
```



Note that many terms are marked by a # symbol as not having full rank, and one of them has zero degrees of freedom and is missing a *p* value. This can happen when there are missing factor combinations and the model has higher-order terms. In this case, the cross-tabulation below shows that there are no cars made in Europe during the early part of the period with other than four cylinders, as indicated by the `0` in `table(2,1,1)`.

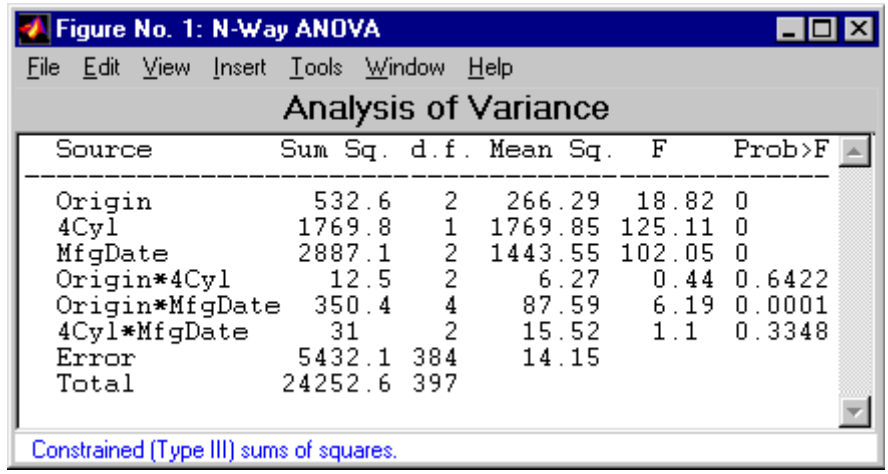
```
[table, chi2, p, factorvals] = crosstab(org,when,cyl4)

table(:,:,1) =

    82    75    25
     0     4     3
     3     3     4
```

```
table(:,:,2) =
    12    22    38
    23    26    17
    12    25    32

chi2 =

  207.7689

p =

     0

factorvals =

    'USA'       'Early'    'Other'
    'Europe'    'Mid'      'Four'
    'Japan'     'Late'          []
```

Consequently it is impossible to estimate the three-way interaction effects, and including the three-way interaction term in the model makes the fit singular.

Using even the limited information available in the ANOVA table, you can see that the three-way interaction has a p value of 0.699, so it is not significant. So this time you examine only two-way interactions.

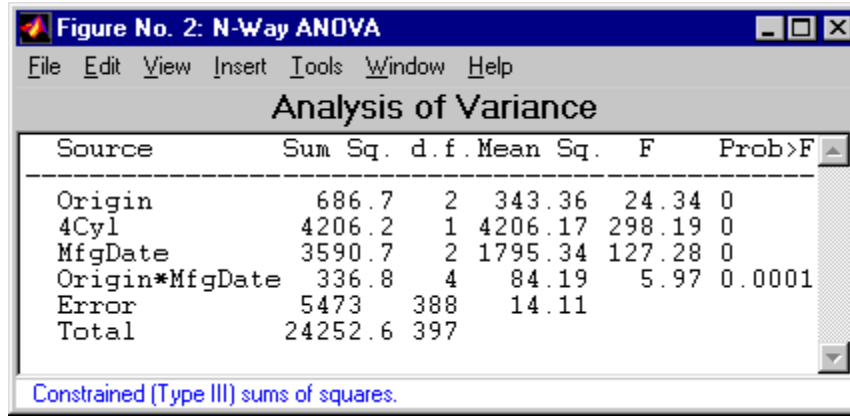
```
[p,tbl,stats,terms] = anovan(MPG,{org cyl4 when},2,3,varnames);
terms

terms =
     1     0     0
     0     1     0
     0     0     1
     1     1     0
     1     0     1
     0     1     1
```



Now all terms are estimable. The *p*-values for interaction term 4 (`Origin*4Cyl`) and interaction term 6 (`4Cyl*MfgDate`) are much larger than a typical cutoff value of 0.05, indicating these terms are not significant. You could choose to omit these terms and pool their effects into the error term. The output `terms` variable returns a matrix of codes, each of which is a bit pattern representing a term. You can omit terms from the model by deleting their entries from `terms` and running `anovan` again, this time supplying the resulting vector as the model argument.

```
terms([4 6],:) = []

terms =

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

anovan(MPG,{org cyl4 when},terms,3,varnames)

ans =

  1.0e-003 *
```

```
    0.0000
         0
         0
    0.1140
```



Now you have a more parsimonious model indicating that the mileage of these cars seems to be related to all three factors, and that the effect of the manufacturing date depends on where the car was made.

ANOVA with Random Effects

Introduction to ANOVA with Random Effects. In an ordinary ANOVA model, each grouping variable represents a fixed factor. The levels of that factor are a fixed set of values. Your goal is to determine whether different factor levels lead to different response values. This section presents an example that shows how to use `anovan` to fit models where a factor's levels represent a random selection from a larger (infinite) set of possible levels.

Setting Up the Model. To set up the example, first load the data, which is stored in a 6-by-3 matrix, `mileage`.

```
load mileage
```

The `anova2` function works only with balanced data, and it infers the values of the grouping variables from the row and column numbers of the input matrix. The `anovan` function, on the other hand, requires you to explicitly create vectors of grouping variable values. To create these vectors, do the following steps:

1. Create an array indicating the factory for each value in `mileage`. This array is 1 for the first column, 2 for the second, and 3 for the third.

   ```
   factory  = repmat(1:3,6,1);
   ```

2. Create an array indicating the car model for each mileage value. This array is 1 for the first three rows of mileage, and 2 for the remaining three rows.

   ```
   carmod = [ones(3,3); 2*ones(3,3)];
   ```

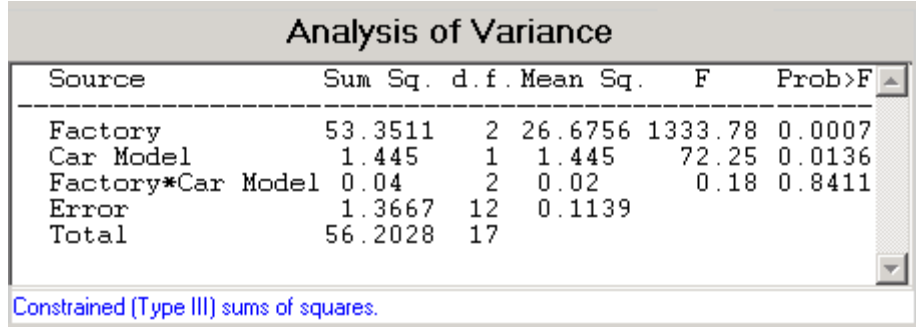
3. Turn these matrices into vectors and display them.

   ```
   mileage = mileage(:);
   factory = factory(:);
   carmod = carmod(:);
   [mileage factory carmod]

   ans =

      33.3000    1.0000    1.0000
      33.4000    1.0000    1.0000
      32.9000    1.0000    1.0000
      32.6000    1.0000    2.0000
      32.5000    1.0000    2.0000
      33.0000    1.0000    2.0000
      34.5000    2.0000    1.0000
      34.8000    2.0000    1.0000
      33.8000    2.0000    1.0000
      33.4000    2.0000    2.0000
      33.7000    2.0000    2.0000
   ```

```
33.9000    2.0000    2.0000
37.4000    3.0000    1.0000
36.8000    3.0000    1.0000
37.6000    3.0000    1.0000
36.6000    3.0000    2.0000
37.0000    3.0000    2.0000
36.7000    3.0000    2.0000
```

Fitting a Random Effects Model. Continuing the example from the preceding section, suppose you are studying a few factories but you want information about what would happen if you build these same car models in a different factory—either one that you already have or another that you might construct. To get this information, fit the analysis of variance model, specifying a model that includes an interaction term and that the `factory` factor is random.

```
[pvals,tbl,stats] = anovan(mileage, {factory carmod}, ...
'model',2, 'random',1,'varnames',{'Factory' 'Car Model'});
```



In the fixed effects version of this fit, which you get by omitting the inputs `'random',1` in the preceding code, the effect of car model is significant, with a p value of 0.0039. But in this example, which takes into account the random variation of the effect of the variable `'Car Model'` from one factory to another, the effect is still significant, but with a higher p value of 0.0136.

F Statistics for Models with Random Effects. The *F* statistic in a model having random effects is defined differently than in a model having all fixed effects. In the fixed effects model, you compute the *F* statistic for any term by taking the ratio of the mean square for that term with the mean square for error. In a random effects model, however, some *F* statistics use a different mean square in the denominator.

In the example described in "Setting Up the Model" on page 8-20, the effect of the variable `'Factory'` could vary across car models. In this case, the interaction mean square takes the place of the error mean square in the *F* statistic. The *F* statistic for factory is:

```
F = 1.445 / 0.02

F =

   72.2500
```

The degrees of freedom for the statistic are the degrees of freedom for the numerator (1) and denominator (2) mean squares. Therefore the *p* value for the statistic is:

```
pval = 1 - fcdf(F,1,2)

pval =

    0.0136
```

With random effects, the expected value of each mean square depends not only on the variance of the error term, but also on the variances contributed by the random effects. You can see these dependencies by writing the expected values as linear combinations of contributions from the various model terms. To find the coefficients of these linear combinations, enter `stats.ems`, which returns the `ems` field of the `stats` structure:

```
stats.ems

ans =

    6.0000    0.0000    3.0000    1.0000
    0.0000    9.0000    3.0000    1.0000
```

```
    0.0000    0.0000    3.0000    1.0000
         0         0         0    1.0000
```

To see text representations of the linear combinations, enter

```
stats.txtems

ans =

    '6*V(Factory)+3*V(Factory*Car Model)+V(Error)'
    '9*Q(Car Model)+3*V(Factory*Car Model)+V(Error)'
    '3*V(Factory*Car Model)+V(Error)'
    'V(Error)'
```

The expected value for the mean square due to car model (second term) includes contributions from a quadratic function of the car model effects, plus three times the variance of the interaction term's effect, plus the variance of the error term. Notice that if the car model effects were all zero, the expression would reduce to the expected mean square for the third term (the interaction term). That is why the *F* statistic for the car model effect uses the interaction mean square in the denominator.

In some cases there is no single term whose expected value matches the one required for the denominator of the*F*statistic. In that case, the denominator is a linear combination of mean squares. The `stats` structure contains fields giving the definitions of the denominators for each *F* statistic. The `txtdenom` field, `stats.txtdenom`, gives a text representation, and the `denom` field gives a matrix that defines a linear combination of the variances of terms in the model. For balanced models like this one, the `denom` matrix, `stats.denom`, contains zeros and ones, because the denominator is just a single term's mean square:

```
stats.txtdenom

ans =

    'MS(Factory*Car Model)'
    'MS(Factory*Car Model)'
    'MS(Error)'

stats.denom
```

```
ans =

   -0.0000    1.0000    0.0000
    0.0000    1.0000   -0.0000
    0.0000         0    1.0000
```

Variance Components. For the model described in "Setting Up the Model" on page 8-20, consider the mileage for a particular car of a particular model made at a random factory. The variance of that car is the sum of components, or contributions, one from each of the random terms.

```
stats.rtnames

ans =

    'Factory'
    'Factory*Car Model'
    'Error'
```

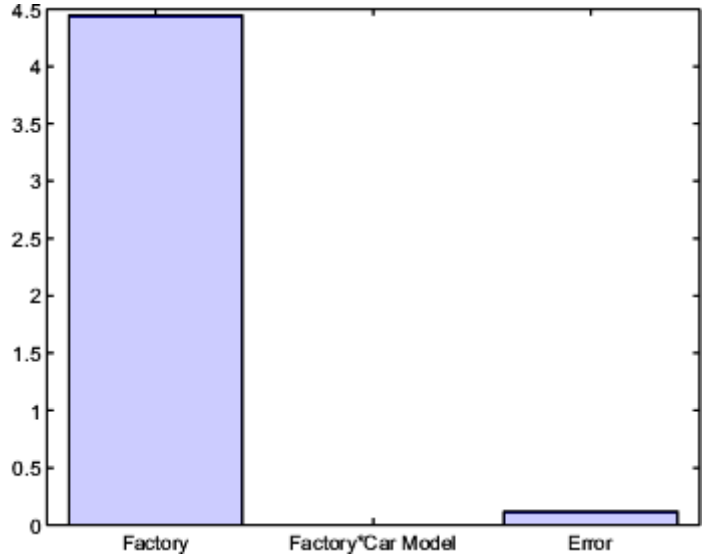
You do not know those variances, but you can estimate them from the data. Recall that the `ems` field of the `stats` structure expresses the expected value of each term's mean square as a linear combination of unknown variances for random terms, and unknown quadratic forms for fixed terms. If you take the expected mean square expressions for the random terms, and equate those expected values to the computed mean squares, you get a system of equations that you can solve for the unknown variances. These solutions are the variance component estimates. The `varest` field contains a variance component estimate for each term. The `rtnames` field contains the names of the random terms.

```
stats.varest

ans =

    4.4426
   -0.0313
    0.1139
```

Under some conditions, the variability attributed to a term is unusually low, and that term's variance component estimate is negative. In those cases it

is common to set the estimate to zero, which you might do, for example, to create a bar graph of the components.

```
bar(max(0,stats.varest))
set(gca,'xtick',1:3,'xticklabel',stats.rtnames)
```



You can also compute confidence bounds for the variance estimate. The `anovan` function does this by computing confidence bounds for the variance expected mean squares, and finding lower and upper limits on each variance component containing all of these bounds. This procedure leads to a set of bounds that is conservative for balanced data. (That is, 95% confidence bounds will have a probability of at least 95% of containing the true variances if the number of observations for each combination of grouping variables is the same.) For unbalanced data, these are approximations that are not guaranteed to be conservative.

```
[{'Term' 'Estimate' 'Lower' 'Upper'};
 stats.rtnames, num2cell([stats.varest stats.varci])]

ans =

    'Term'                 'Estimate'    'Lower'     'Upper'
```

```
'Factory'              [  4.4426]    [1.0736]    [175.6038]
'Factory*Car Model'    [ -0.0313]    [   NaN]    [     NaN]
'Error'                [  0.1139]    [0.0586]    [  0.3103]
```

Other ANOVA Models

The anovan function also has arguments that enable you to specify two other types of model terms. First, the 'nested' argument specifies a matrix that indicates which factors are nested within other factors. A nested factor is one that takes different values within each level its nested factor.

For example, the mileage data from the previous section assumed that the two car models produced in each factory were the same. Suppose instead, each factory produced two distinct car models for a total of six car models, and we numbered them 1 and 2 for each factory for convenience. Then, the car model is nested in factory. A more accurate and less ambiguous numbering of car model would be as follows:

Factory	Car Model
1	1
1	2
2	3
2	4
3	5
3	6

However, it is common with nested models to number the nested factor the same way in each nested factor.

Second, the 'continuous' argument specifies that some factors are to be treated as continuous variables. The remaining factors are categorical variables. Although the anovan function can fit models with multiple continuous and categorical predictors, the simplest model that combines one predictor of each type is known as an *analysis of covariance* model. The next section describes a specialized tool for fitting this model.

Analysis of Covariance

Introduction to Analysis of Covariance

Analysis of covariance is a technique for analyzing grouped data having a response (*y*, the variable to be predicted) and a predictor (*x*, the variable used to do the prediction). Using analysis of covariance, you can model *y* as a linear function of *x*, with the coefficients of the line possibly varying from group to group.

Analysis of Covariance Tool

The `aoctool` function opens an interactive graphical environment for fitting and prediction with analysis of covariance (ANOCOVA) models. It fits the following models for the *i*th group:

Same mean	$y = a + \varepsilon$
Separate means	$y = (a + a_i) + \varepsilon$
Same line	$y = a + \beta x + \varepsilon$
Parallel lines	$y = (a + a_i) + \beta x + \varepsilon$
Separate lines	$y = (a + a_i) + (\beta + \beta_i)x + \varepsilon$

For example, in the parallel lines model the intercept varies from one group to the next, but the slope is the same for each group. In the same mean model, there is a common intercept and no slope. In order to make the group coefficients well determined, the tool imposes the constraints

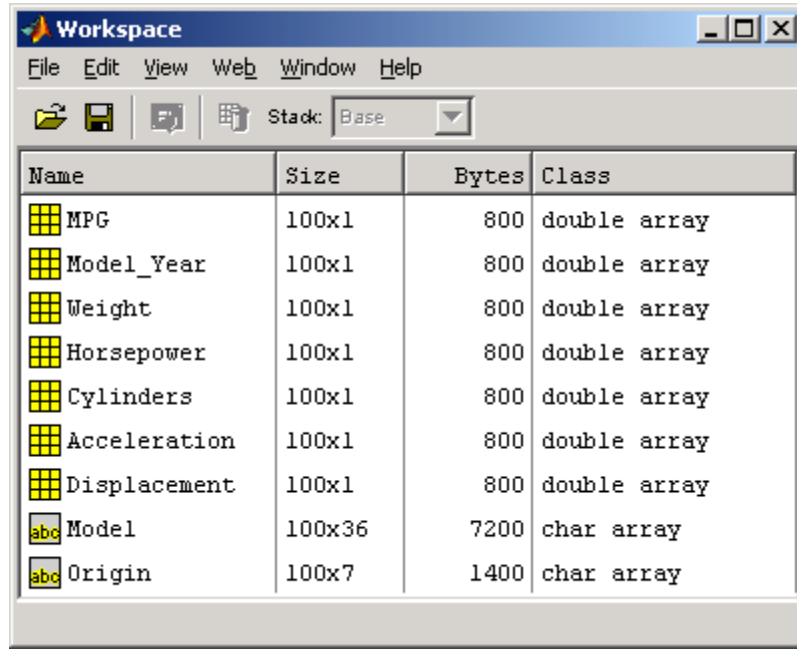
$$\sum \alpha_j = \sum \beta_j = 0$$

The following steps describe the use of `aoctool`.

1 **Load the data.** The Statistics Toolbox data set `carsmall.mat` contains information on cars from the years 1970, 1976, and 1982. This example studies the relationship between the weight of a car and its mileage, and whether this relationship has changed over the years. To start the demonstration, load the data set.

```
load carsmall
```

The Workspace Browser shows the variables in the data set.



Name	Size	Bytes	Class
MPG	100x1	800	double array
Model_Year	100x1	800	double array
Weight	100x1	800	double array
Horsepower	100x1	800	double array
Cylinders	100x1	800	double array
Acceleration	100x1	800	double array
Displacement	100x1	800	double array
Model	100x36	7200	char array
Origin	100x7	1400	char array

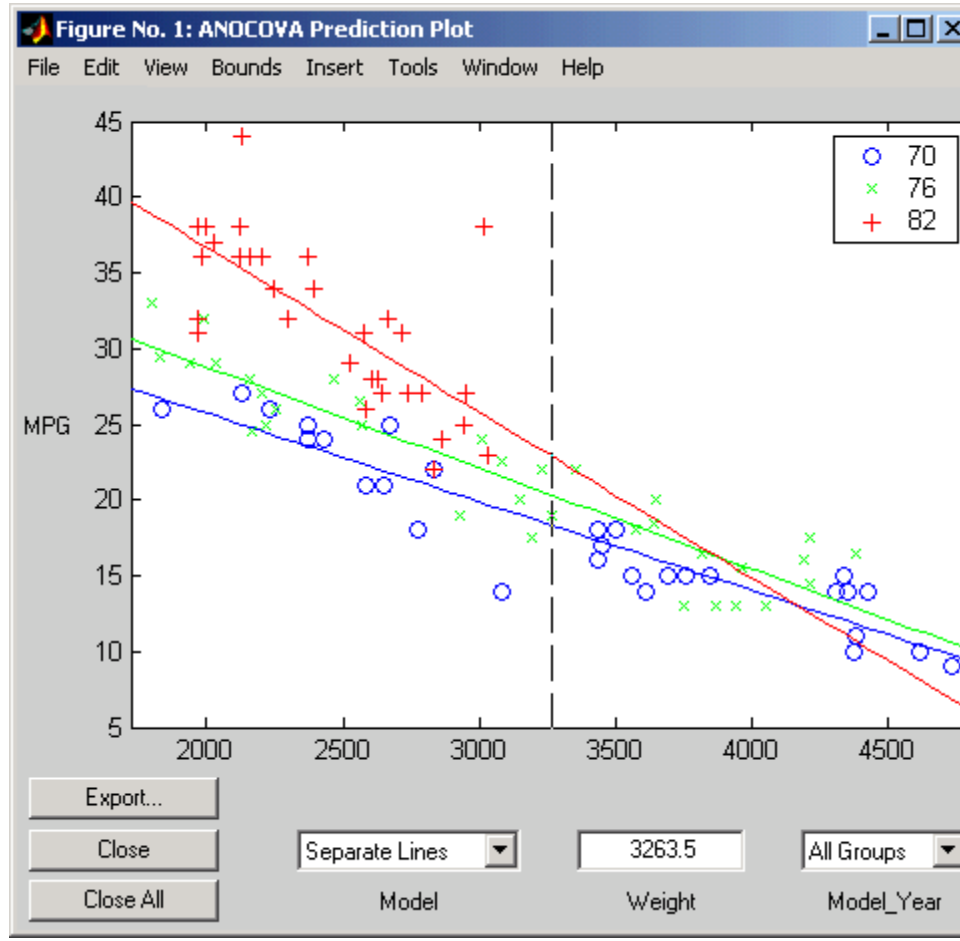
You can also use `aoctool` with your own data.

2 **Start the tool.** The following command calls `aoctool` to fit a separate line to the column vectors `Weight` and `MPG` for each of the three model group defined in `Model_Year`. The initial fit models the *y* variable, `MPG`, as a linear function of the *x* variable, `Weight`.

```
[h,atab,ctab,stats] = aoctool(Weight,MPG,Model_Year);
```

See the `aoctool` function reference page for detailed information about calling `aoctool`.

3 **Examine the output.** The graphical output consists of a main window with a plot, a table of coefficient estimates, and an analysis of variance table. In the plot, each `Model_Year` group has a separate line. The data points for each group are coded with the same color and symbol, and the fit for each group has the same color as the data points.



The coefficients of the three lines appear in the figure titled ANOCOVA Coefficients. You can see that the slopes are roughly –0.0078, with a small deviation for each group:

- Model year 1970: $y = (45.9798 - 8.5805) + (-0.0078 + 0.002)x + \varepsilon$
- Model year 1976: $y = (45.9798 - 3.8902) + (-0.0078 + 0.0011)x + \varepsilon$
- Model year 1982: $y = (45.9798 + 12.4707) + (-0.0078 - 0.0031)x + \varepsilon$

Figure No. 3: ANOCOVA Coefficients

File Edit View Insert Tools Window Help

Coefficient Estimates

Term	Estimate	Std. Err.	T	Prob>|T|
Intercept	45.9798	1.52085	30.23	0
70	-8.5805	1.96186	-4.37	0
76	-3.8902	1.86864	-2.08	0.0403
82	12.4707	2.5568	4.88	0
Slope	-0.0078	0.00056	-14	0
70	0.002	0.00066	2.96	0.0039
76	0.0011	0.00065	1.74	0.0849
82	-0.0031	0.001	-3.1	0.0026

Because the three fitted lines have slopes that are roughly similar, you may wonder if they really are the same. The `Model_Year*Weight` interaction expresses the difference in slopes, and the ANOVA table shows a test for the significance of this term. With an F statistic of 5.23 and a p value of 0.0072, the slopes are significantly different.

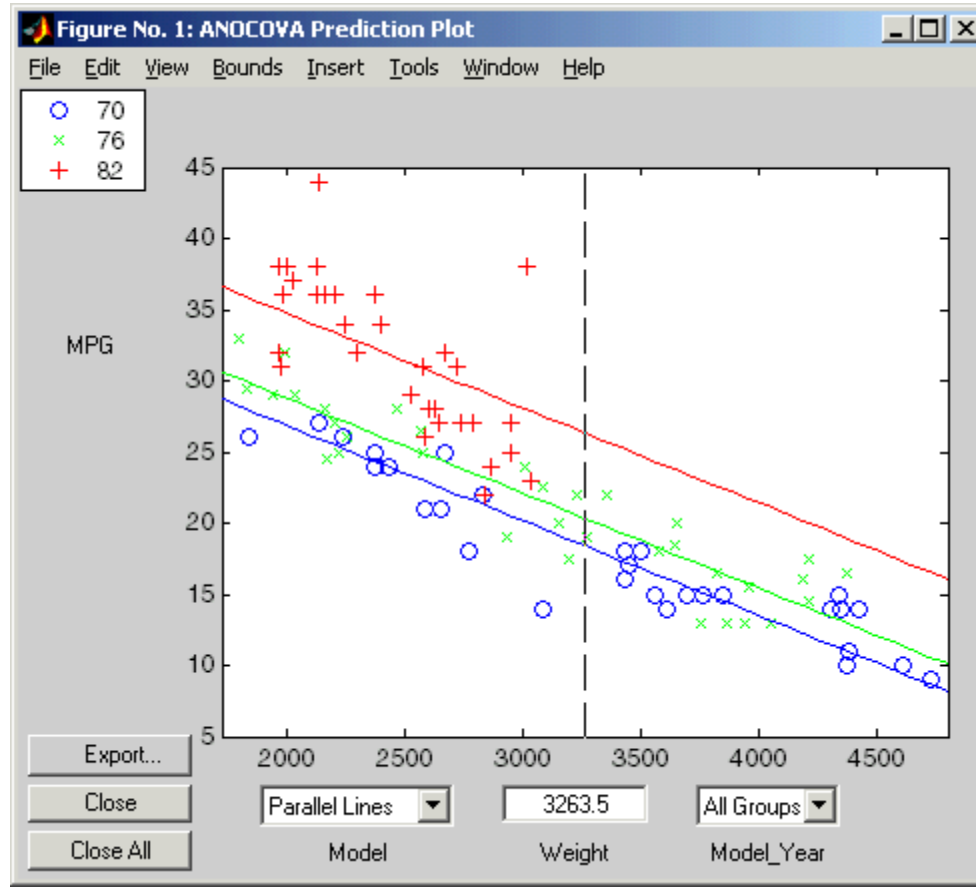
Figure No. 2: ANOCOVA Test Results

File Edit View Insert Tools Window Help

ANOVA Table

Source	d.f	Sum Sq	Mean Sq	F	Prob>F
Model_Year	2	807.69	403.84	51.98	0
Weight	1	2050.2	2050.2	263.87	0
Model_Year*Weigh	2	81.22	40.61	5.23	0.0072
Error	88	683.74	7.77		

4 Constrain the slopes to be the same. To examine the fits when the slopes are constrained to be the same, return to the ANOCOVA Prediction Plot window and use the **Model** pop-up menu to select a `Parallel Lines` model. The window updates to show the following graph.

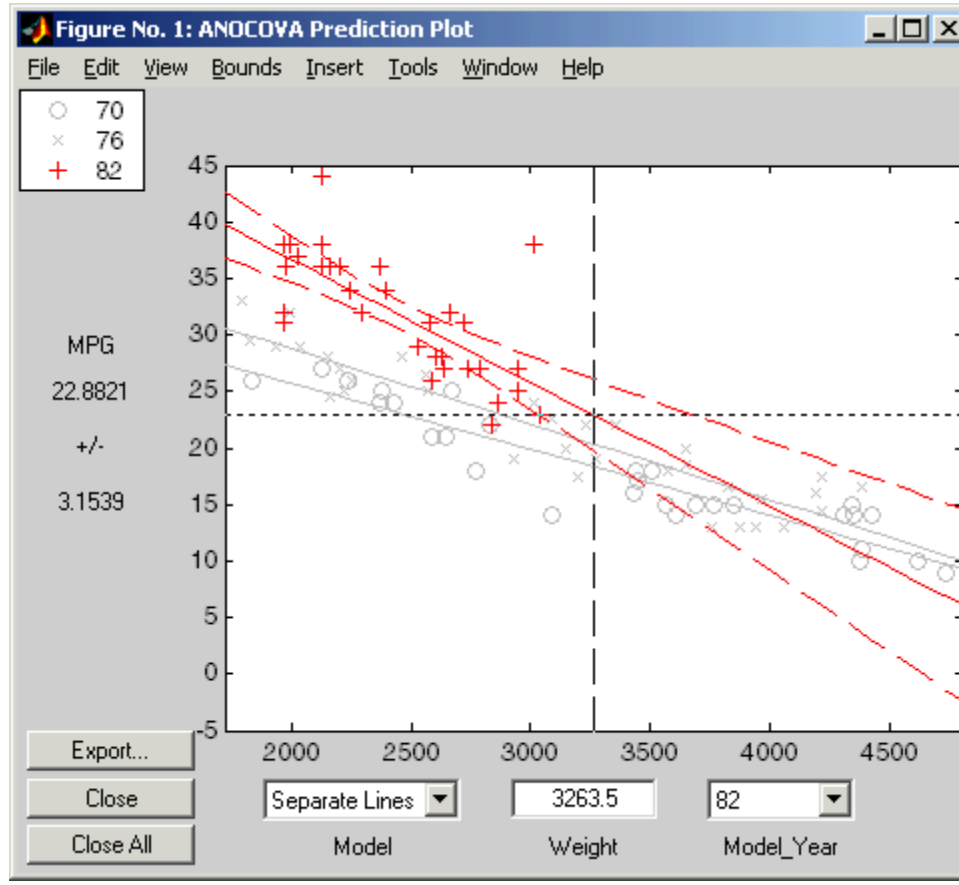


Though this fit looks reasonable, it is significantly worse than the `Separate Lines` model. Use the **Model** pop-up menu again to return to the original model.

Confidence Bounds

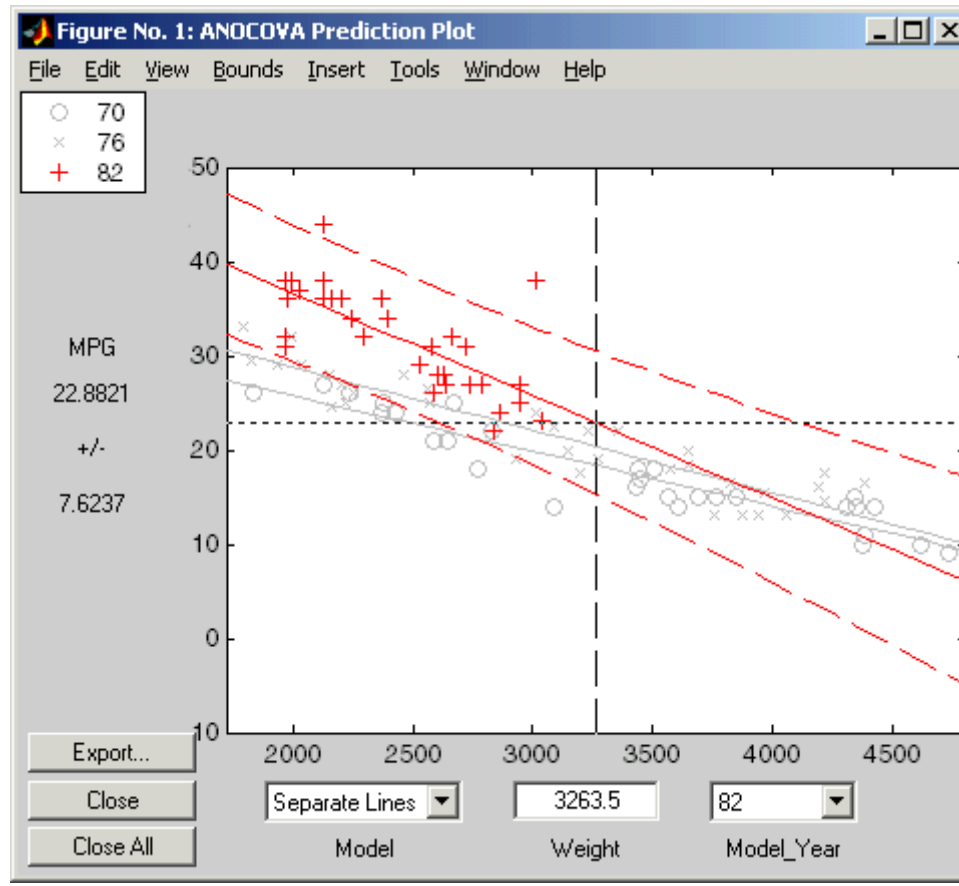
The example in "Analysis of Covariance Tool" on page 8-27 provides estimates of the relationship between `MPG` and `Weight` for each `Model_Year`, but how accurate are these estimates? To find out, you can superimpose confidence bounds on the fits by examining them one group at a time.

1. In the **Model_Year** menu at the lower right of the figure, change the setting from `All Groups` to 82. The data and fits for the other groups are dimmed, and confidence bounds appear around the 82 fit.



The dashed lines form an envelope around the fitted line for model year 82. Under the assumption that the true relationship is linear, these bounds provide a 95% confidence region for the true line. Note that the fits for the other model years are well outside these confidence bounds for `Weight` values between `2000` and `3000`.

2 Sometimes it is more valuable to be able to predict the response value for a new observation, not just estimate the average response value. Use the `aoctool` function **Bounds** menu to change the definition of the confidence bounds from `Line` to `Observation`. The resulting wider intervals reflect the uncertainty in the parameter estimates as well as the randomness of a new observation.



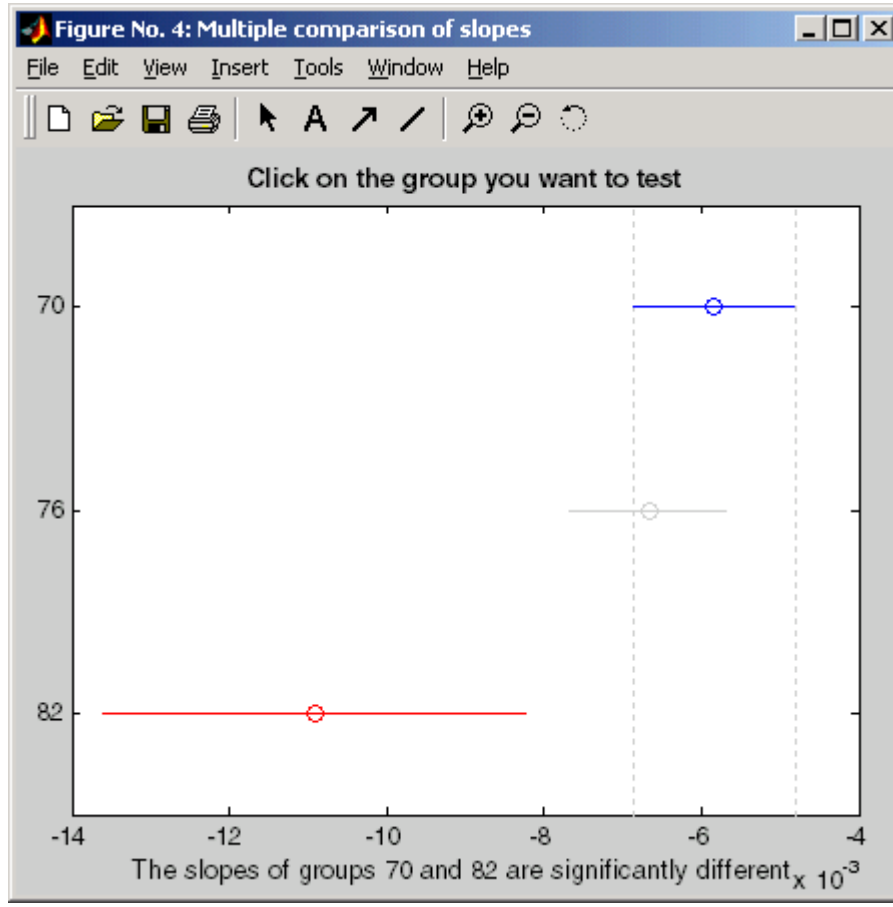
Like the `polytool` function, the `aoctool` function has cross hairs that you can use to manipulate the `Weight` and watch the estimate and confidence bounds along the *y*-axis update. These values appear only when a single group is selected, not when `All Groups` is selected.

Multiple Comparisons

You can perform a multiple comparison test by using the `stats` output structure from `aoctool` as input to the `multcompare` function. The `multcompare` function can test either slopes, intercepts, or population marginal means (the predicted MPG of the mean weight for each group). The example in "Analysis of Covariance Tool" on page 8-27 shows that the slopes are not all the same, but could it be that two are the same and only the other one is different? You can test that hypothesis.

```
multcompare(stats,0.05,'on','','s')

ans =
    1.0000    2.0000   -0.0012    0.0008    0.0029
    1.0000    3.0000    0.0013    0.0051    0.0088
    2.0000    3.0000    0.0005    0.0042    0.0079
```

This matrix shows that the estimated difference between the intercepts of groups 1 and 2 (1970 and 1976) is 0.0008, and a confidence interval for the difference is [–0.0012, 0.0029]. There is no significant difference between the two. There are significant differences, however, between the intercept for 1982 and each of the other two. The graph shows the same information.



Note that the `stats` structure was created in the initial call to the `aoctool` function, so it is based on the initial model fit (typically a separate-lines model). If you change the model interactively and want to base your multiple comparisons on the new model, you need to run `aoctool` again to get another `stats` structure, this time specifying your new model as the initial model.

Nonparametric Methods

- "Introduction to Nonparametric Methods" on page 8-36

Introduction to Nonparametric Methods

Statistics Toolbox functions include nonparametric versions of one-way and two-way analysis of variance. Unlike classical tests, nonparametric tests make only mild assumptions about the data, and are appropriate when the distribution of the data is non-normal. On the other hand, they are less powerful than classical methods for normally distributed data.

Both of the nonparametric functions described here will return a `stats` structure that can be used as an input to the `multcompare` function for multiple comparisons.

Kruskal-Wallis Test

The example "Example: One-Way ANOVA" on page 8-4 uses one-way analysis of variance to determine if the bacteria counts of milk varied from shipment to shipment. The one-way analysis rests on the assumption that the measurements are independent, and that each has a normal distribution with a common variance and with a mean that was constant in each column. You can conclude that the column means were not all the same. The following example repeats that analysis using a nonparametric procedure.

The Kruskal-Wallis test is a nonparametric version of one-way analysis of variance. The assumption behind this test is that the measurements come from a continuous distribution, but not necessarily a normal distribution. The test is based on an analysis of variance using the ranks of the data values, not the data values themselves. Output includes a table similar to an ANOVA table, and a box plot.

You can run this test as follows:

```
load hogg

p = kruskalwallis(hogg)
p =
    0.0020
```

The low p value means the Kruskal-Wallis test results agree with the one-way analysis of variance results.

Friedman's Test

"Example: Two-Way ANOVA" on page 8-10 uses two-way analysis of variance to study the effect of car model and factory on car mileage. The example tests whether either of these factors has a significant effect on mileage, and whether there is an interaction between these factors. The conclusion of the example is there is no interaction, but that each individual factor has a significant effect. The next example examines whether a nonparametric analysis leads to the same conclusion.

Friedman's test is a nonparametric test for data having a two-way layout (data grouped by two categorical factors). Unlike two-way analysis of variance, Friedman's test does not treat the two factors symmetrically and it does not test for an interaction between them. Instead, it is a test for whether the columns are different after adjusting for possible row differences. The test is based on an analysis of variance using the ranks of the data across categories of the row factor. Output includes a table similar to an ANOVA table.

You can run Friedman's test as follows.

```
load mileage
p = friedman(mileage,3)
p =
  7.4659e-004
```

Recall the classical analysis of variance gave a p value to test column effects, row effects, and interaction effects. This p value is for column effects. Using either this p value or the p value from ANOVA ($p < 0.0001$), you conclude that there are significant column effects.

In order to test for row effects, you need to rearrange the data to swap the roles of the rows in columns. For a data matrix `x` with no replications, you could simply transpose the data and type

```
p = friedman(x')
```

With replicated data it is slightly more complicated. A simple way is to transform the matrix into a three-dimensional array with the first dimension

representing the replicates, swapping the other two dimensions, and restoring the two-dimensional shape.

```
x = reshape(mileage, [3 2 3]);
x = permute(x,[1 3 2]);
x = reshape(x,[9 2])
x =
   33.3000   32.6000
   33.4000   32.5000
   32.9000   33.0000
   34.5000   33.4000
   34.8000   33.7000
   33.8000   33.9000
   37.4000   36.6000
   36.8000   37.0000
   37.6000   36.7000

friedman(x,3)
ans =
    0.0082
```

Again, the conclusion is similar to that of the classical analysis of variance. Both this p value and the one from ANOVA ($p = 0.0039$) lead you to conclude that there are significant row effects.

You cannot use Friedman's test to test for interactions between the row and column factors.

MANOVA

In this section...

Introduction to MANOVA

The analysis of variance technique in "Example: One-Way ANOVA" on page 8-4 takes a set of grouped data and determine whether the mean of a variable differs significantly among groups. Often there are multiple response variables, and you are interested in determining whether the entire set of means is different from one group to the next. There is a multivariate version of analysis of variance that can address the problem.

ANOVA with Multiple Responses

The `carsmall` data set has measurements on a variety of car models from the years 1970, 1976, and 1982. Suppose you are interested in whether the characteristics of the cars have changed over time.

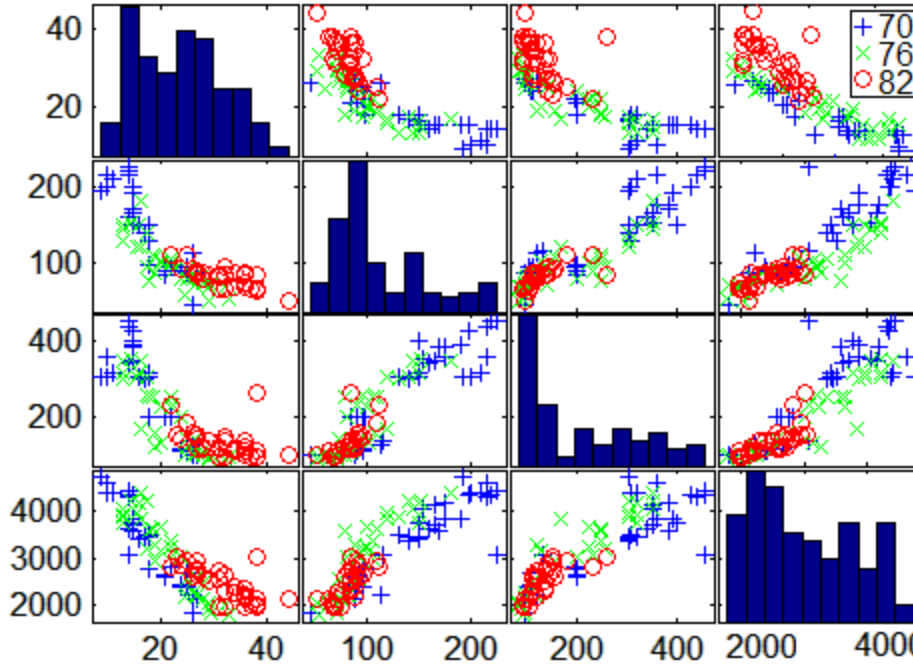
First, load the data.

```
load carsmall
whos
  Name              Size          Bytes  Class
  Acceleration     100x1            800  double array
  Cylinders        100x1            800  double array
  Displacement     100x1            800  double array
  Horsepower       100x1            800  double array
  MPG              100x1            800  double array
  Model            100x36          7200  char array
  Model_Year       100x1            800  double array
  Origin           100x7           1400  char array
  Weight           100x1            800  double array
```

Four of these variables (`Acceleration`, `Displacement`, `Horsepower`, and `MPG`) are continuous measurements on individual car models. The variable

`Model_Year` indicates the year in which the car was made. You can create a grouped plot matrix of these variables using the `gplotmatrix` function.

```
x = [MPG Horsepower Displacement Weight];
gplotmatrix(x,[],Model_Year,[],'+xo')
```



(When the second argument of `gplotmatrix` is empty, the function graphs the columns of the `x` argument against each other, and places histograms along the diagonals. The empty fourth argument produces a graph with the default colors. The fifth argument controls the symbols used to distinguish between groups.)

It appears the cars do differ from year to year. The upper right plot, for example, is a graph of `MPG` versus `Weight`. The 1982 cars appear to have higher mileage than the older cars, and they appear to weigh less on average. But as a group, are the three years significantly different from one another? The `manova1` function can answer that question.

```
[d,p,stats] = manova1(x,Model_Year)
```

```
d =
     2
p =
  1.0e-006 *
         0
    0.1141
stats =
           W: [4x4 double]
           B: [4x4 double]
           T: [4x4 double]
         dfW: 90
         dfB: 2
         dfT: 92
      lambda: [2x1 double]
       chisq: [2x1 double]
     chisqdf: [2x1 double]
    eigenval: [4x1 double]
    eigenvec: [4x4 double]
       canon: [100x4 double]
       mdist: [100x1 double]
      gmdist: [3x3 double]
```

The `manova1` function produces three outputs:

- The first output, `d`, is an estimate of the dimension of the group means. If the means were all the same, the dimension would be 0, indicating that the means are at the same point. If the means differed but fell along a line, the dimension would be 1. In the example the dimension is 2, indicating that the group means fall in a plane but not along a line. This is the largest possible dimension for the means of three groups.
- The second output, `p`, is a vector of *p*-values for a sequence of tests. The first *p* value tests whether the dimension is 0, the next whether the dimension is 1, and so on. In this case both *p*-values are small. That's why the estimated dimension is 2.
- The third output, `stats`, is a structure containing several fields, described in the following section.

The Fields of the stats Structure

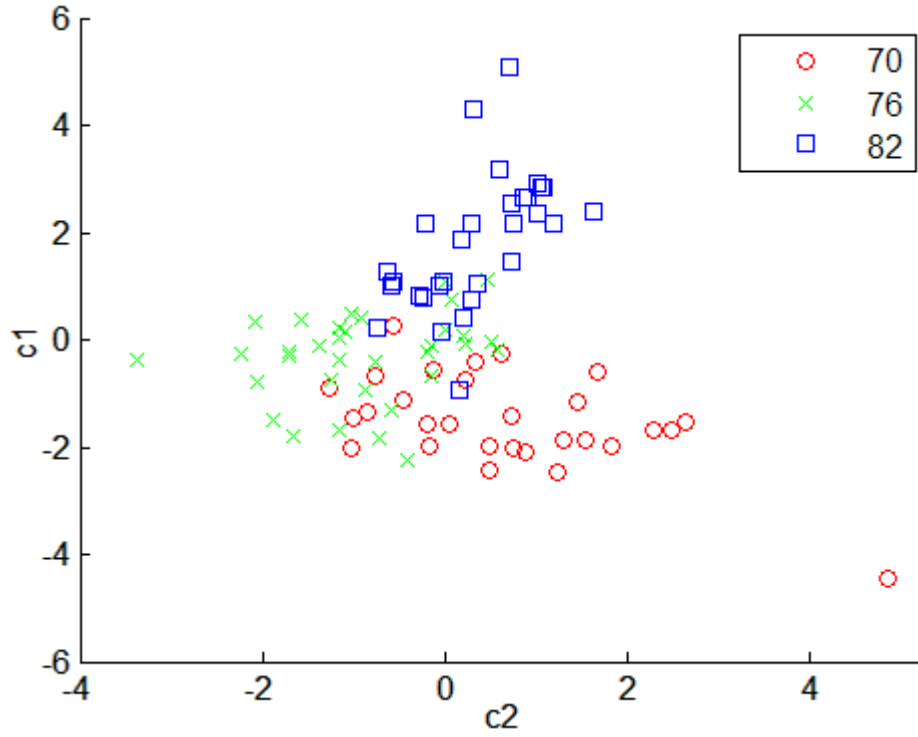
The `W`, `B`, and `T` fields are matrix analogs to the within, between, and total sums of squares in ordinary one-way analysis of variance. The next three fields are the degrees of freedom for these matrices. Fields `lambda`, `chisq`, and `chisqdf` are the ingredients of the test for the dimensionality of the group means. (The *p*-values for these tests are the first output argument of `manova1`.)

The next three fields are used to do a canonical analysis. Recall that in principal components analysis ("Principal Component Analysis (PCA)" on page 10-31) you look for the combination of the original variables that has the largest possible variation. In multivariate analysis of variance, you instead look for the linear combination of the original variables that has the largest separation between groups. It is the single variable that would give the most significant result in a univariate one-way analysis of variance. Having found that combination, you next look for the combination with the second highest separation, and so on.

The `eigenvec` field is a matrix that defines the coefficients of the linear combinations of the original variables. The `eigenval` field is a vector measuring the ratio of the between-group variance to the within-group variance for the corresponding linear combination. The `canon` field is a matrix of the canonical variable values. Each column is a linear combination of the mean-centered original variables, using coefficients from the `eigenvec` matrix.

A grouped scatter plot of the first two canonical variables shows more separation between groups then a grouped scatter plot of any pair of original variables. In this example it shows three clouds of points, overlapping but with distinct centers. One point in the bottom right sits apart from the others. By using the `gname` function, you can see that this is the 20th point.

```
c1 = stats.canon(:,1);
c2 = stats.canon(:,2);
gscatter(c2,c1,Model_Year,[],'oxs')
gname
```



Roughly speaking, the first canonical variable, `c1`, separates the 1982 cars (which have high values of `c1`) from the older cars. The second canonical variable, `c2`, reveals some separation between the 1970 and 1976 cars.

The final two fields of the `stats` structure are Mahalanobis distances. The `mdist` field measures the distance from each point to its group mean. Points with large values may be outliers. In this data set, the largest outlier is the one in the scatter plot, the Buick Estate station wagon. (Note that you could have supplied the model name to the `gname` function above if you wanted to label the point with its model name rather than its row number.)

```
max(stats.mdist)
ans =
   31.5273
find(stats.mdist == ans)
ans =
```

```
   20
Model(20,:)
ans =
   buick_estate_wagon_(sw)
```

The `gmdist` field measures the distances between each pair of group means. The following commands examine the group means and their distances:

```
grpstats(x, Model_Year)
ans =
  1.0e+003 *
    0.0177    0.1489    0.2869    3.4413
    0.0216    0.1011    0.1978    3.0787
    0.0317    0.0815    0.1289    2.4535
stats.gmdist
ans =
         0    3.8277   11.1106
    3.8277         0    6.1374
   11.1106    6.1374         0
```

As might be expected, the multivariate distance between the extreme years 1970 and 1982 (11.1) is larger than the difference between more closely spaced years (3.8 and 6.1). This is consistent with the scatter plots, where the points seem to follow a progression as the year changes from 1970 through 1976 to 1982. If you had more groups, you might find it instructive to use the `manovacluster` function to draw a diagram that presents clusters of the groups, formed using the distances between their means.

9

Parametric Regression Analysis

Introduction to Parametric Regression Analysis

Regression is the process of fitting models to data. The process depends on the model. If a model is parametric, regression estimates the parameters from the data. If a model is linear in the parameters, estimation is based on methods from linear algebra that minimize the norm of a residual vector. If a model is nonlinear in the parameters, estimation is based on search methods from optimization that minimize the norm of a residual vector. Nonparametric models, like "Classification Trees and Regression Trees" on page 13-27, use methods all their own.

This chapter considers data and models with continuous predictors and responses. Categorical predictors are the subject of Chapter 8, "Analysis of Variance". Categorical responses are the subject of Chapter 12, "Parametric Classification" and Chapter 13, "Nonparametric Supervised Learning".

Linear Regression

In this section...

Linear Regression Models

In statistics, linear regression models often take the form of something like this:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_1 x_2 + \beta_4 x_1^2 + \beta_5 x_2^2 + \varepsilon$$

Here a response variable y is modeled as a combination of constant, linear, interaction, and quadratic terms formed from two predictor variables x_1 and x_2. Uncontrolled factors and experimental errors are modeled by ε. Given data on x_1, x_2, and y, *regression* estimates the model parameters β_j (j = 1, ..., 5).

More general linear regression models represent the relationship between a continuous response y and a continuous or categorical predictor $\boldsymbol{x}$ in the form:

$$y = \beta_1 f_1(\boldsymbol{x}) + \ldots + \beta_p f_p(\boldsymbol{x}) + \varepsilon$$

The response is modeled as a linear combination of (not necessarily linear) functions of the predictor, plus a random error ε. The expressions $f_j(\boldsymbol{x})$ ($j = 1, \ldots, p$) are the *terms* of the model. The β_j ($j = 1, \ldots, p$) are the *coefficients*. Errors ε are assumed to be uncorrelated and distributed with mean 0 and constant (but unknown) variance.

Examples of linear regression models with a scalar predictor variable x include:

- Linear additive (straight-line) models — Terms are $f_1(x) = 1$ and $f_2(x) = x$.
- Polynomial models — Terms are $f_1(x) = 1$, $f_2(x) = x$, …, $f_p(x) = x^{p-1}$.
- Chebyshev orthogonal polynomial models — Terms are $f_1(x) = 1$, $f_2(x) = x$, …, $f_p(x) = 2xf_{p-1}(x) - f_{p-2}(x)$.
- Fourier trigonometric polynomial models — Terms are $f_1(x) = 1/2$ and sines and cosines of different frequencies.

Examples of linear regression models with a vector of predictor variables $\boldsymbol{x} = (x_1, \ldots, x_N)$ include:

- Linear additive (hyperplane) models — Terms are $f_1(\boldsymbol{x}) = 1$ and $f_{k+1}(\boldsymbol{x}) = x_k$ ($k = 1, \ldots, N$).
- Pairwise interaction models — Terms are linear additive terms plus $g_{k_1k_2}(\boldsymbol{x}) = x_{k_1}x_{k_2}$ ($k_1, k_2 = 1, \ldots, N, k_1 \neq k_2$).
- Quadratic models — Terms are pairwise interaction terms plus $h_k(\boldsymbol{x}) = x_k^2$ ($k = 1, \ldots, N$).
- Pure quadratic models — Terms are quadratic terms minus the $g_{k_1k_2}(\boldsymbol{x})$ terms.

Whether or not the predictor $\boldsymbol{x}$ is a vector of predictor variables, *multivariate regression* refers to the case where the response $\boldsymbol{y} = (y_1, \ldots, y_M)$ is a vector of M response variables. See "Multivariate Regression" on page 9-71 for more on multivariate regression models.

Given n independent observations $(\boldsymbol{x}_1, y_1), \ldots, (\boldsymbol{x}_n, y_n)$ of the predictor $\boldsymbol{x}$ and the response y, the linear regression model becomes an n-by-p system of equations:

$$\underbrace{\begin{pmatrix} y_1 \\ \vdots \\ y_n \end{pmatrix}}_{y} = \underbrace{\begin{pmatrix} f_1(\boldsymbol{x}_1) & \cdots & f_p(\boldsymbol{x}_1) \\ \vdots & \ddots & \vdots \\ f_1(\boldsymbol{x}_n) & \cdots & f_p(\boldsymbol{x}_n) \end{pmatrix}}_{X} \underbrace{\begin{pmatrix} \beta_1 \\ \vdots \\ \beta_p \end{pmatrix}}_{\beta} + \underbrace{\begin{pmatrix} \varepsilon_1 \\ \vdots \\ \varepsilon_n \end{pmatrix}}_{\varepsilon}$$

X is the *design matrix* of the system. The columns of X are the terms of the model evaluated at the predictors. To fit the model to the data, the system must be solved for the p coefficient values in $\beta = (\beta_1, \ldots, \beta_p)^T$.

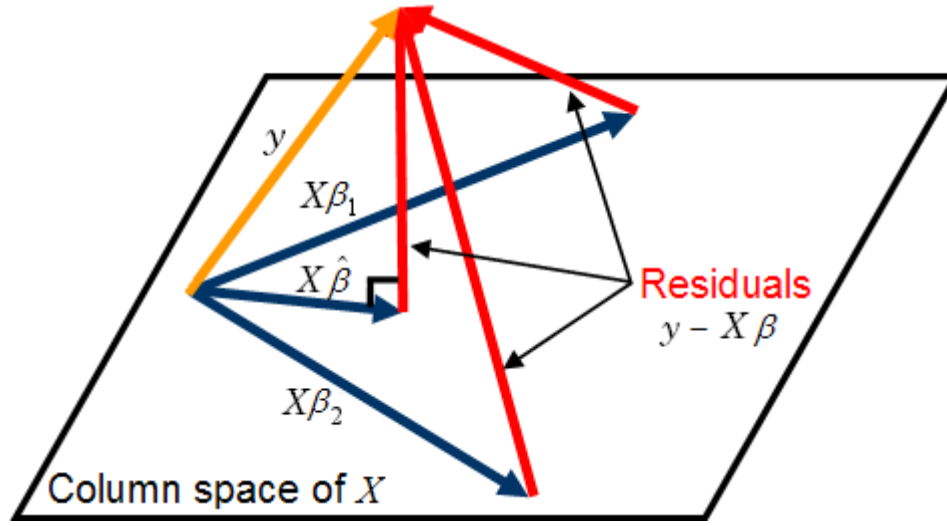
The MATLAB backslash operator `\` (`mldivide`) solves systems of linear equations. Ignoring the unknown error ε, MATLAB estimates model coefficients in $y = X\beta$ using

```
betahat = X\y
```

where `X` is the design matrix and `y` is the vector of observed responses. MATLAB returns the least-squares solution to the system; `betahat` minimizes the norm of the *residual* vector `y-X*beta` over all `beta`. If the system is consistent, the norm is `0` and the solution is exact. In this case, the regression model interpolates the data. In more typical regression cases where $n > p$ and the system is overdetermined, the least-squares solution estimates model coefficients obscured by the error ε.

The least-squares estimator `betahat` has several important statistical properties. First, it is unbiased, with expected value β. Second, by the Gauss-Markov theorem, it has minimum variance among all unbiased estimators formed from linear combinations of the response data. Under the additional assumption that ε is normally distributed, `betahat` is a maximum likelihood estimator. The assumption also implies that the estimates themselves are normally distributed, which is useful for computing confidence intervals. Even without the assumption, by the Central Limit theorem, the estimates have an approximate normal distribution if the sample size is large enough.

Visualize the least-squares estimator as follows.



For `betahat` to minimize `norm(y-X*beta)`, `y-X*betahat` must be perpendicular to the column space of `X`, which contains all linear combinations of the model terms. This requirement is summarized in the *normal equations*, which express vanishing inner products between `y-X*betahat` and the columns of `X`:

$$X^T\left(y - X\hat{\beta}\right) = 0$$

or

$$X^T X\hat{\beta} = X^T y$$

If `X` is *n*-by-*p*, the normal equations are a *p*-by-*p* square system with solution `betahat = inv(X'*X)*X'*y`, where `inv` is the MATLAB inverse operator. The matrix `inv(X'*X)*X'` is the *pseudoinverse* of `X`, computed by the MATLAB function `pinv`.

The normal equations are often badly conditioned relative to the original system $y = X\beta$ (the coefficient estimates are much more sensitive to the model error ε), so the MATLAB backslash operator avoids solving them directly.

Instead, a QR (orthogonal, triangular) decomposition of `X` is used to create a simpler, more stable triangular system:

$$\begin{aligned} X^T X\hat{\beta} &= X^T y \\ (QR)^T (QR)\hat{\beta} &= (QR)^T y \\ R^T Q^T QR\hat{\beta} &= R^T Q^T y \\ R^T R\hat{\beta} &= R^T Q^T y \\ R\hat{\beta} &= Q^T y \end{aligned}$$

Statistics Toolbox functions like `regress` and `regstats` call the MATLAB backslash operator to perform linear regression. The QR decomposition is also used for efficient computation of confidence intervals.

Once `betahat` is computed, the model can be evaluated at the predictor data:

```
yhat = X*betahat
```

or

```
yhat = X*inv(X'*X)*X'*y
```

`H = X*inv(X'*X)*X'` is the *hat matrix*. It is a square, symmetric n-by-n matrix determined by the predictor data. The diagonal elements `H(i,i)` (i = 1, ..., n) give the *leverage* of the ith observation. Since `yhat = H*y`, leverage values determine the influence of the observed response `y(i)` on the predicted response `yhat(i)`. For leverage values near 1, the predicted response approximates the observed response. The Statistics Toolbox function `leverage` computes leverage values from a QR decomposition of `X`.

Component residual values in `y-yhat` are useful for detecting failures in model assumptions. Like the errors in ε, residuals have an expected value of 0. Unlike the errors, however, residuals are correlated, with nonconstant variance. Residuals may be "Studentized" (scaled by an estimate of their standard deviation) for comparison. Studentized residuals are used by Statistics Toolbox functions like `regress` and `robustfit` to identify outliers in the data.

Multiple Linear Regression

Introduction to Multiple Linear Regression

The system of linear equations

$$\underbrace{\begin{pmatrix} y_1 \\ \vdots \\ y_n \end{pmatrix}}_{y} = \underbrace{\begin{pmatrix} f_1(\boldsymbol{x}_1) & \cdots & f_p(\boldsymbol{x}_1) \\ \vdots & \ddots & \vdots \\ f_1(\boldsymbol{x}_n) & \cdots & f_p(\boldsymbol{x}_n) \end{pmatrix}}_{X} \underbrace{\begin{pmatrix} \beta_1 \\ \vdots \\ \beta_p \end{pmatrix}}_{\beta} + \underbrace{\begin{pmatrix} \varepsilon_1 \\ \vdots \\ \varepsilon_n \end{pmatrix}}_{\varepsilon}$$

in "Linear Regression Models" on page 9-3 expresses a response y as a linear combination of model terms $f_j(\boldsymbol{x})$ (j = 1, ..., p) at each of the observations ($\boldsymbol{x}_1$, y_1), …, ($\boldsymbol{x}_n$, y_n).

If the predictor $\boldsymbol{x}$ is multidimensional, so are the functions f_j that form the terms of the model. For example, if the predictor is $\boldsymbol{x} = (x_1, x_2)$, terms for the model might include $f_1(\boldsymbol{x}) = x_1$ (a linear term), $f_2(\boldsymbol{x}) = x_1^2$ (a quadratic term), and $f_3(\boldsymbol{x}) = x_1x_2$ (a pairwise interaction term). Typically, the function $f(\boldsymbol{x}) = 1$ is included among the f_j, so that the design matrix X contains a column of 1s and the model contains a constant (y-intercept) term.

Multiple linear regression models are useful for:

- Understanding which terms $f_j(\boldsymbol{x})$ have greatest effect on the response (coefficients β_j with greatest magnitude)
- Finding the direction of the effects (signs of the β_j)
- Predicting unobserved values of the response ($y(\boldsymbol{x})$ for new $\boldsymbol{x}$)

The Statistics Toolbox functions `regress` and `regstats` are used for multiple linear regression analysis.

Programmatic Multiple Linear Regression

For example, the file `moore.mat` contains the 20-by-6 data matrix `moore`. The first five columns are measurements of biochemical oxygen demand on five predictor variables. The final column contains the observed responses. Use `regress` to find coefficient estimates `betahat` for a linear additive model as follows. Before using `regress` give the design matrix `X1` a first column of 1s to include a constant term in the model, `betahat(1)`.

```
load moore
X1 = [ones(size(moore,1),1) moore(:,1:5)];
y = moore(:,6);
betahat = regress(y,X1)
betahat =
   -2.1561
   -0.0000
    0.0013
    0.0001
    0.0079
    0.0001
```

The MATLAB backslash (`mldivide`) operator, which `regress` calls, obtains the same result:

```
betahat = X1\y
betahat =
   -2.1561
   -0.0000
    0.0013
    0.0001
    0.0079
    0.0001
```

The advantage of working with `regress` is that it allows for additional inputs and outputs relevant to statistical analysis of the regression. For example:

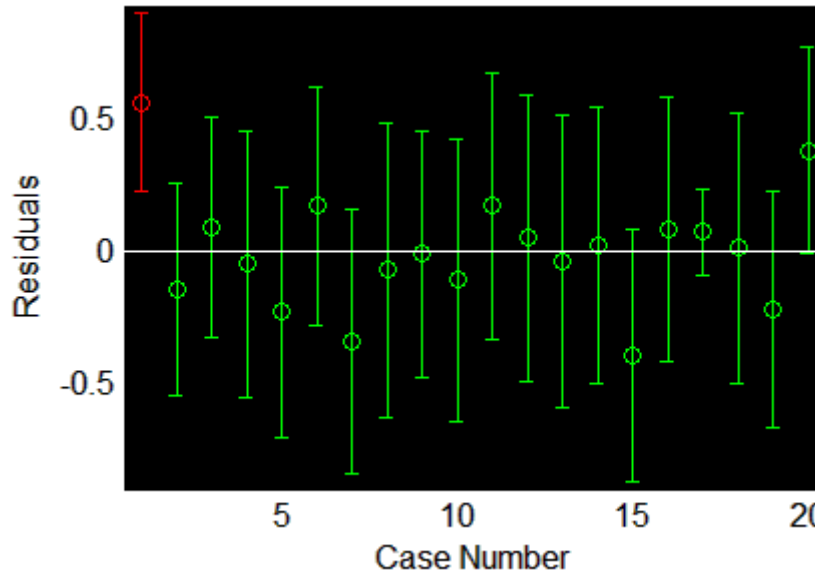
```
alpha = 0.05;
[betahat,Ibeta,res,Ires,stats] = regress(y,X1,alpha);
```

returns not only the coefficient estimates in `betahat`, but also

- `Ibeta` — A p-by-2 matrix of 95% confidence intervals for the coefficient estimates, using a `100*(1-alpha)`% confidence level. The first column contains lower confidence bounds for each of the p coefficient estimates; the second column contains upper confidence bounds.
- `res` — An n-by-1 vector of residuals.
- `Ires` — An n-by-2 matrix of intervals that can be used to diagnose outliers. If the interval `Ires(i,:)` for observation `i` does not contain zero, the corresponding residual is larger than expected in `100*(1-alpha)`% of new observations, suggesting an outlier.
- `stats` — A 1-by-4 vector that contains, in order, the R^2 statistic, the F statistic and its p value, and an estimate of the error variance. The statistics are computed assuming the model contains a constant term, and are incorrect otherwise.

Visualize the residuals, in case (row number) order, with the `rcoplot` function:

```
rcoplot(res,Ires)
```



The interval around the first residual, shown in red when plotted, does not contain zero. This indicates that the residual is larger than expected in 95% of new observations, and suggests the data point is an outlier.

Outliers in regression appear for a variety of reasons:

1. If there is sufficient data, 5% of the residuals, by the definition of `rint`, are too big.
2. If there is a systematic error in the model (that is, if the model is not appropriate for generating the data under model assumptions), the mean of the residuals is not zero.
3. If the errors in the model are not normally distributed, the distributions of the residuals may be skewed or leptokurtic (with heavy tails and more outliers).

When errors are normally distributed, `Ires(i,:)` is a confidence interval for the mean of `res(i)` and checking if the interval contains zero is a test of the null hypothesis that the residual has zero mean.

Interactive Multiple Linear Regression

The function `regstats` also performs multiple linear regression, but computes more statistics than `regress`. By default, `regstats` automatically adds a first column of 1s to the design matrix (necessary for computing the F statistic and its p value), so a constant term should not be included explicitly as for `regress`. For example:

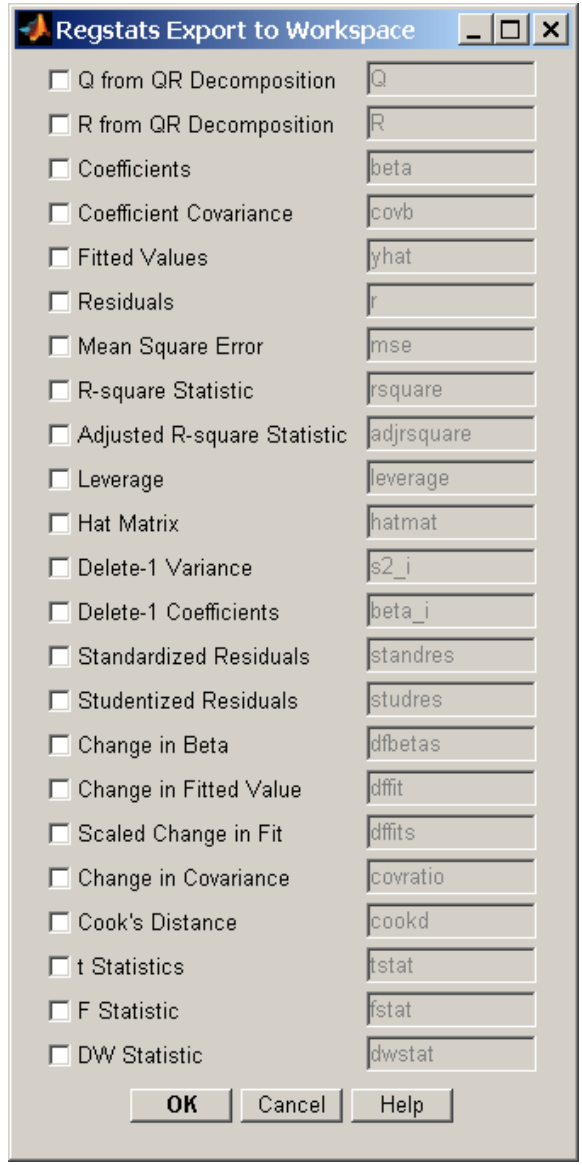
```
X2 = moore(:,1:5);
stats = regstats(y,X2);
```

creates a structure `stats` with fields containing regression statistics. An optional input argument allows you to specify which statistics are computed.

To interactively specify the computed statistics, call `regstats` without an output argument. For example:

```
regstats(y,X2)
```

opens the following interface.



Select the check boxes corresponding to the statistics you want to compute and click **OK**. Selected statistics are returned to the MATLAB workspace. Names

of container variables for the statistics appear on the right-hand side of the interface, where they can be changed to any valid MATLAB variable name.

Tabulating Diagnostic Statistics

The `regstats` function computes statistics that are typically used in regression diagnostics. Statistics can be formatted into standard tabular displays in a variety of ways. For example, the `tstat` field of the `stats` output structure of `regstats` is itself a structure containing statistics related to the estimated coefficients of the regression. Dataset arrays (see "Dataset Arrays" on page 2-23) provide a natural tabular format for the information:

```
t = stats.tstat;
CoeffTable = dataset({t.beta,'Coef'},{t.se,'StdErr'}, ...
                     {t.t,'tStat'},{t.pval,'pVal'})
CoeffTable =
    Coef            StdErr         tStat        pVal
         -2.1561        0.91349      -2.3603      0.0333
    -9.0116e-006     0.00051835    -0.017385     0.98637
       0.0013159      0.0012635       1.0415     0.31531
       0.0001278    7.6902e-005       1.6618     0.11876
       0.0078989          0.014      0.56421     0.58154
      0.00014165    7.3749e-005       1.9208    0.075365
```

The MATLAB function `fprintf` gives you control over tabular formatting. For example, the `fstat` field of the `stats` output structure of `regstats` is a structure with statistics related to the analysis of variance (ANOVA) of the regression. The following commands produce a standard regression ANOVA table:

```
f = stats.fstat;

fprintf('\n')
fprintf('Regression ANOVA');
fprintf('\n\n')

fprintf('%6s','Source');
fprintf('%10s','df','SS','MS','F','P');
fprintf('\n')

fprintf('%6s','Regr');
```

```
fprintf('%10.4f',f.dfr,f.ssr,f.ssr/f.dfr,f.f,f.pval);
fprintf('\n')

fprintf('%6s','Resid');
fprintf('%10.4f',f.dfe,f.sse,f.sse/f.dfe);
fprintf('\n')

fprintf('%6s','Total');
fprintf('%10.4f',f.dfe+f.dfr,f.sse+f.ssr);
fprintf('\n')
```

The result looks like this:

```
Regression ANOVA

Source        df        SS        MS         F         P
  Regr    5.0000    4.1084    0.8217   11.9886    0.0001
 Resid   14.0000    0.9595    0.0685
 Total   19.0000    5.0679
```

Robust Regression

Introduction to Robust Regression

The models described in "Linear Regression Models" on page 9-3 are based on certain assumptions, such as a normal distribution of errors in the observed responses. If the distribution of errors is asymmetric or prone to outliers, model assumptions are invalidated, and parameter estimates, confidence intervals, and other computed statistics become unreliable. The Statistics Toolbox function `robustfit` is useful in these cases. The function implements a robust fitting method that is less sensitive than ordinary least squares to large changes in small parts of the data.

Robust regression works by assigning a weight to each data point. Weighting is done automatically and iteratively using a process called *iteratively*

reweighted least squares. In the first iteration, each point is assigned equal weight and model coefficients are estimated using ordinary least squares. At subsequent iterations, weights are recomputed so that points farther from model predictions in the previous iteration are given lower weight. Model coefficients are then recomputed using weighted least squares. The process continues until the values of the coefficient estimates converge within a specified tolerance.

Programmatic Robust Regression

The example in "Multiple Linear Regression" on page 9-8 shows an outlier when ordinary least squares is used to model the response variable as a linear combination of the five predictor variables. To determine the influence of the outlier, compare the coefficient estimates computed by `regress`:

```
load moore
X1 = [ones(size(moore,1),1) moore(:,1:5)];
y = moore(:,6);
betahat = regress(y,X1)
betahat =
   -2.1561
   -0.0000
    0.0013
    0.0001
    0.0079
    0.0001
```

to those computed by `robustfit`:

```
X2 = moore(:,1:5);
robustbeta = robustfit(X2,y)
robustbeta =
   -1.7516
    0.0000
    0.0009
    0.0002
    0.0060
    0.0001
```

By default, `robustfit` automatically adds a first column of 1s to the design matrix, so a constant term does not have to be included explicitly as for

`regress`. In addition, the order of inputs is reversed for `robustfit` and `regress`.

To understand the difference in the coefficient estimates, look at the final weights given to the data points in the robust fit:

```
[robustbeta,stats] = robustfit(X2,y);
stats.w'
ans =
  Columns 1 through 5
    0.0246    0.9986    0.9763    0.9323    0.9704
  Columns 6 through 10
    0.8597    0.9180    0.9992    0.9590    0.9649
  Columns 11 through 15
    0.9769    0.9868    0.9999    0.9976    0.8122
  Columns 16 through 20
    0.9733    0.9892    0.9988    0.8974    0.6774
```

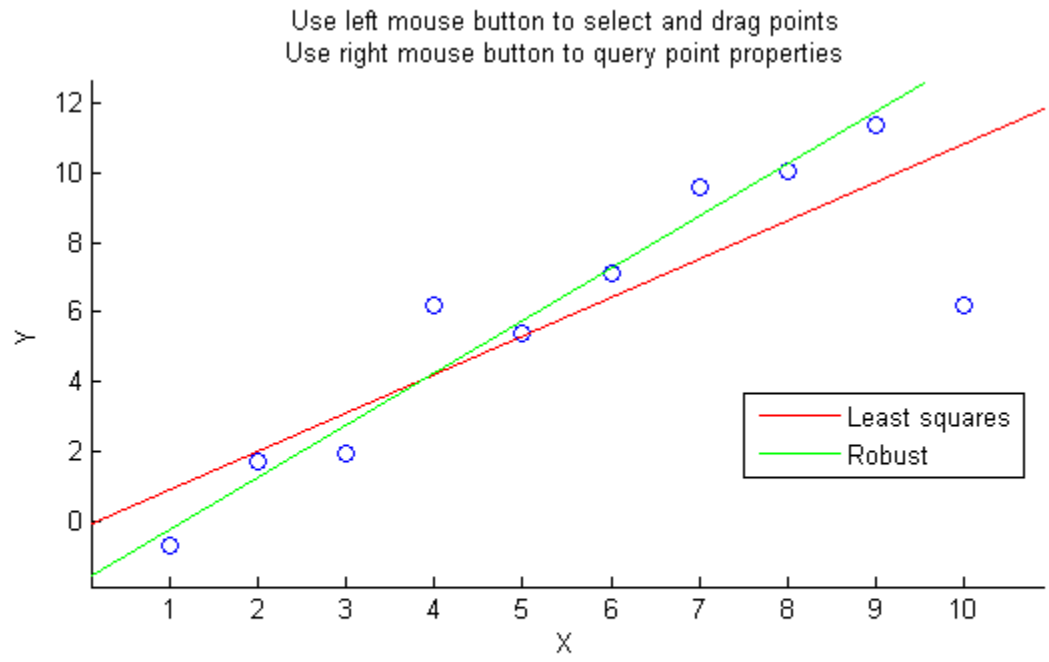
The first data point has a very low weight compared to the other data points, and so is effectively ignored in the robust regression.

Interactive Robust Regression

The `robustdemo` function shows the difference between ordinary least squares and robust fitting for data with a single predictor. You can use data provided with the demo, or you can supply your own data. The following steps show you how to use `robustdemo`.

1. **Start the demo.** To begin using `robustdemo` with the built-in data, simply enter the function name at the command line:

   ```
   robustdemo
   ```

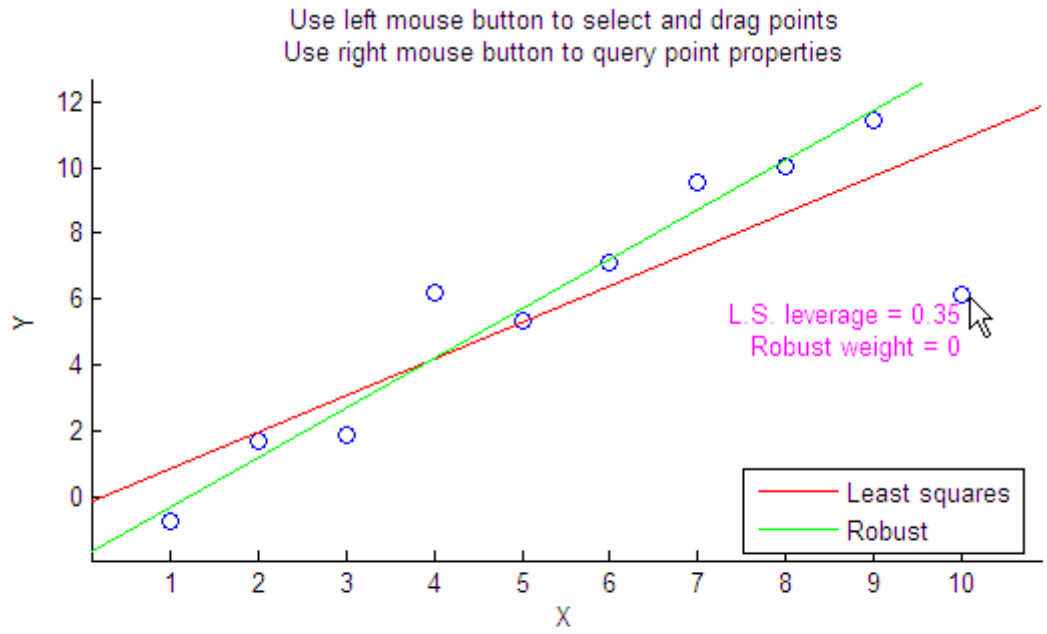


Least squares: Y = -0.188327 + 1.10351*X RMS error = 2.21375

Robust: Y = -1.77278 + 1.50415*X RMS error = 1.43663

The resulting figure shows a scatter plot with two fitted lines. The red line is the fit using ordinary least-squares regression. The green line is the fit using robust regression. At the bottom of the figure are the equations for the fitted lines, together with the estimated root mean squared errors for each fit.

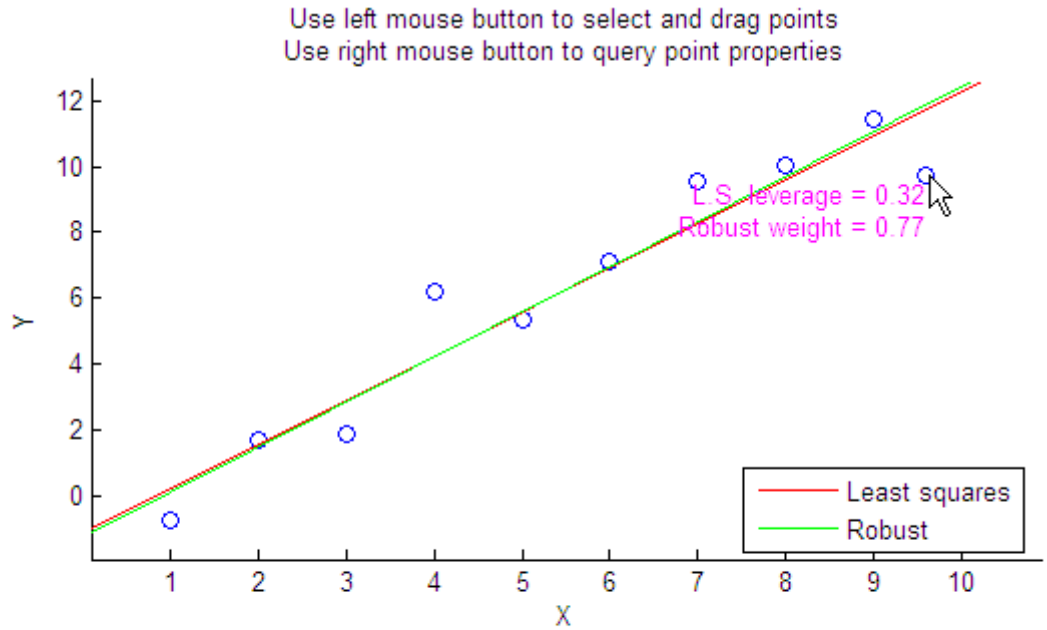
2 View leverages and robust weights. Right-click on any data point to see its least-squares leverage and robust weight.



Least squares:	Y = -0.188327 + 1.10351*X	RMS error = 2.21375
Robust:	Y = -1.77278 + 1.50415*X	RMS error = 1.43663

In the built-in data, the rightmost point has a relatively high leverage of 0.35. The point exerts a large influence on the least-squares fit, but its small robust weight shows that it is effectively excluded from the robust fit.

3 **See how changes in the data affect the fits.** With the left mouse button, click and hold on any data point and drag it to a new location. When you release the mouse button, the displays update.



Least squares:	Y = -1.0661 + 1.33785*X	RMS error = 1.21477
Robust:	Y = -1.18916 + 1.36459*X	RMS error = 1.27697

Bringing the rightmost data point closer to the least-squares line makes the two fitted lines nearly identical. The adjusted rightmost data point has significant weight in the robust fit.

Stepwise Regression

Introduction to Stepwise Regression

Multiple linear regression models, as described in "Multiple Linear Regression" on page 9-8, are built from a potentially large number of predictive terms. The number of interaction terms, for example, increases exponentially with the number of predictor variables. If there is no theoretical basis for choosing the form of a model, and no assessment of correlations among terms, it is possible to include redundant terms in a model that confuse the identification of significant effects.

Stepwise regression is a systematic method for adding and removing terms from a multilinear model based on their statistical significance in a regression. The method begins with an initial model and then compares the explanatory power of incrementally larger and smaller models. At each step, the p value of an F-statistic is computed to test models with and without a potential term. If a term is not currently in the model, the null hypothesis is that the term would have a zero coefficient if added to the model. If there is sufficient evidence to reject the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model. The method proceeds as follows:

1. Fit the initial model.
2. If any terms not in the model have p-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest p value and repeat this step; otherwise, go to step 3.
3. If any terms in the model have p-values greater than an exit tolerance (that is, if it is unlikely that the hypothesis of a zero coefficient can be rejected), remove the one with the largest p value and go to step 2; otherwise, end.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method may build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but may not be globally optimal.

Statistics Toolbox functions for stepwise regression are:

- `stepwisefit` — A function that proceeds automatically from a specified initial model and entrance/exit tolerances
- `stepwise` — An interactive tool that allows you to explore individual steps in the regression

Programmatic Stepwise Regression

For example, load the data in `hald.mat`, which contains observations of the heat of reaction of various cement mixtures:

```
load hald
whos
  Name          Size    Bytes   Class   Attributes

  Description   22x58   2552    char
  hald          13x5     520    double
  heat          13x1     104    double
  ingredients   13x4     416    double
```

The response (`heat`) depends on the quantities of the four predictors (the columns of `ingredients`).

Use `stepwisefit` to carry out the stepwise regression algorithm, beginning with no terms in the model and using entrance/exit tolerances of 0.05/0.10 on the *p*-values:

```
stepwisefit(ingredients,heat,...
            'penter',0.05,'premove',0.10);
Initial columns included:  none
Step 1, added column 4, p=0.000576232
Step 2, added column 1, p=1.10528e-006
Final columns included:  1 4
    'Coeff'      'Std.Err.'    'Status'    'P'
    [ 1.4400]    [  0.1384]    'In'        [1.1053e-006]
    [ 0.4161]    [  0.1856]    'Out'       [     0.0517]
    [-0.4100]    [  0.1992]    'Out'       [     0.0697]
    [-0.6140]    [  0.0486]    'In'        [1.8149e-007]
```

`stepwisefit` automatically includes an intercept term in the model, so you do not add it explicitly to `ingredients` as you would for `regress`. For terms not

in the model, coefficient estimates and their standard errors are those that result if the term is added.

The `inmodel` parameter is used to specify terms in an initial model:

```
initialModel = ...
           [false true false false]; % Force in 2nd term
stepwisefit(ingredients,heat,...
            'inmodel',initialModel,...
            'penter',.05,'premove',0.10);
Initial columns included:  2
Step 1, added column 1, p=2.69221e-007
Final columns included:  1 2
    'Coeff'      'Std.Err.'    'Status'    'P'
    [ 1.4683]    [  0.1213]    'In'        [2.6922e-007]
    [ 0.6623]    [  0.0459]    'In'        [5.0290e-008]
    [ 0.2500]    [  0.1847]    'Out'       [     0.2089]
    [-0.2365]    [  0.1733]    'Out'       [     0.2054]
```

The preceding two models, built from different initial models, use different subsets of the predictive terms. Terms 2 and 4, swapped in the two models, are highly correlated:

```
term2 = ingredients(:,2);
term4 = ingredients(:,4);
R = corrcoef(term2,term4)
R =
    1.0000   -0.9730
   -0.9730    1.0000
```

To compare the models, use the `stats` output of `stepwisefit`:

```
[betahat1,se1,pval1,inmodel1,stats1] = ...
          stepwisefit(ingredients,heat,...
          'penter',.05,'premove',0.10,...
          'display','off');
[betahat2,se2,pval2,inmodel2,stats2] = ...
          stepwisefit(ingredients,heat,...
                      'inmodel',initialModel,...
                      'penter',.05,'premove',0.10,...
                      'display','off');
```

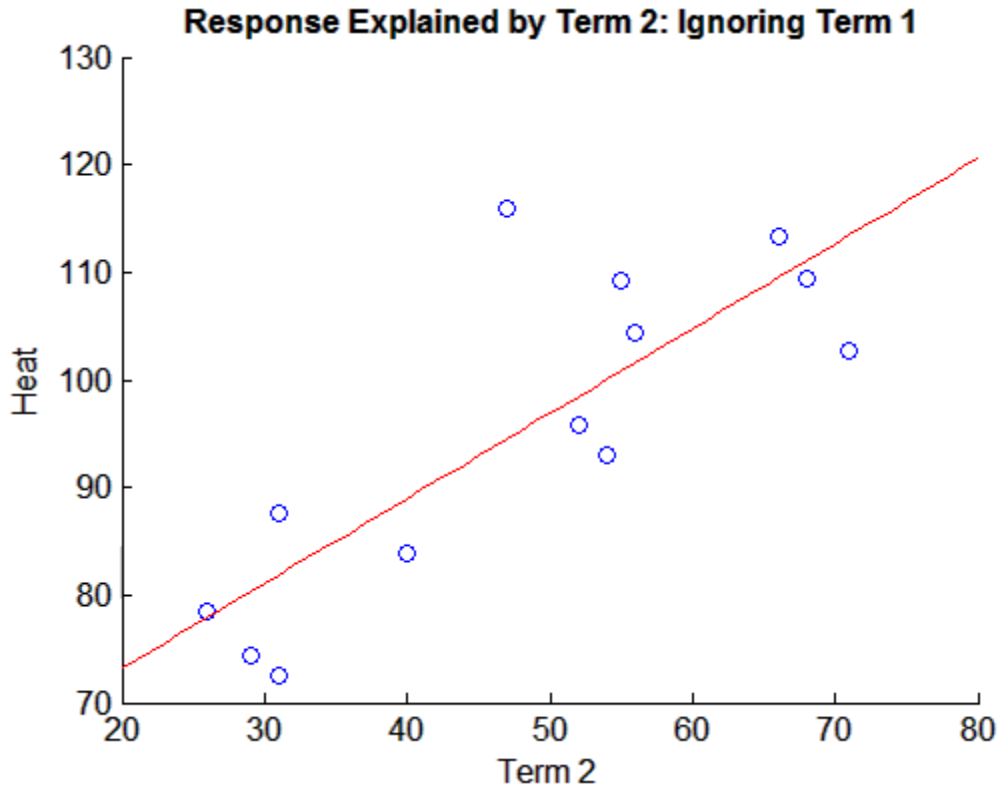
```
RMSE1 = stats1.rmse
RMSE1 =
    2.7343
RMSE2 = stats2.rmse
RMSE2 =
    2.4063
```

The second model has a lower Root Mean Square Error (RMSE).

An *added variable plot* is used to determine the unique effect of adding a new term to a model. The plot shows the relationship between the part of the response unexplained by terms already in the model and the part of the new term unexplained by terms already in the model. The "unexplained" parts are measured by the residuals of the respective regressions. A scatter of the residuals from the two regressions forms the added variable plot.

For example, suppose you want to add `term2` to a model that already contains the single term `term1`. First, consider the ability of `term2` alone to explain the response:

```
load hald
term2 = ingredients(:,2);

[b2,Ib2,res2] = regress(heat,[ones(size(term2)) term2]);

scatter(term2,heat)
xlabel('Term 2')
ylabel('Heat')
hold on
x2 = 20:80;
y2 = b2(1) + b2(2)*x2;
plot(x2,y2,'r')
title('{\bf Response Explained by Term 2: Ignoring Term 1}')
```



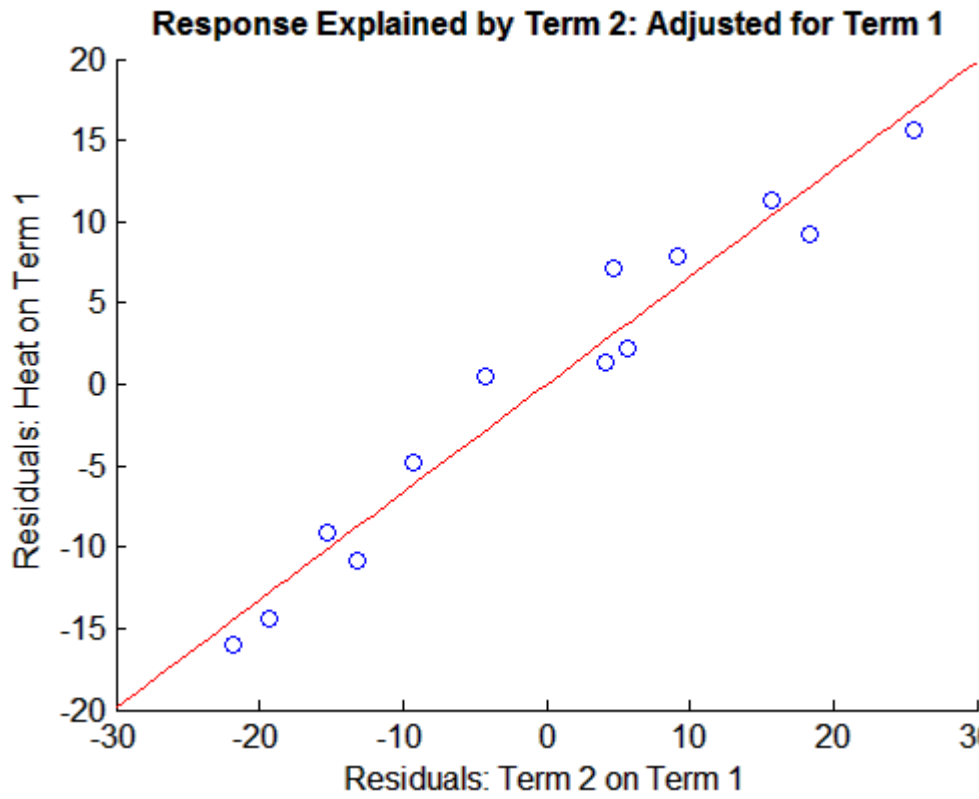
Next, consider the following regressions involving the model term `term1`:

```
term1 = ingredients(:,1);
[b1,Ib1,res1] = regress(heat,[ones(size(term1)) term1]);
[b21,Ib21,res21] = regress(term2,[ones(size(term1)) term1]);
bres = regress(res1,[ones(size(res21)) res21]);
```

A scatter of the residuals `res1` vs. the residuals `res12` forms the added variable plot:

```
figure
scatter(res21,res1)
xlabel('Residuals: Term 2 on Term 1')
ylabel('Residuals: Heat on Term 1')
hold on
```

```
xres = -30:30;
yres = bres(1) + bres(2)*xres;
plot(xres,yres,'r')
title('{\bf Response Explained by Term 2: Adjusted for Term 1}')
```

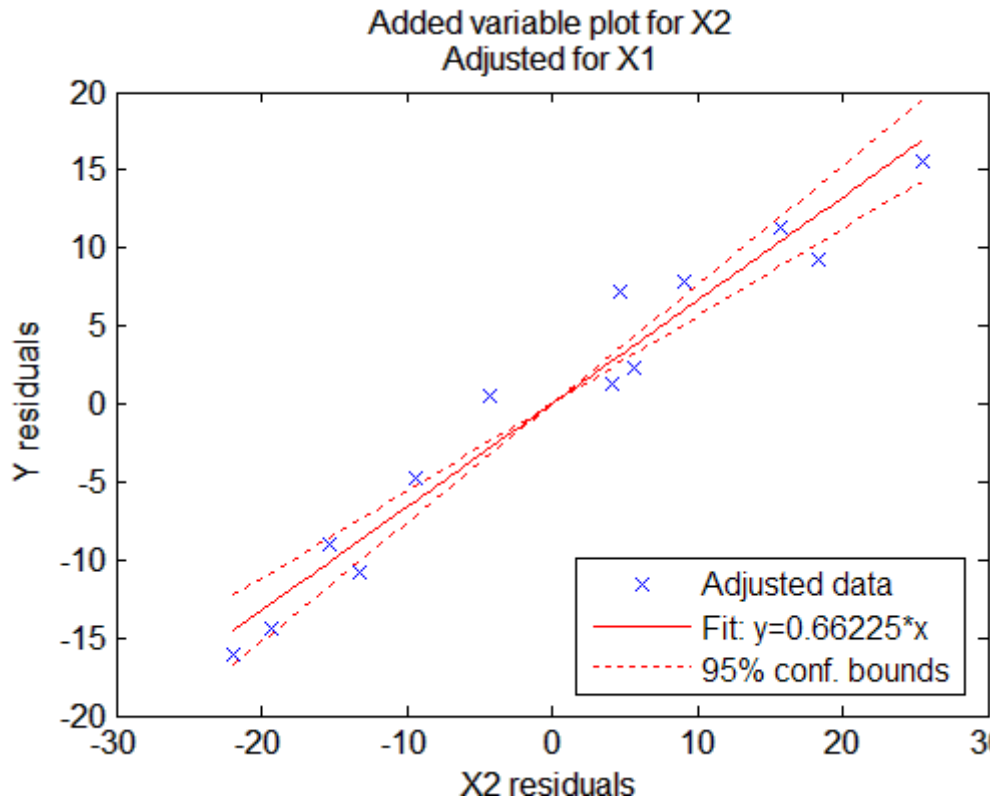


Since the plot adjusted for `term1` shows a stronger relationship (less variation along the fitted line) than the plot ignoring `term1`, the two terms act jointly to explain extra variation. In this case, adding `term2` to a model consisting of `term1` would reduce the RMSE.

The Statistics Toolbox function `addedvarplot` produces added variable plots. The previous plot is essentially the one produced by the following:

```
figure
```

```
inmodel = [true false false false];
addedvarplot(ingredients,heat,2,inmodel)
```



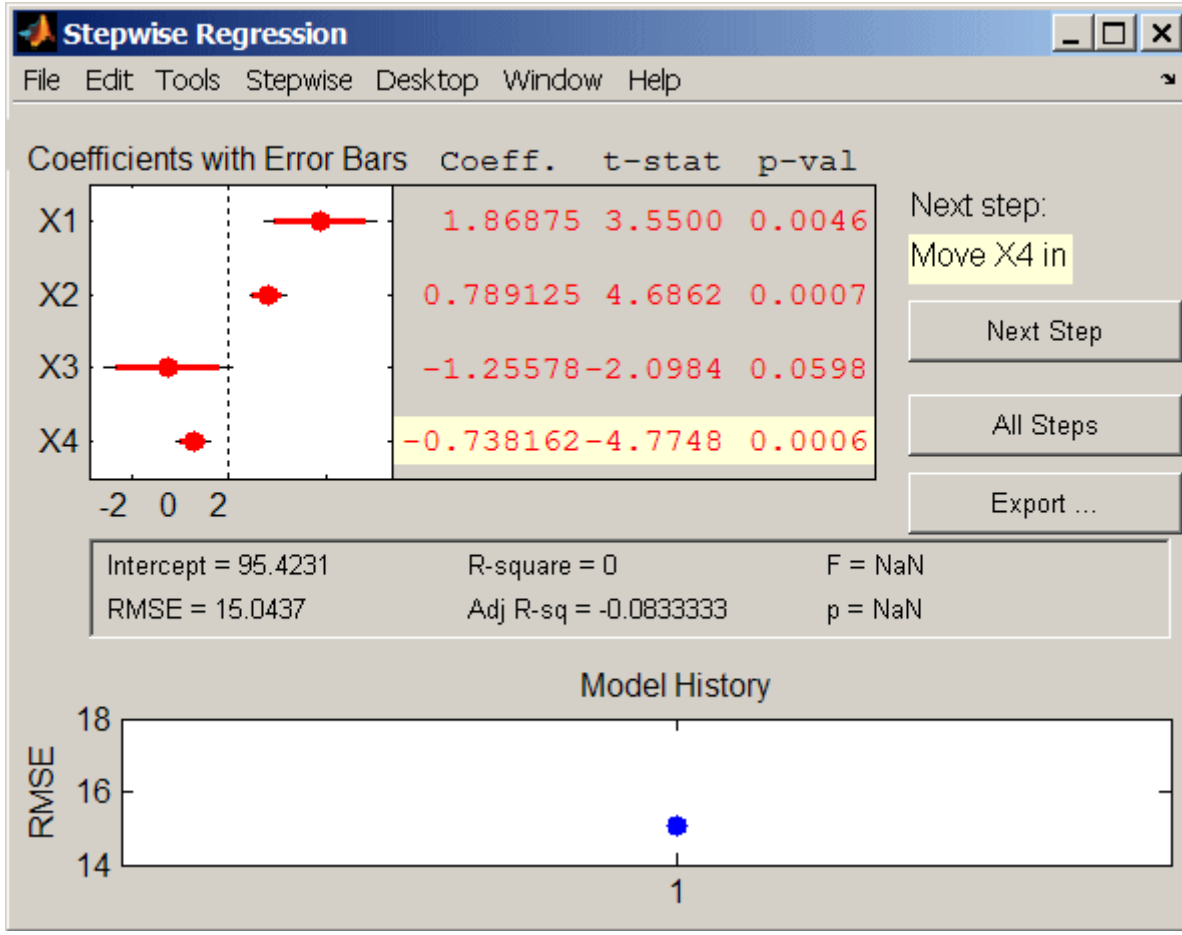
In addition to the scatter of residuals, the plot shows 95% confidence intervals on predictions from the fitted line. The fitted line has intercept zero because, under the assumptions outlined in "Linear Regression Models" on page 9-3, both of the plotted variables have mean zero. The slope of the fitted line is the coefficient that `term2` would have if it was added to the model with `term1`.

The `addevarplot` function is useful for considering the unique effect of adding a new term to an existing model with any number of terms.

Interactive Stepwise Regression

The `stepwise` interface provides interactive features that allow you to investigate individual steps in a stepwise regression, and to build models from arbitrary subsets of the predictive terms. To open the interface with data from `hald.mat`:

```
load hald
stepwise(ingredients,heat)
```



The upper left of the interface displays estimates of the coefficients for all potential terms, with horizontal bars indicating 90% (colored) and 95% (grey) confidence intervals. The red color indicates that, initially, the terms are not in the model. Values displayed in the table are those that would result if the terms were added to the model.

The middle portion of the interface displays summary statistics for the entire model. These statistics are updated with each step.

The lower portion of the interface, **Model History**, displays the RMSE for the model. The plot tracks the RMSE from step to step, so you can compare the optimality of different models. Hover over the blue dots in the history to see which terms were in the model at a particular step. Click on a blue dot in the history to open a copy of the interface initialized with the terms in the model at that step.

Initial models, as well as entrance/exit tolerances for the p-values of F-statistics, are specified using additional input arguments to `stepwise`. Defaults are an initial model with no terms, an entrance tolerance of 0.05, and an exit tolerance of 0.10.

To center and scale the input data (compute z-scores) to improve conditioning of the underlying least-squares problem, select `Scale Inputs` from the **Stepwise** menu.

You proceed through a stepwise regression in one of two ways:

1. Click **Next Step** to select the recommended next step. The recommended next step either adds the most significant term or removes the least significant term. When the regression reaches a local minimum of RMSE, the recommended next step is "Move no terms." You can perform all of the recommended steps at once by clicking **All Steps**.

2. Click a line in the plot or in the table to toggle the state of the corresponding term. Clicking a red line, corresponding to a term not currently in the model, adds the term to the model and changes the line to blue. Clicking a blue line, corresponding to a term currently in the model, removes the term from the model and changes the line to red.

To call `addedvarplot` and produce an added variable plot from the `stepwise` interface, select **Added Variable Plot** from the **Stepwise** menu. A list of terms is displayed. Select the term you want to add, and then click **OK**.

Click **Export** to display a dialog box that allows you to select information from the interface to save to the MATLAB workspace. Check the information you want to export and, optionally, change the names of the workspace variables to be created. Click **OK** to export the information.

Ridge Regression

Introduction to Ridge Regression

Coefficient estimates for the models described in "Multiple Linear Regression" on page 9-8 rely on the independence of the model terms. When terms are correlated and the columns of the design matrix X have an approximate linear dependence, the matrix $(X^TX)^{-1}$ becomes close to singular. As a result, the least-squares estimate

$$\hat{\beta} = (X^T X)^{-1} X^T y$$

becomes highly sensitive to random errors in the observed response y, producing a large variance. This situation of *multicollinearity* can arise, for example, when data are collected without an experimental design.

Ridge regression addresses the problem by estimating regression coefficients using

$$\hat{\beta} = (X^T X + kI)^{-1} X^T y$$

where k is the *ridge parameter* and I is the identity matrix. Small positive values of k improve the conditioning of the problem and reduce the variance of the estimates. While biased, the reduced variance of ridge estimates often result in a smaller mean square error when compared to least-squares estimates.

The Statistics Toolbox function `ridge` carries out ridge regression.

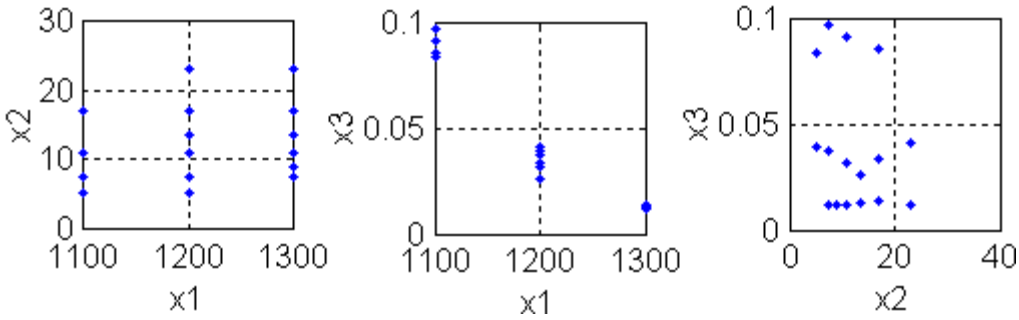
Example: Ridge Regression

For example, load the data in `acetylene.mat`, with observations of the predictor variables `x1`, `x2`, `x3`, and the response variable `y`:

```
load acetylene
```

Plot the predictor variables against each other:

```
subplot(1,3,1)
plot(x1,x2,'.')
xlabel('x1'); ylabel('x2'); grid on; axis square

subplot(1,3,2)
plot(x1,x3,'.')
xlabel('x1'); ylabel('x3'); grid on; axis square

subplot(1,3,3)
plot(x2,x3,'.')
xlabel('x2'); ylabel('x3'); grid on; axis square
```



Note the correlation between `x1` and the other two predictor variables.

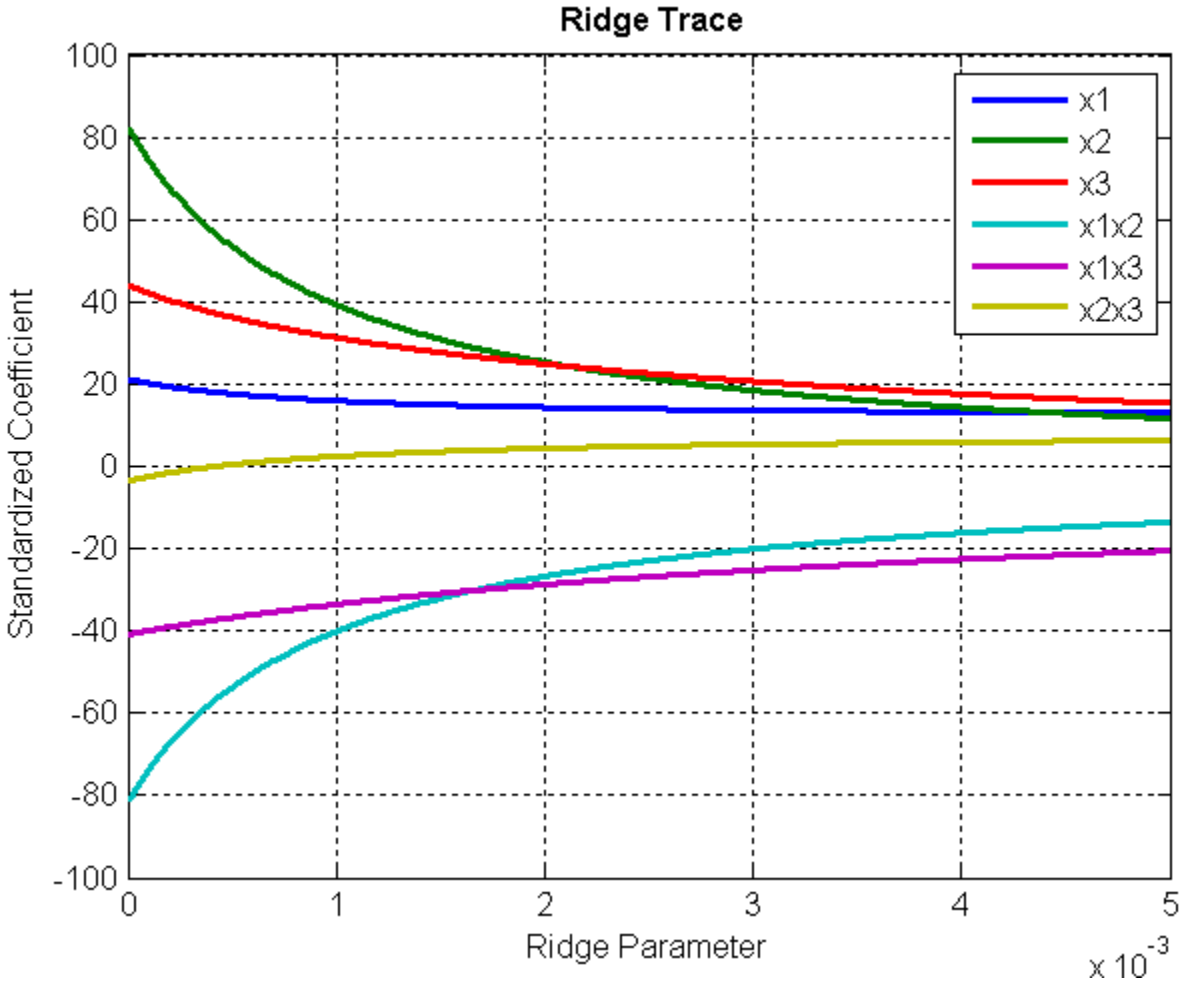
Use `ridge` and `x2fx` to compute coefficient estimates for a multilinear model with interaction terms, for a range of ridge parameters:

```
X = [x1 x2 x3];
D = x2fx(X,'interaction');
```

```
D(:,1) = []; % No constant term
k = 0:1e-5:5e-3;
betahat = ridge(y,D,k);
```

Plot the ridge trace:

```
figure
plot(k,betahat,'LineWidth',2)
ylim([-100 100])
grid on
xlabel('Ridge Parameter')
ylabel('Standardized Coefficient')
title('{\bf Ridge Trace}')
legend('x1','x2','x3','x1x2','x1x3','x2x3')
```



The estimates stabilize to the right of the plot. Note that the coefficient of the `x2x3` interaction term changes sign at a value of the ridge parameter $\approx 5 \times 10^{-4}$.

Lasso and Elastic Net

Lasso is a regularization technique. Use `lasso` to:

- Reduce the number of predictors in a regression model.
- Identify important predictors.
- Select among redundant predictors.
- Produce shrinkage estimates with potentially lower predictive errors than ordinary least squares.

Elastic net is a related technique. Use elastic net when you have several highly correlated variables. `lasso` provides elastic net regularization when you set the `Alpha` name-value pair to a number strictly between `0` and `1`.

See "Lasso and Elastic Net Details" on page 9-44.

Example: Lasso Regularization

To see how `lasso` identifies and discards unnecessary predictors:

1 Generate `200` samples of five-dimensional artificial data `X` from exponential distributions with various means:

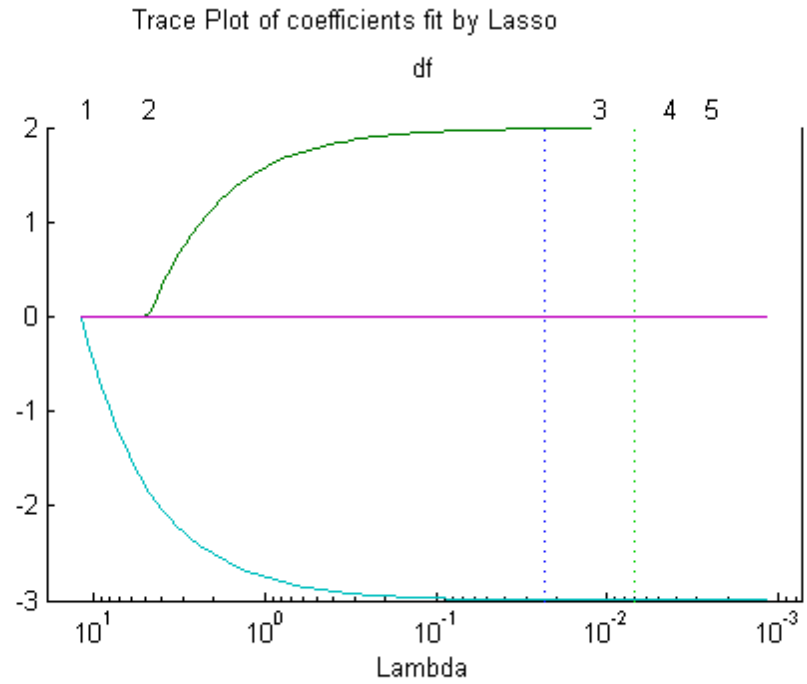
```
rng(3,'twister') % for reproducibility
X = zeros(200,5);
for ii = 1:5
    X(:,ii) = exprnd(ii,200,1);
end
```

2 Generate response data `Y = X*r + eps` where `r` has just two nonzero components, and the noise `eps` is normal with standard deviation `0.1`:

```
r = [0;2;0;-3;0];
Y = X*r + randn(200,1)*.1;
```

3 Fit a cross-validated sequence of models with `lasso`, and plot the result:

```
[b fitinfo] = lasso(X,Y,'CV',10);
lassoPlot(b,fitinfo,'PlotType','Lambda','XScale','log');
```



The plot shows the nonzero coefficients in the regression for various values of the `Lambda` regularization parameter. Larger values of `Lambda` appear on the left side of the graph, meaning more regularization, resulting in fewer nonzero regression coefficients.

The dashed vertical lines represent the `Lambda` value with minimal mean squared error (on the right), and the `Lambda` value with minimal mean squared error plus one standard deviation. This latter value is a recommended setting for `Lambda`. These lines appear only when you perform cross validation. Cross validate by setting the `'CV'` name-value pair. This example uses 10-fold cross validation.

The upper part of the plot shows the degrees of freedom (df), meaning the number of nonzero coefficients in the regression, as a function of Lambda. On the left, the large value of Lambda causes all but one coefficient to be

0. On the right all five coefficients are nonzero, though the plot shows only two clearly. The other three coefficients are so small that you cannot visually distinguish them from 0.

For small values of `Lambda` (toward the right in the plot), the coefficient values are close to the least-squares estimate. See step 5 on page 9-35.

4 Find the `Lambda` value of the minimal cross-validated mean squared error plus one standard deviation. Examine the MSE and coefficients of the fit at that `Lambda`:

```
lam = fitinfo.Index1SE;
fitinfo.MSE(lam)

ans =
    0.0101

b(:,lam)

ans =
         0
    1.9850
         0
   -2.9946
         0
```

`lasso` did a good job finding the coefficient vector `r`.

5 For comparison, find the least-squares estimate of `r`:

```
rhat = X\Y

rhat =

   -0.0038
    1.9952
    0.0014
   -2.9993
    0.0031
```

The estimate `b(:,lam)` has slightly more mean squared error than the mean squared error of `rhat`:

```
res = X*rhat - Y; % calculate residuals
MSEmin = res'*res/200 % b(:,lam) value is 0.0101

MSEmin =
    0.0088
```

But `b(:,lam)` has only two nonzero components, and therefore can provide better predictive estimates on new data.

Example: Lasso and Elastic Net Regularization with Cross Validation

Consider predicting the mileage (`MPG`) of a car based on its weight, displacement, horsepower, and acceleration. The `carbig` data contains these measurements. The data seem likely to be correlated, making elastic net an attractive choice.

1 Load the data:

```
load carbig
```

2 Extract the continuous (noncategorical) predictors (`lasso` does not handle categorical predictors):

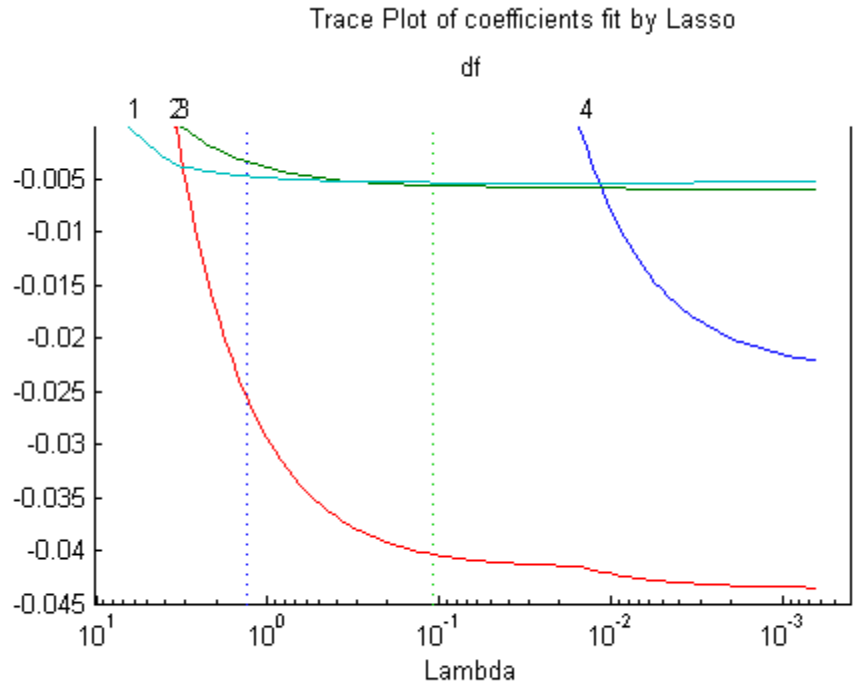
```
X = [Acceleration Displacement Horsepower Weight];
```

3 Perform a lasso fit with 10-fold cross validation:

```
[b fitinfo] = lasso(X,MPG,'CV',10);
```

4 Plot the result:

```
lassoPlot(b,fitinfo,'PlotType','Lambda','XScale','log');
```



5 Calculate the correlation of the predictors:

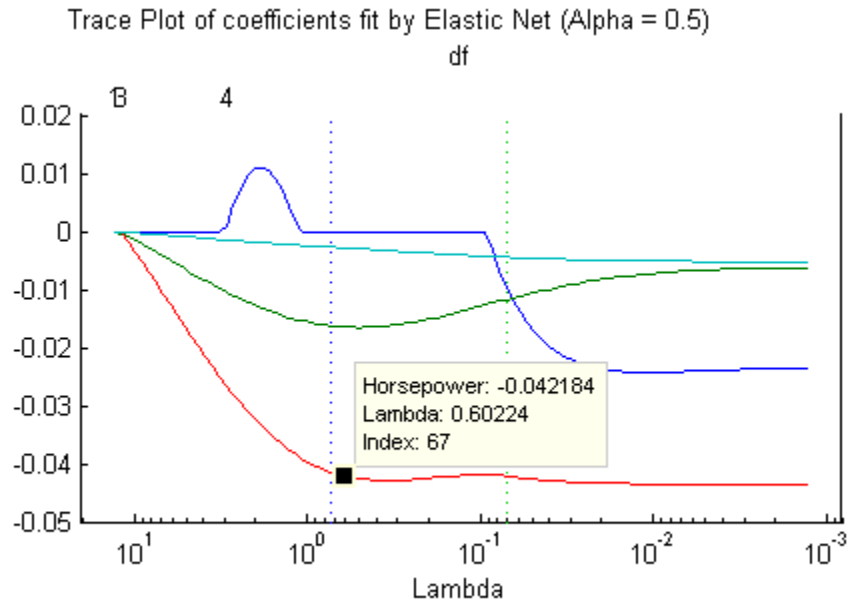
```
% Eliminate NaNs so corr runs
nonan = ~any(isnan([X MPG]),2);
Xnonan = X(nonan,:);
MPGnonan = MPG(nonan,:);
corr(Xnonan)

ans =
    1.0000   -0.5438   -0.6892   -0.4168
   -0.5438    1.0000    0.8973    0.9330
   -0.6892    0.8973    1.0000    0.8645
   -0.4168    0.9330    0.8645    1.0000
```

6 Because some predictors are highly correlated, perform elastic net fitting. Use `Alpha = 0.5`:

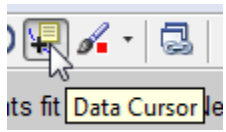
```
[ba fitinfoa] = lasso(X,MPG,'CV',10,'Alpha',.5);
```

7 Plot the result. Name each predictor so you can tell which curve is which:

```
pnames = {'Acceleration','Displacement',...
    'Horsepower','Weight'};
lassoPlot(ba,fitinfoa,'PlotType','Lambda',...
    'XScale','log','PredictorNames',pnames);
```



When you activate the data cursor



and click the plot, you see the name of the predictor, the coefficient, the value of `Lambda`, and the index of that point, meaning the column in `b` associated with that fit.

Here, the elastic net and lasso results are not very similar. Also, the elastic net plot reflects a notable qualitative property of the elastic net technique. The elastic net retains three nonzero coefficients as `Lambda` increases (toward the left of the plot), and these three coefficients reach `0` at about the same `Lambda` value. In contrast, the lasso plot shows two of the three coefficients becoming `0` at the same value of `Lambda`, while another coefficient remains nonzero for higher values of `Lambda`.

This behavior exemplifies a general pattern. In general, elastic net tends to retain or drop groups of highly correlated predictors as `Lambda` increases. In contrast, lasso tends to drop smaller groups, or even individual predictors.

Example: Wide Data via Lasso and Parallel Computing

Lasso and elastic net are especially well suited to *wide* data, meaning data with more predictors than observations. Obviously, there are redundant predictors in this type of data. Use `lasso` along with cross validation to identify important predictors.

Cross validation can be slow. If you have a Parallel Computing Toolbox™ license, speed the computation using parallel computing.

1 Load the `spectra` data:

```
load spectra
Description

Description =

== Spectral and octane data of gasoline ==

NIR spectra and octane numbers of 60 gasoline samples

NIR:     NIR spectra, measured in 2 nm intervals from 900 nm to 1700 nm
octane:  octane numbers
spectra: a dataset array containing variables for NIR and octane
```

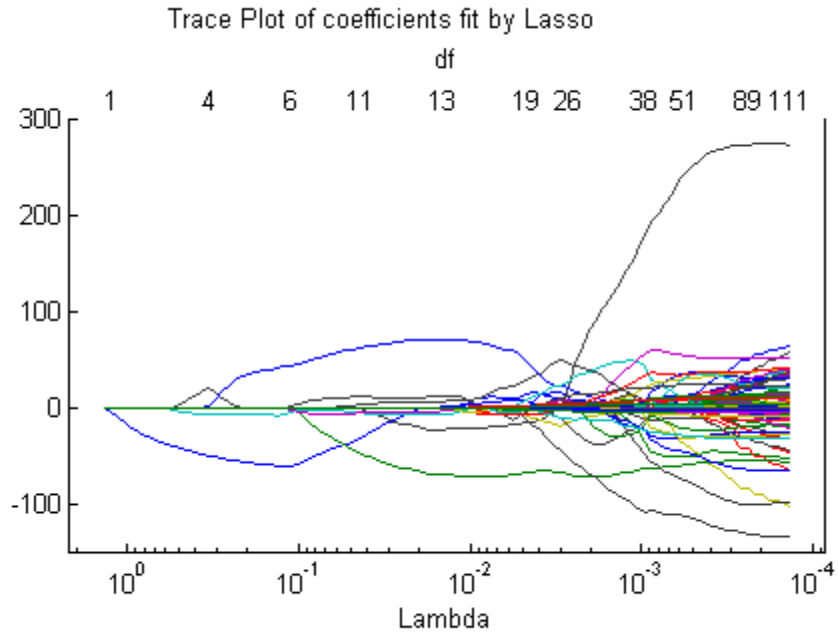
```
Reference:
Kalivas, John H., "Two Data Sets of Near Infrared Spectra," Chemometrics
and Intelligent Laboratory Systems, v.37 (1997) pp.255 259
```

2 Compute the default `lasso` fit:

```
[b fitinfo] = lasso(NIR,octane);
```

3 Plot the number of predictors in the fitted lasso regularization as a function of `Lambda`, using a logarithmic *x*-axis:

```
lassoPlot(b,fitinfo,'PlotType','Lambda','XScale','log');
```



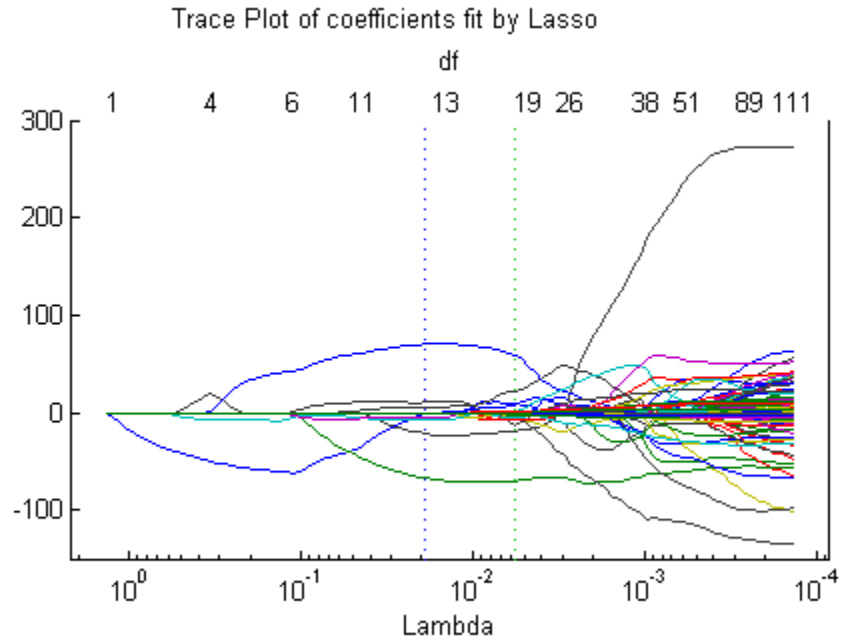
4 It is difficult to tell which value of `Lambda` is appropriate. To determine a good value, try fitting with cross validation:

```
tic
```

```
[b fitinfo] = lasso(NIR,octane,'CV',10);
% A time-consuming operation
toc

Elapsed time is 161.933311 seconds.
```

5 Plot the result:

```
lassoPlot(b,fitinfo,'PlotType','Lambda','XScale','log');
```



You can see the suggested value of `Lambda` is over `1e-2`, and the `Lambda` with minimal MSE is under `1e-2`. These values are in the `fitinfo` structure:

```
fitinfo.LambdaMinMSE
ans =
    0.0057
```

```
fitinfo.Lambda1SE
ans =
    0.0190
```

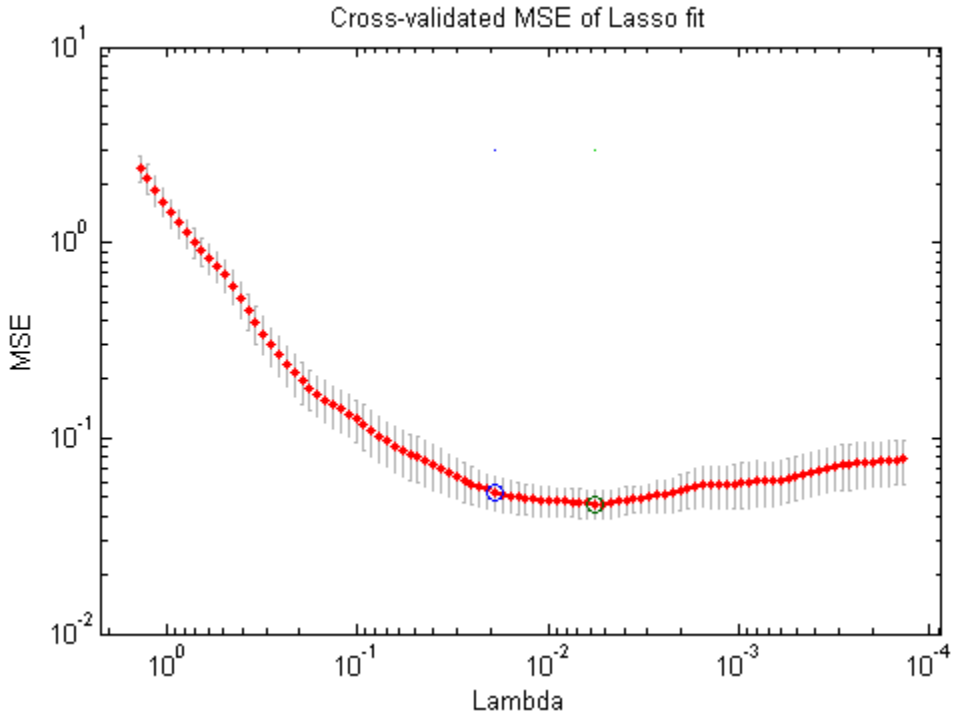
6 Examine the quality of the fit for the suggested value of `Lambda`:

```
lambdaindex = fitinfo.Index1SE;
fitinfo.MSE(lambdaindex)

ans =
    0.0532

fitinfo.DF(lambdaindex)

ans =
    11
```

The fit uses just 11 of the 401 predictors, and achieves a cross-validated MSE of `0.0532`.

7 Examine the plot of cross-validated MSE:

```
lassoPlot(b,fitinfo,'PlotType','CV');
% Use a log scale for MSE to see small MSE values better
set(gca,'YScale','log');
```



As `Lambda` increases (toward the left), MSE increases rapidly. The coefficients are reduced too much and they do not adequately fit the responses.

As `Lambda` decreases, the models are larger (have more nonzero coefficients). The increasing MSE suggests that the models are overfitted.

The default set of `Lambda` values does not include values small enough to include all predictors. In this case, there does not appear to be a reason to look at smaller values. However, if you want smaller values than the default, use the `LambdaRatio` parameter, or supply a sequence of `Lambda` values using the `Lambda` parameter. For details, see the `lasso` reference page.

8 To compute the cross-validated lasso estimate faster, use parallel computing (available with a Parallel Computing Toolbox license):

```
matlabpool open
Starting matlabpool using the 'local' configuration ...
    connected to 4 labs.

opts = statset('UseParallel','always');
tic;
[b fitinfo] = lasso(NIR,octane,'CV',10,'Options',opts);
toc

Elapsed time is 77.910882 seconds.
```

Computing in parallel is more than twice as fast on this problem using a quad-core processor.

Lasso and Elastic Net Details

Overview of Lasso and Elastic Net. Lasso is a regularization technique for performing linear regression. Lasso includes a penalty term that constrains the size of the estimated coefficients. Therefore, it resembles ridge regression. Lasso is a *shrinkage estimator*: it generates coefficient estimates that are biased to be small. Nevertheless, a lasso estimator can have smaller mean squared error than an ordinary least-squares estimator when you apply it to new data.

Unlike ridge regression, as the penalty term increases, lasso sets more coefficients to zero. This means that the lasso estimator is a smaller model, with fewer predictors. As such, lasso is an alternative to stepwise regression and other model selection and dimensionality reduction techniques.

Elastic net is a related technique. Elastic net is a hybrid of ridge regression and lasso regularization. Like lasso, elastic net can generate reduced models by generating zero-valued coefficients. Empirical studies have suggested that the elastic net technique can outperform lasso on data with highly intercorrelated predictors.

Definition of Lasso. The *lasso* technique solves this regularization problem. For a given value of λ, a nonnegative parameter, `lasso` solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{2N}\sum_{i=1}^{N}\left(y_i-\beta_0-x_i^T\beta\right)+\lambda\sum_{j=1}^{p}\left|\beta_j\right|\right),$$

where

- N is the number of observations.
- y_i is the response at observation i.
- x_i is data, a vector of p values at observation i.
- λ is a positive regularization parameter corresponding to one value of `Lambda`.
- The parameters β_0 and β are scalar and p-vector respectively.

As λ increases, the number of nonzero components of β decreases.

The lasso problem involves the L^1 norm of β, as contrasted with the elastic net algorithm.

Definition of Elastic Net. The *elastic net* technique solves this regularization problem. For an α strictly between 0 and 1, and a nonnegative λ, elastic net solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{2N}\sum_{i=1}^{N}\left(y_i-\beta_0-x_i^T\beta\right)+\lambda P_\alpha(\beta)\right),$$

where

$$P_\alpha(\beta)=\frac{(1-\alpha)}{2}\|\beta\|_2^2+\alpha\|\beta\|_1=\sum_{j=1}^{p}\left(\frac{(1-\alpha)}{2}\beta_j^2+\alpha\left|\beta_j\right|\right).$$

Elastic net is the same as lasso when $\alpha = 1$. As α shrinks toward 0, elastic net approaches `ridge` regression. For other values of α, the penalty term $P_\alpha(\beta)$ interpolates between the L^1 norm of β and the squared L^2 norm of β.

References

[1] Tibshirani, R. *Regression shrinkage and selection via the lasso.* Journal of the Royal Statistical Society, Series B, Vol 58, No. 1, pp. 267–288, 1996.

[2] Zou, H. and T. Hastie. *Regularization and variable selection via the elastic net.* Journal of the Royal Statistical Society, Series B, Vol. 67, No. 2, pp. 301–320, 2005.

[3] Friedman, J., R. Tibshirani, and T. Hastie. *Regularization paths for generalized linear models via coordinate descent.* Journal of Statistical Software, Vol 33, No. 1, 2010. `http://www.jstatsoft.org/v33/i01`

[4] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning,* 2nd edition. Springer, New York, 2008.

Partial Least Squares

Introduction to Partial Least Squares

Partial least-squares (*PLS*) regression is a technique used with data that contain correlated predictor variables. This technique constructs new predictor variables, known as *components*, as linear combinations of the original predictor variables. PLS constructs these components while considering the observed response values, leading to a parsimonious model with reliable predictive power.

The technique is something of a cross between multiple linear regression and principal component analysis:

- Multiple linear regression finds a combination of the predictors that best fit a response.
- Principal component analysis finds combinations of the predictors with large variance, reducing correlations. The technique makes no use of response values.

- PLS finds combinations of the predictors that have a large covariance with the response values.

PLS therefore combines information about the variances of both the predictors and the responses, while also considering the correlations among them.

PLS shares characteristics with other regression and feature transformation techniques. It is similar to ridge regression in that it is used in situations with correlated predictors. It is similar to stepwise regression (or more general feature selection techniques) in that it can be used to select a smaller set of model terms. PLS differs from these methods, however, by transforming the original predictor space into the new component space.

The Statistics Toolbox function `plsregress` carries out PLS regression.

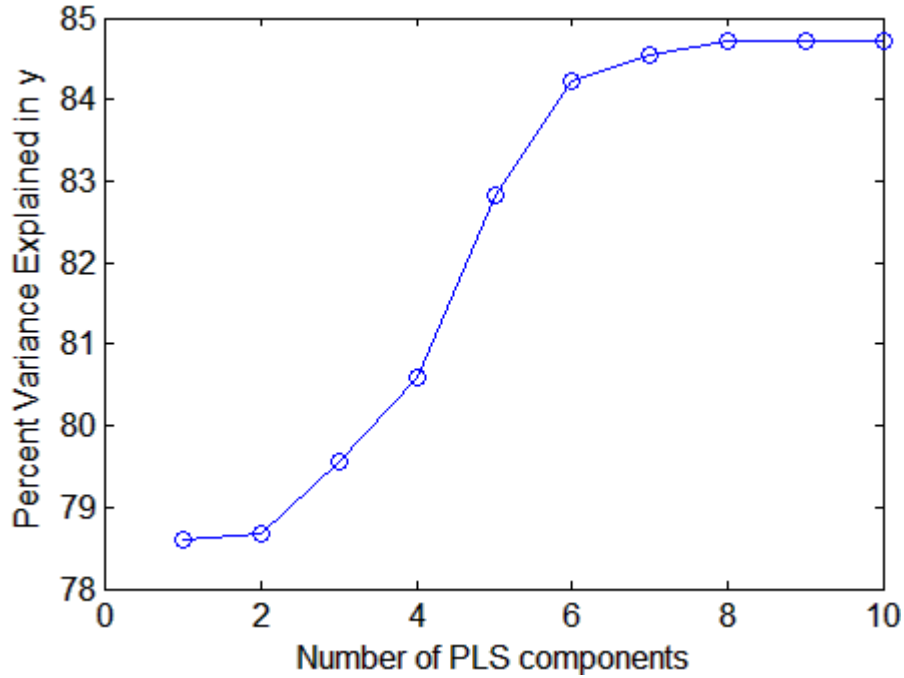
Example: Partial Least Squares

For example, consider the data on biochemical oxygen demand in `moore.mat`, padded with noisy versions of the predictors to introduce correlations:

```
load moore
y = moore(:,6);              % Response
X0 = moore(:,1:5);           % Original predictors
X1 = X0+10*randn(size(X0));  % Correlated predictors
X = [X0,X1];
```

Use `plsregress` to perform PLS regression with the same number of components as predictors, then plot the percentage variance explained in the response as a function of the number of components:

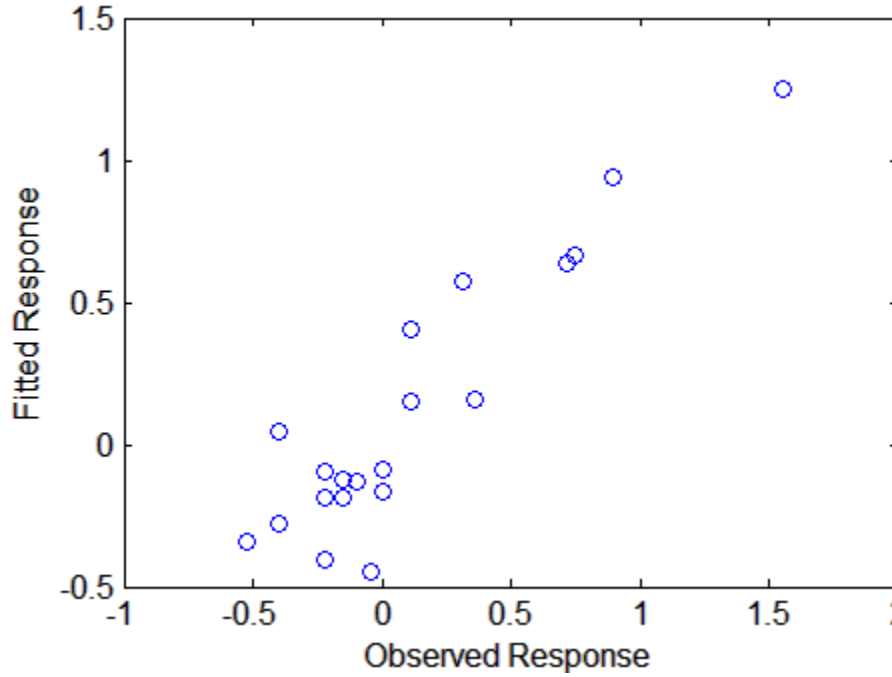
```
[XL,yl,XS,YS,beta,PCTVAR] = plsregress(X,y,10);

plot(1:10,cumsum(100*PCTVAR(2,:)),'-bo');
xlabel('Number of PLS components');
ylabel('Percent Variance Explained in y');
```



Choosing the number of components in a PLS model is a critical step. The plot gives a rough indication, showing nearly 80% of the variance in `y` explained by the first component, with as many as five additional components making significant contributions.

The following computes the six-component model:

```
[XL,yl,XS,YS,beta,PCTVAR,MSE,stats] = plsregress(X,y,6);
yfit = [ones(size(X,1),1) X]*beta;

plot(y,yfit,'o')
```

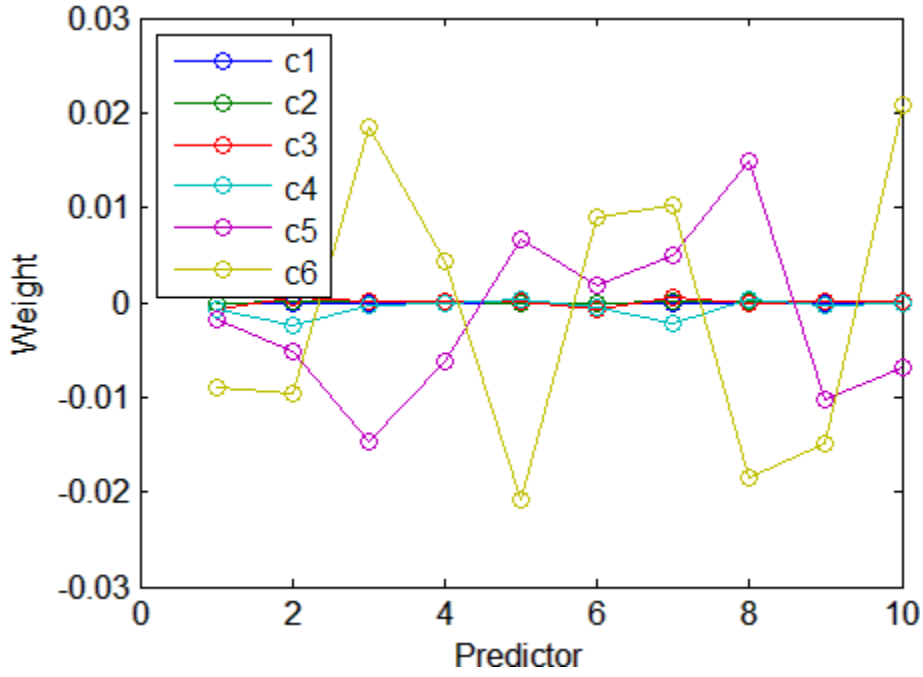


The scatter shows a reasonable correlation between fitted and observed responses, and this is confirmed by the R^2 statistic:

```
TSS = sum((y-mean(y)).^2);
RSS = sum((y-yfit).^2);
Rsquared = 1 - RSS/TSS
Rsquared =
    0.8421
```

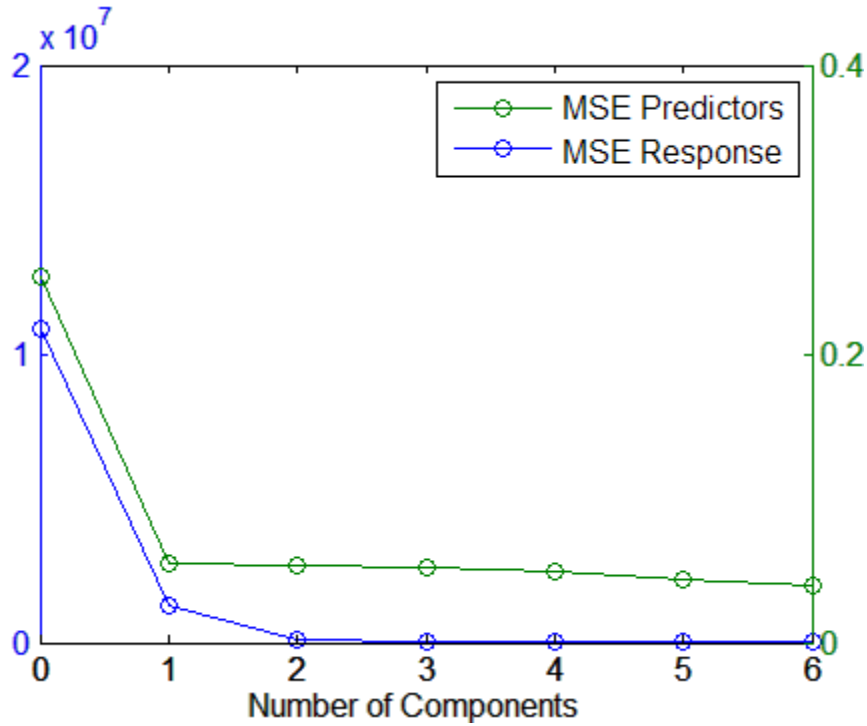
A plot of the weights of the ten predictors in each of the six components shows that two of the components (the last two computed) explain the majority of the variance in `X`:

```
plot(1:10,stats.W,'o-');
legend({'c1','c2','c3','c4','c5','c6'},'Location','NW')
xlabel('Predictor');
ylabel('Weight');
```



A plot of the mean-squared errors suggests that as few as two components may provide an adequate model:

```
[axes,h1,h2] = plotyy(0:6,MSE(1,:),0:6,MSE(2,:));
set(h1,'Marker','o')
set(h2,'Marker','o')
legend('MSE Predictors','MSE Response')
xlabel('Number of Components')
```



The calculation of mean-squared errors by `plsregress` is controlled by optional parameter name/value pairs specifying cross-validation type and the number of Monte Carlo repetitions.

Polynomial Models

Introduction to Polynomial Models

Polynomial models are a special case of the linear models discussed in "Linear Regression Models" on page 9-3. Polynomial models have the advantages of being simple, familiar in their properties, and reasonably flexible for following

data trends. They are also robust with respect to changes in the location and scale of the data (see "Conditioning Polynomial Fits" on page 9-55). However, polynomial models may be poor predictors of new values. They oscillate between data points, especially as the degree is increased to improve the fit. Asymptotically, they follow power functions, leading to inaccuracies when extrapolating other long-term trends. Choosing a polynomial model is often a trade-off between a simple description of overall data trends and the accuracy of predictions made from the model.

Programmatic Polynomial Regression

Functions for Polynomial Fitting. To fit polynomials to data, MATLAB and Statistics Toolbox software offer a number of dedicated functions. The MATLAB function `polyfit` computes least-squares coefficient estimates for polynomials of arbitrary degree. For example:

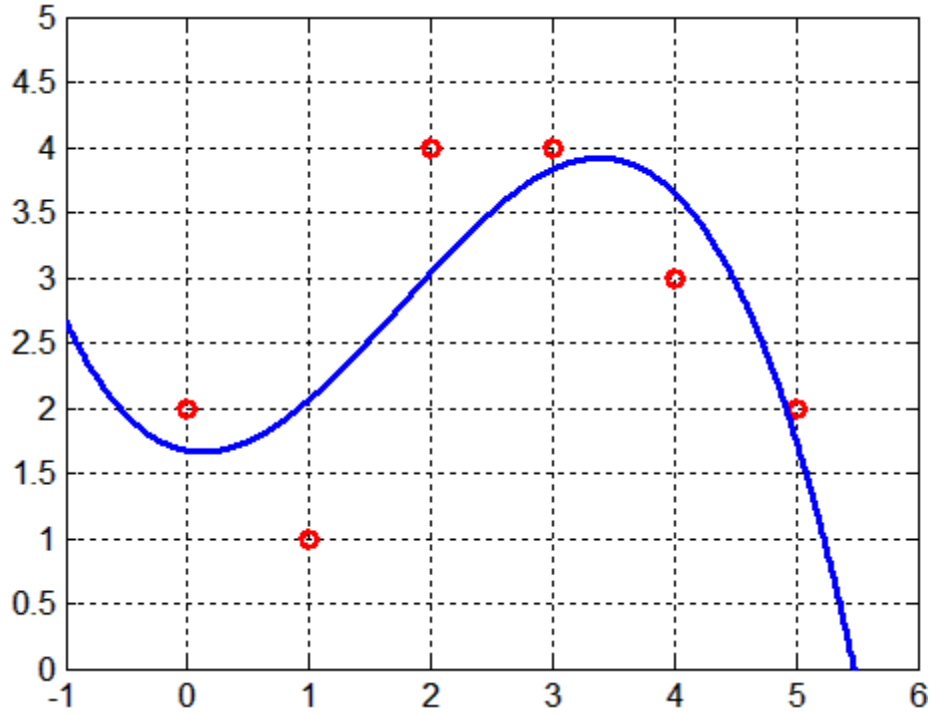
```
x = 0:5; % x data
y = [2 1 4 4 3 2]; % y data
p = polyfit(x,y,3) % Degree 3 fit
p =
   -0.1296    0.6865   -0.1759    1.6746
```

Polynomial coefficients in `p` are listed from highest to lowest degree, so $p(x) \approx -0.13\,x^3 + 0.69\,x^2 - 0.18\,x + 1.67$. For convenience, `polyfit` sets up the Vandermonde design matrix (`vander`) and calls backslash (`mldivide`) to perform the fit.

Once the coefficients of a polynomial are collected in a vector `p`, use the MATLAB function `polyval` to evaluate the polynomial at arbitrary inputs. For example, the following plots the data and the fit over a range of inputs:

```
plot(x,y,'ro','LineWidth',2) % Plot data
hold on
xfit = -1:0.01:6;
yfit = polyval(p,xfit);
```

```
plot(xfit,yfit,'LineWidth',2) % Plot fit
ylim([0,5])
grid on
```



Use the MATLAB function `roots` to find the roots of `p`:

```
r = roots(p)
r =
   5.4786
  -0.0913 + 1.5328i
  -0.0913 - 1.5328i
```

The MATLAB function `poly` solves the inverse problem, finding a polynomial with specified roots. `poly` is the inverse of `roots` up to ordering, scaling, and round-off error.

An optional output from `polyfit` is passed to `polyval` or to the Statistics Toolbox function `polyconf` to compute prediction intervals for the fit. For example, the following computes 95% prediction intervals for new observations at each value of the predictor `x`:

```
[p,S] = polyfit(x,y,3);
[yhat,delta] = polyconf(p,x,S);
PI = [yhat-delta;yhat+delta]'
PI =
   -5.3022    8.6514
   -4.2068    8.3179
   -2.9899    9.0534
   -2.1963    9.8471
   -2.6036    9.9211
   -5.2229    8.7308
```

Optional input arguments to `polyconf` allow you to compute prediction intervals for estimated values (`yhat`) as well as new observations, and to compute the bounds simultaneously for all `x` instead of nonsimultaneously (the default). The confidence level for the intervals can also be set.

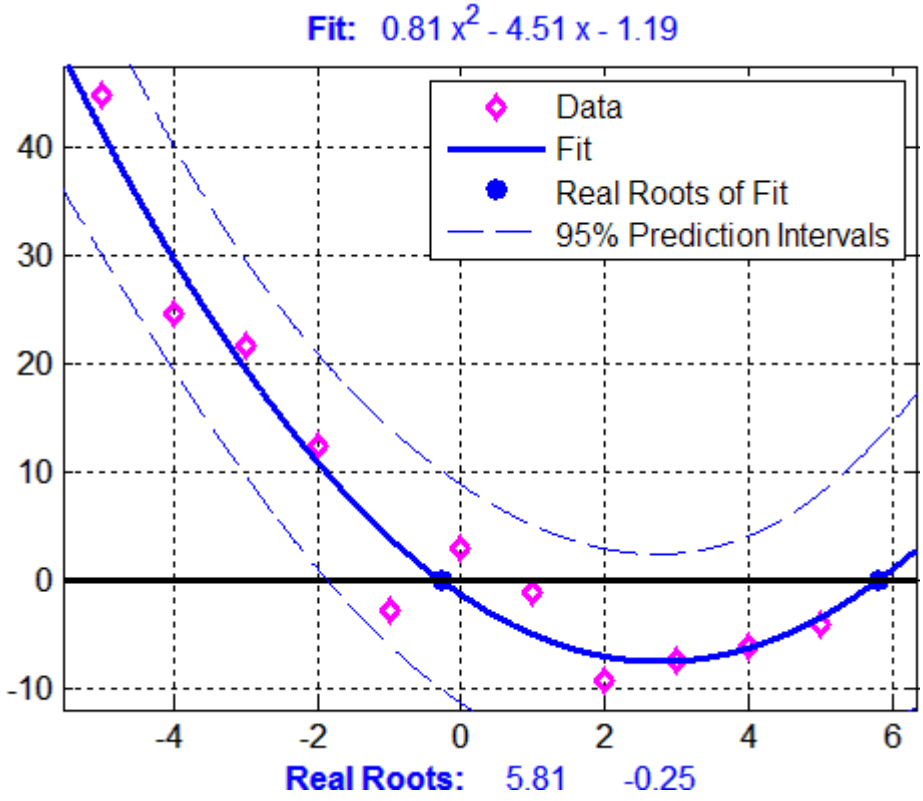
Displaying Polynomial Fits. The documentation example function `polydemo` combines the functions `polyfit`, `polyval`, `roots`, and `polyconf` to produce a formatted display of data with a polynomial fit.

Note Statistics Toolbox documentation example files are located in the `\help\toolbox\stats\examples` subdirectory of your MATLAB root folder (`matlabroot`). This subdirectory is not on the MATLAB path at installation. To use the files in this subdirectory, either add the subdirectory to the MATLAB path (`addpath`) or make the subdirectory your current working folder (`cd`).

For example, the following uses `polydemo` to produce a display of simulated data with a quadratic trend, a fitted polynomial, and 95% prediction intervals for new observations:

```
x = -5:5;
y = x.^2 - 5*x - 3 + 5*randn(size(x));
p = polydemo(x,y,2,0.05)
```

```
p =
    0.8107   -4.5054   -1.1862
```



`polydemo` calls the documentation example function `polystr` to convert the coefficient vector `p` into a string for the polynomial expression displayed in the figure title.

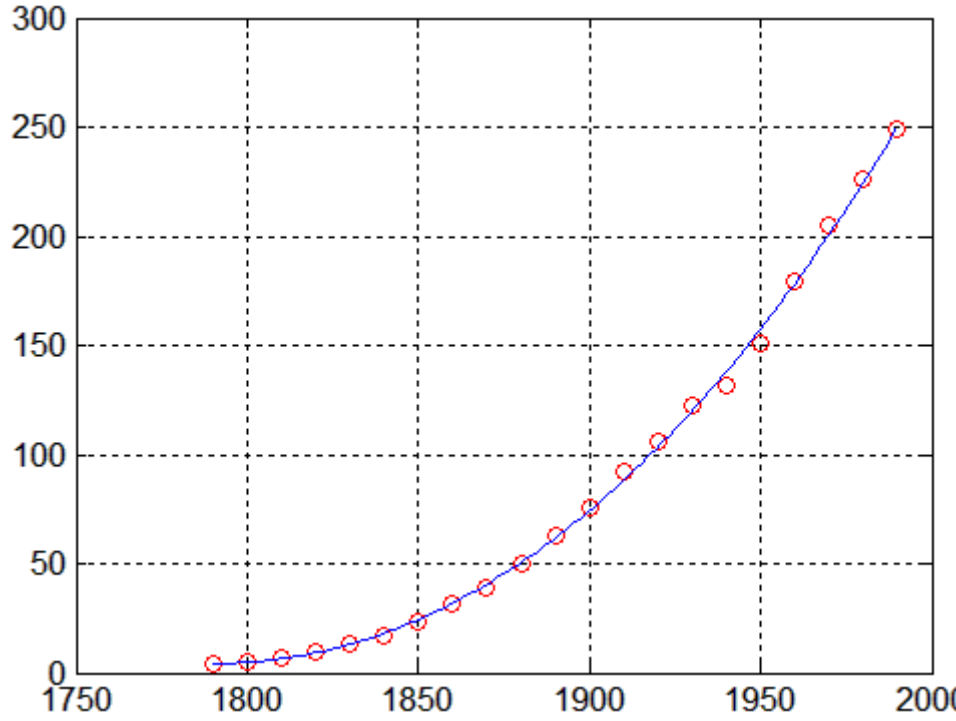
Conditioning Polynomial Fits. If `x` and `y` data are on very different scales, polynomial fits may be badly conditioned, in the sense that coefficient estimates are very sensitive to random errors in the data. For example, using `polyfit` to estimate coefficients of a cubic fit to the U.S. census data in `census.mat` produces the following warning:

```
load census
x = cdate;
```

```
y = pop;
p = polyfit(x,y,3);
Warning: Polynomial is badly conditioned.
         Add points with distinct X values,
         reduce the degree of the polynomial,
         or try centering and scaling as
         described in HELP POLYFIT.
```

The following implements the suggested centering and scaling, and demonstrates the robustness of polynomial fits under these transformations:

```
plot(x,y,'ro') % Plot data
hold on

z = zscore(x); % Compute z-scores of x data
zfit = linspace(z(1),z(end),100);
pz = polyfit(z,y,3); % Compute conditioned fit
yfit = polyval(pz,zfit);

xfit = linspace(x(1),x(end),100);
plot(xfit,yfit,'b-') % Plot conditioned fit vs. x data
grid on
```



Interactive Polynomial Regression

The functions `polyfit`, `polyval`, and `polyconf` are interactively applied to data using two graphical interfaces for polynomial fitting:

- "The Basic Fitting Tool" on page 9-57
- "The Polynomial Fitting Tool" on page 9-58

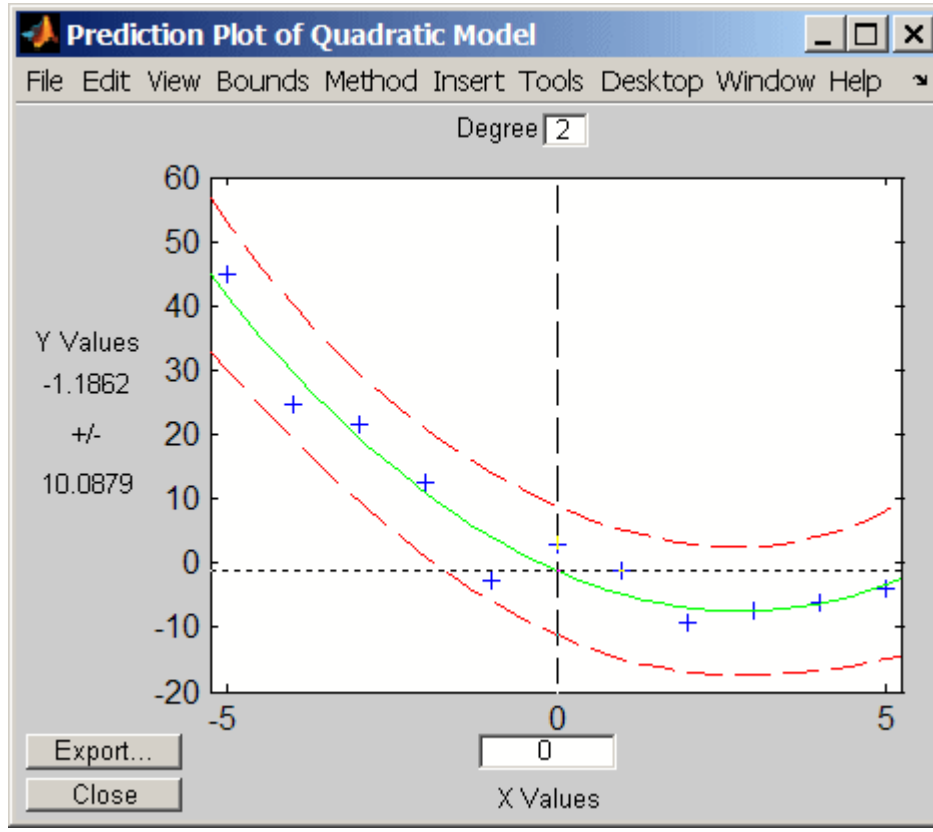
The Basic Fitting Tool. The Basic Fitting Tool is a MATLAB interface, discussed in "Interactive Fitting" in the MATLAB documentation. The tool allows you to:

- Fit interpolants and polynomials of degree ≤ 10
- Plot residuals and compute their norm
- Interpolate or extrapolate values from the fit

- Save results to the MATLAB workspace

The Polynomial Fitting Tool. The Statistics Toolbox function `polytool` opens the Polynomial Fitting Tool. For example, the following opens the interface using simulated data with a quadratic trend and displays a fitted polynomial with 95% prediction intervals for new observations:

```
x = -5:5;
y = x.^2 - 5*x - 3 + 5*randn(size(x));
polytool(x,y,2,0.05)
```



The tool allows you to:

- Interactively change the degree of the fit. Change the value in the **Degree** text box at the top of the figure.
- Evaluate the fit and the bounds using a movable crosshair. Click, hold, and drag the crosshair to change its position.
- Export estimated coefficients, predicted values, prediction intervals, and residuals to the MATLAB workspace. Click **Export** to a open a dialog box with choices for exporting the data.

Options for the displayed bounds and the fitting method are available through menu options at the top of the figure:

- The **Bounds** menu lets you choose between bounds on new observations (the default) and bounds on estimated values. It also lets you choose between nonsimultaneous (the default) and simultaneous bounds. See `polyconf` for a description of these options.
- The **Method** menu lets you choose between ordinary least-squares regression and robust regression, as described in "Robust Regression" on page 9-14.

Response Surface Models

Introduction to Response Surface Models

Polynomial models are generalized to any number of predictor variables x_i (i = 1, ..., N) as follows:

$$y(x) = a_0 + \sum_{i=0}^{N} a_i x_i + \sum_{i<j}^{N} a_{ij} x_i x_j + \sum_{i=0}^{N} a_{ii} x_i^2 + \dots$$

The model includes, from left to right, an intercept, linear terms, quadratic interaction terms, and squared terms. Higher order terms would follow, as necessary.

Response surface models are multivariate polynomial models. They typically arise in the design of experiments (see Chapter 15, "Design of Experiments"), where they are used to determine a set of design variables that optimize a response. Linear terms alone produce models with response surfaces that are hyperplanes. The addition of interaction terms allows for warping of the hyperplane. Squared terms produce the simplest models in which the response surface has a maximum or minimum, and so an optimal response.

Response surface methodology (RSM) is the process of adjusting predictor variables to move the response in a desired direction and, iteratively, to an optimum. The method generally involves a combination of both computation and visualization. The use of quadratic response surface models makes the method much simpler than standard nonlinear techniques for determining optimal designs.

Programmatic Response Surface Methodology

The file `reaction.mat` contains simulated data on the rate of a chemical reaction:

```
load reaction
```

The variables include:

- `rate` — A 13-by-1 vector of observed reaction rates
- `reactants` — A 13-by-3 matrix of reactant concentrations
- `xn` — The names of the three reactants
- `yn` — The name of the response

In "Nonlinear Regression" on page 9-72, the nonlinear Hougen-Watson model is fit to the data using `nlinfit`. However, there may be no theoretical basis for choosing a particular model to fit the data. A quadratic response surface model provides a simple way to determine combinations of reactants that lead to high reaction rates.

As described in "Multiple Linear Regression" on page 9-8, the `regress` and `regstats` functions fit linear models—including response surface models—to data using a design matrix of model terms evaluated at predictor data. The

`x2fx` function converts predictor data to design matrices for quadratic models. The `regstats` function calls `x2fx` when instructed to do so.

For example, the following fits a quadratic response surface model to the data in `reaction.mat`:

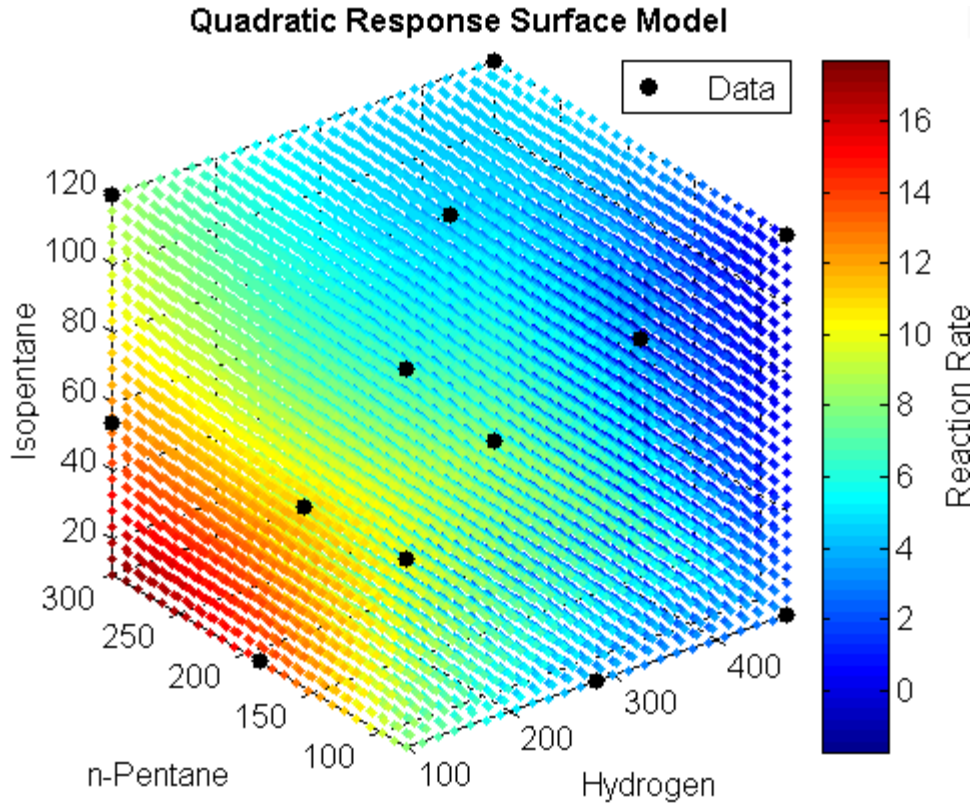
```
stats = regstats(rate,reactants,'quadratic','beta');
b = stats.beta; % Model coefficients
```

The 10-by-1 vector `b` contains, in order, a constant term and then the coefficients for the model terms x_1, x_2, x_3, x_1x_2, x_1x_3, x_2x_3, ${x_1}^2$, ${x_2}^2$, and ${x_3}^2$, where x_1, x_2, and x_3 are the three columns of `reactants`. The order of coefficients for quadratic models is described in the reference page for `x2fx`.

Since the model involves only three predictors, it is possible to visualize the entire response surface using a color dimension for the reaction rate:

```
x1 = reactants(:,1);
x2 = reactants(:,2);
x3 = reactants(:,3);

xx1 = linspace(min(x1),max(x1),25);
xx2 = linspace(min(x2),max(x2),25);
xx3 = linspace(min(x3),max(x3),25);

[X1,X2,X3] = meshgrid(xx1,xx2,xx3);

RATE = b(1) + b(2)*X1 + b(3)*X2 + b(4)*X3 + ...
       b(5)*X1.*X2 + b(6)*X1.*X3 + b(7)*X2.*X3 + ...
       b(8)*X1.^2 + b(9)*X2.^2 + b(10)*X3.^2;

hmodel = scatter3(X1(:),X2(:),X3(:),5,RATE(:),'filled');
hold on
hdata = scatter3(x1,x2,x3,'ko','filled');
axis tight
xlabel(xn(1,:))
ylabel(xn(2,:))
zlabel(xn(3,:))
hbar = colorbar;
ylabel(hbar,yn);
title('{\bf Quadratic Response Surface Model}')
```

```
legend(hdata,'Data','Location','NE')
```

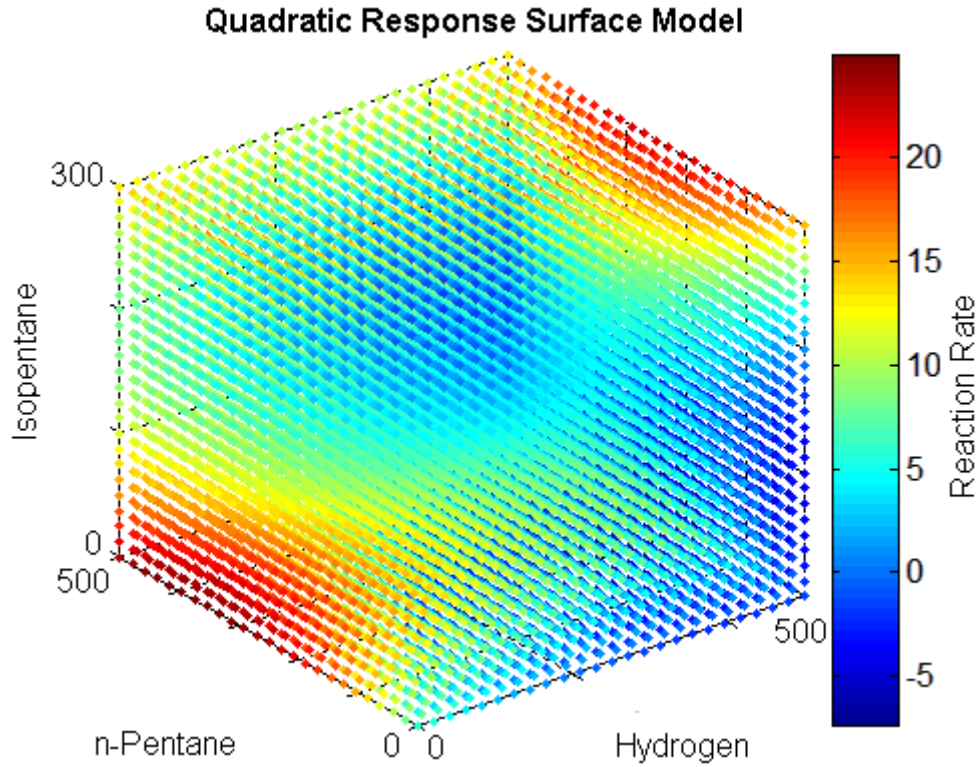


The plot show a general increase in model response, within the space of the observed data, as the concentration of *n*-pentane increases and the concentrations of hydrogen and isopentane decrease.

Before trying to determine optimal values of the predictors, perhaps by collecting more data in the direction of increased reaction rate indicated by the plot, it is helpful to evaluate the geometry of the response surface. If $x = (x_1, x_2, x_3)^T$ is the vector of predictors, and H is the matrix such that x^THx gives the quadratic terms of the model, the model has a unique optimum if and only if H is positive definite. For the data in this example, the model does not have a unique optimum:

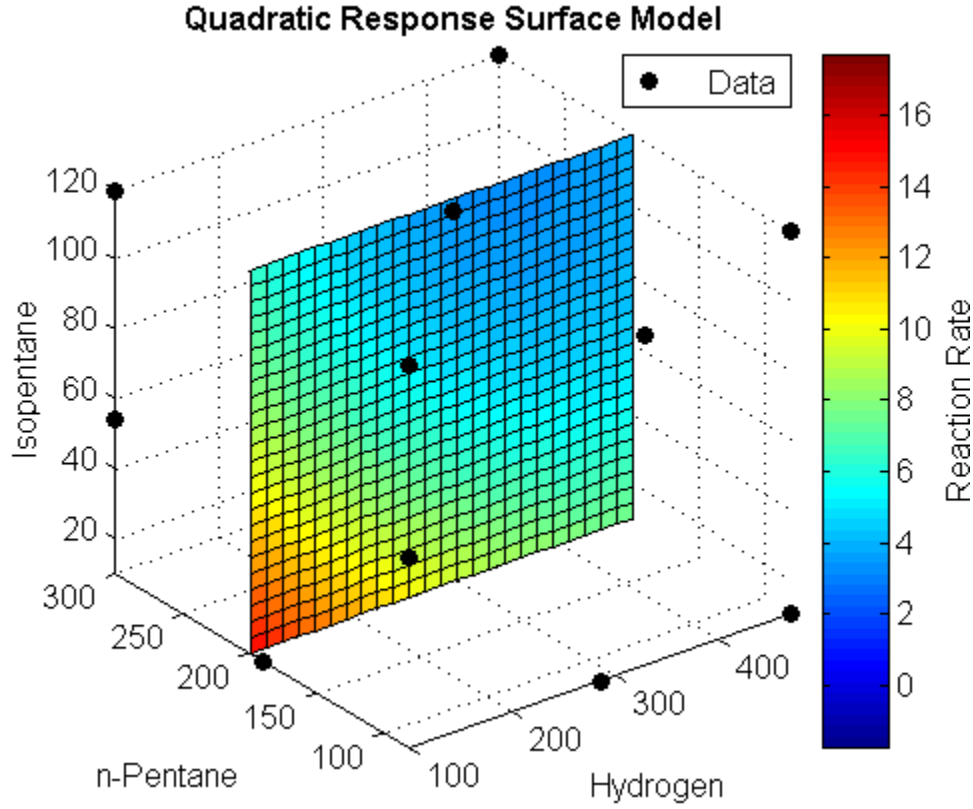
```
H = [b(8),b(5)/2,b(6)/2; ...
     b(5)/2,b(9),b(7)/2; ...
     b(6)/2,b(7)/2,b(10)];
lambda = eig(H)
lambda =
  1.0e-003 *
   -0.1303
    0.0412
    0.4292
```

The negative eigenvalue shows a lack of positive definiteness. The saddle in the model is visible if the range of the predictors in the plot (`xx1`, `xx2`, and `xx3`) is expanded:



When the number of predictors makes it impossible to visualize the entire response surface, 3-, 2-, and 1-dimensional slices provide local views. The MATLAB function `slice` displays 2-dimensional contours of the data at fixed values of the predictors:

```
delete(hmodel)
X2slice = 200; % Fix n-Pentane concentration
slice(X1,X2,X3,RATE,[],X2slice,[])
```

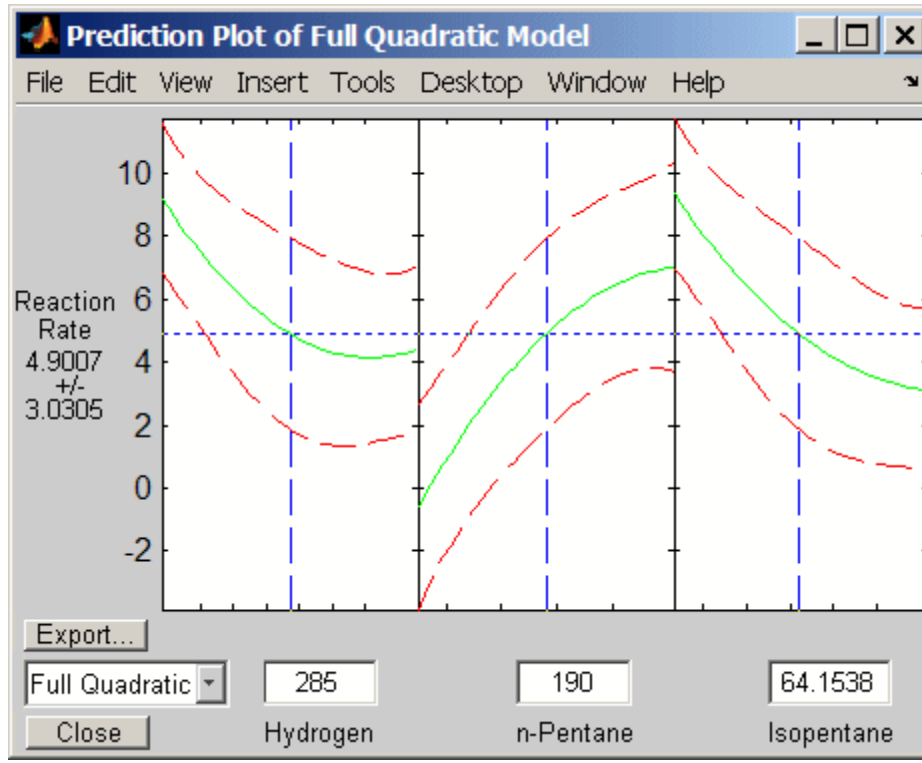


One-dimensional contours are displayed by the Response Surface Tool, `rstool`, described in the next section.

Interactive Response Surface Methodology

The Statistics Toolbox function `rstool` opens a GUI for interactively investigating simultaneous one-dimensional contours of multidimensional response surface models. For example, the following opens the interface with a quadratic response surface fit to the data in `reaction.mat`:

```
load reaction
alpha = 0.01; % Significance level
rstool(reactants,rate,'quadratic',alpha,xn,yn)
```



A sequence of plots is displayed, each showing a contour of the response surface against a single predictor, with all other predictors held fixed. Confidence intervals for new observations are shown as dashed red curves above and below the response. Predictor values are displayed in the text boxes on the horizontal axis and are marked by vertical dashed blue lines

in the plots. Predictor values are changed by editing the text boxes or by dragging the dashed blue lines. When you change the value of a predictor, all plots update to show the new point in predictor space.

Note The Statistics Toolbox demonstration function `rsmdemo` generates simulated data for experimental settings specified by either the user or by a *D*-optimal design generated by `cordexch`. It uses the `rstool` interface to visualize response surface models fit to the data, and it uses the `nlintool` interface to visualize a nonlinear model fit to the data.

Generalized Linear Models

Introduction to Generalized Linear Models

Linear regression models describe a linear relationship between a response and one or more predictive terms. Many times, however, a nonlinear relationship exists. "Nonlinear Regression" on page 9-72 describes general nonlinear models. A special class of nonlinear models, known as *generalized linear models*, makes use of linear methods.

Recall that linear models have the following characteristics:

- At each set of values for the predictors, the response has a normal distribution with mean μ.
- A coefficient vector b defines a linear combination Xb of the predictors X.
- The model is $\mu = Xb$.

In generalized linear models, these characteristics are generalized as follows:

- At each set of values for the predictors, the response has a distribution that may be normal, binomial, Poisson, gamma, or inverse Gaussian, with parameters including a mean μ.
- A coefficient vector b defines a linear combination Xb of the predictors X.

- A *link function* f defines the model as $f(\mu) = Xb$.

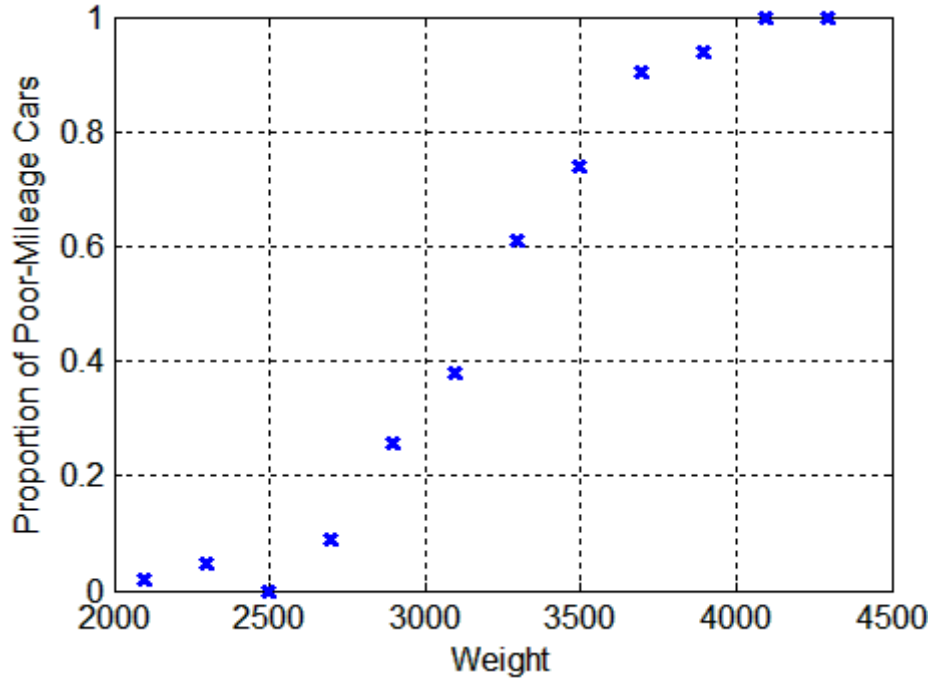
Example: Generalized Linear Models

The following data are derived from `carbig.mat`, which contains measurements of large cars of various weights. Each weight in `w` has a corresponding number of cars in `total` and a corresponding number of poor-mileage cars in `poor`:

```
w = [2100 2300 2500 2700 2900 3100 ...
     3300 3500 3700 3900 4100 4300]';
total = [48 42 31 34 31 21 23 23 21 16 17 21]';
poor = [1 2 0 3 8 8 14 17 19 15 17 21]';
```

A plot shows that the proportion of poor-mileage cars follows an S-shaped sigmoid:

```
plot(w,poor./total,'x','LineWidth',2)
grid on
xlabel('Weight')
ylabel('Proportion of Poor-Mileage Cars')
```

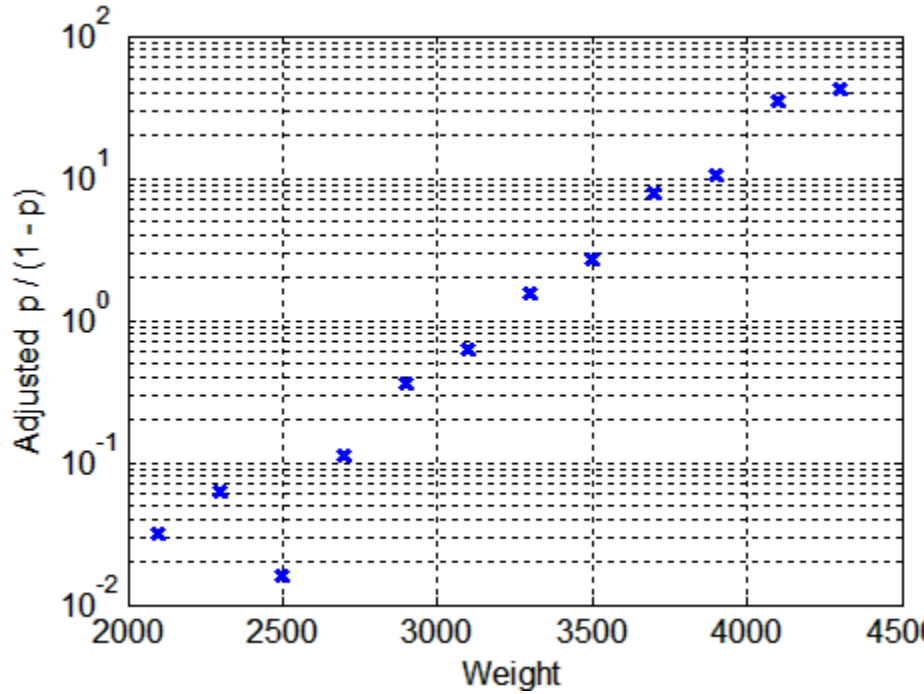


The *logistic model* is useful for proportion data. It defines the relationship between the proportion p and the weight w by:

$$\log[p/(1-p)] = b_1 + b_2 w$$

Some of the proportions in the data are `0` and `1`, making the left-hand side of this equation undefined. To keep the proportions within range, add relatively small perturbations to the `poor` and `total` values. A semi-log plot then shows a nearly linear relationship, as predicted by the model:

```
p_adjusted = (poor+.5)./(total+1);
semilogy(w,p_adjusted./(1-p_adjusted),'x','LineWidth',2)
grid on
xlabel('Weight')
ylabel('Adjusted  p / (1 - p)')
```



It is reasonable to assume that the values of `poor` follow binomial distributions, with the number of trials given by `total` and the percentage of successes depending on `w`. This distribution can be accounted for in the context of a logistic model by using a generalized linear model with link function $\log(\mu/(1-\mu)) = Xb$.

Use the `glmfit` function to carry out the associated regression:

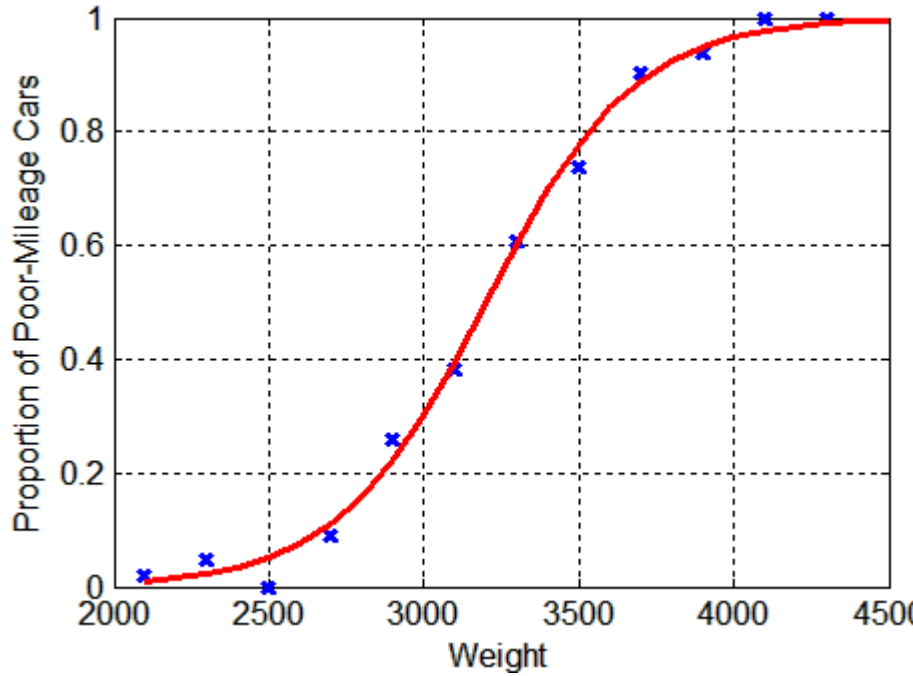
```
b = glmfit(w,[poor total],'binomial','link','logit')
b =
  -13.3801
    0.0042
```

To use the coefficients in `b` to compute fitted proportions, invert the logistic relationship:

$$p = 1/(1 + \exp(-b_1 - b_2 w))$$

Use the `glmval` function to compute the fitted values:

```
x = 2100:100:4500;
y = glmval(b,x,'logit');

plot(w,poor./total,'x','LineWidth',2)
hold on
plot(x,y,'r-','LineWidth',2)
grid on
xlabel('Weight')
ylabel('Proportion of Poor-Mileage Cars')
```



The previous is an example of *logistic regression*. For an example of a kind of *stepwise logistic regression*, analogous to stepwise regression for linear models, see “Sequential Feature Selection” on page 10-23.

Multivariate Regression

Whether or not the predictor $\boldsymbol{x}$ is a vector of predictor variables, *multivariate regression* refers to the case where the response $\boldsymbol{y} = (y_1, ..., y_M)$ is a vector of M response variables.

The Statistics Toolbox functions `mvregress` and `mvregresslike` are used for multivariate regression analysis.

Nonlinear Regression

In this section...

Nonlinear Regression Models

The models described in "Linear Regression Models" on page 9-3 are often called *empirical models*, because they are based solely on observed data. Model parameters typically have no relationship to any mechanism producing the data. To increase the accuracy of a linear model within the range of observations, the number of terms is simply increased.

Nonlinear models, on the other hand, typically involve parameters with specific physical interpretations. While they require *a priori* assumptions about the data-producing process, they are often more parsimonious than linear models, and more accurate outside the range of observed data.

Parametric nonlinear models represent the relationship between a continuous response variable and one or more predictor variables (either continuous or categorical) in the form $y = f(X, \beta) + \varepsilon$, where

- y is an n-by-1 vector of observations of the response variable.
- X is an n-by-p design matrix determined by the predictors.
- β is a p-by-1 vector of unknown parameters to be estimated.
- f is any function of X and β.
- ε is an n-by-1 vector of independent, identically distributed random disturbances.

Nonparametric models do not attempt to characterize the relationship between predictors and response with model parameters. Descriptions are often graphical, as in the case of "Classification Trees and Regression Trees" on page 13-27.

Parametric Models

A Parametric Nonlinear Model

The Hougen-Watson model (Bates and Watts, [2], pp. 271–272) for reaction kinetics is an example of a parametric nonlinear model. The form of the model is

$$rate = \frac{\beta_1 x_2 - x_3 / \beta_5}{1 + \beta_2 x_1 + \beta_3 x_2 + \beta_4 x_3}$$

where *rate* is the reaction rate, x_1, x_2, and x_3 are concentrations of hydrogen, n-pentane, and isopentane, respectively, and β_1, β_2, ... , β_5 are the unknown parameters.

The file `reaction.mat` contains simulated reaction data:

```
load reaction
```

The variables are:

- `rate` — A 13-by-1 vector of observed reaction rates
- `reactants` — A 13-by-3 matrix of reactant concentrations
- `beta` — A 5-by-1 vector of initial parameter estimates
- `model` — The name of a function file for the model
- `xn` — The names of the reactants
- `yn` — The name of the response

The function for the model is `hougen`, which looks like this:

```
type hougen
```

```
function yhat = hougen(beta,x)
%HOUGEN Hougen-Watson model for reaction kinetics.
%   YHAT = HOUGEN(BETA,X) gives the predicted values of the
%   reaction rate, YHAT, as a function of the vector of
%   parameters, BETA, and the matrix of data, X.
%   BETA must have five elements and X must have three
%   columns.
%
%   The model form is:
%   y = (b1*x2 - x3/b5)./(1+b2*x1+b3*x2+b4*x3)

b1 = beta(1);
b2 = beta(2);
b3 = beta(3);
b4 = beta(4);
b5 = beta(5);

x1 = x(:,1);
x2 = x(:,2);
x3 = x(:,3);

yhat = (b1*x2 - x3/b5)./(1+b2*x1+b3*x2+b4*x3);
```

The function `nlinfit` is used to find least-squares parameter estimates for nonlinear models. It uses the Gauss-Newton algorithm with Levenberg-Marquardt modifications for global convergence.

`nlinfit` requires the predictor data, the responses, and an initial guess of the unknown parameters. It also requires a function handle to a function that takes the predictor data and parameter estimates and returns the responses predicted by the model.

To fit the `reaction` data, call `nlinfit` using the following syntax:

```
load reaction
betahat = nlinfit(reactants,rate,@hougen,beta)
betahat =
    1.2526
    0.0628
```

```
    0.0400
    0.1124
    1.1914
```

The output vector `betahat` contains the parameter estimates.

The function `nlinfit` has robust options, similar to those for `robustfit`, for fitting nonlinear models to data with outliers.

Confidence Intervals for Parameter Estimates

To compute confidence intervals for the parameter estimates, use the function `nlparci`, together with additional outputs from `nlinfit`:

```
[betahat,resid,J] = nlinfit(reactants,rate,@hougen,beta);
betaci = nlparci(betahat,resid,J)
betaci =
   -0.7467    3.2519
   -0.0377    0.1632
   -0.0312    0.1113
   -0.0609    0.2857
   -0.7381    3.1208
```

The columns of the output `betaci` contain the lower and upper bounds, respectively, of the (default) 95% confidence intervals for each parameter.

Confidence Intervals for Predicted Responses

The function `nlpredci` is used to compute confidence intervals for predicted responses:

```
[yhat,delta] = nlpredci(@hougen,reactants,betahat,resid,J);
opd = [rate yhat delta]
opd =
    8.5500    8.4179    0.2805
    3.7900    3.9542    0.2474
    4.8200    4.9109    0.1766
    0.0200   -0.0110    0.1875
    2.7500    2.6358    0.1578
   14.3900   14.3402    0.4236
    2.5400    2.5662    0.2425
```

```
    4.3500    4.0385    0.1638
   13.0000   13.0292    0.3426
    8.5000    8.3904    0.3281
    0.0500   -0.0216    0.3699
   11.3200   11.4701    0.3237
    3.1300    3.4326    0.1749
```

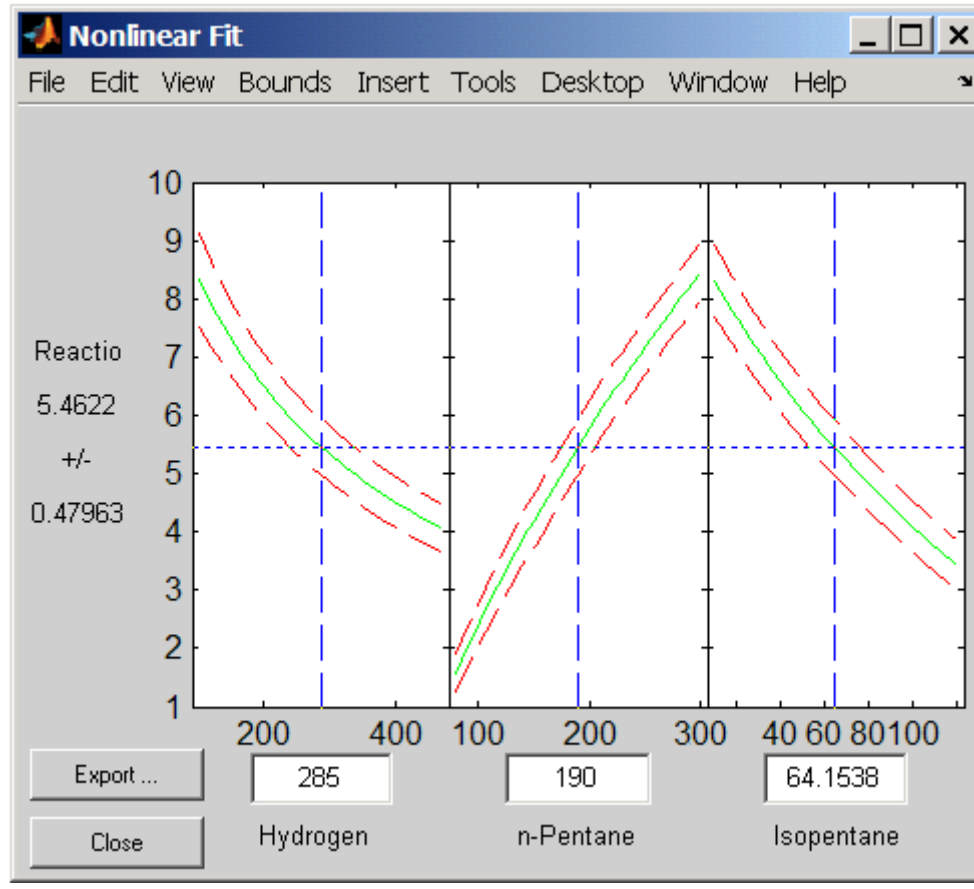
The output `opd` contains the observed rates in the first column and the predicted rates in the second column. The (default) 95% simultaneous confidence intervals on the predictions are the values in the second column ± the values in the third column. These are not intervals for new observations at the predictors, even though most of the confidence intervals do contain the original observations.

Interactive Nonlinear Parametric Regression

Calling `nlintool` opens a graphical user interface (GUI) for interactive exploration of multidimensional nonlinear functions, and for fitting parametric nonlinear models. The GUI calls `nlinfit`, and requires the same inputs. The interface is analogous to `polytool` and `rstool` for polynomial models.

Open `nlintool` with the `reaction` data and the `hougen` model by typing

```
load reaction
nlintool(reactants,rate,@hougen,beta,0.01,xn,yn)
```



You see three plots. The response variable for all plots is the reaction rate, plotted in green. The red lines show confidence intervals on predicted responses. The first plot shows hydrogen as the predictor, the second shows *n*-pentane, and the third shows isopentane.

Each plot displays the fitted relationship of the reaction rate to one predictor at a fixed value of the other two predictors. The fixed values are in the text boxes below each predictor axis. Change the fixed values by typing in a new value or by dragging the vertical lines in the plots to new positions. When you change the value of a predictor, all plots update to display the model at the new point in predictor space.

While this example uses only three predictors, `nlintool` can accommodate any number of predictors.

Note The Statistics Toolbox demonstration function `rsmdemo` generates simulated data for experimental settings specified by either the user or by a *D*-optimal design generated by `cordexch`. It uses the `rstool` interface to visualize response surface models fit to the data, and it uses the `nlintool` interface to visualize a nonlinear model fit to the data.

Mixed-Effects Models

Introduction to Mixed-Effects Models

In statistics, an *effect* is anything that influences the value of a response variable at a particular setting of the predictor variables. Effects are translated into model parameters. In linear models, effects become coefficients, representing the proportional contributions of model terms. In nonlinear models, effects often have specific physical interpretations, and appear in more general nonlinear combinations.

Fixed effects represent population parameters, assumed to be the same each time data is collected. Estimating fixed effects is the traditional domain of regression modeling. *Random effects*, by comparison, are sample-dependent random variables. In modeling, random effects act like additional error terms, and their distributions and covariances must be specified.

For example, consider a model of the elimination of a drug from the bloodstream. The model uses time t as a predictor and the concentration of the drug C as the response. The nonlinear model term C_0e^{-rt} combines parameters C_0 and r, representing, respectively, an initial concentration and an elimination rate. If data is collected across multiple individuals, it is reasonable to assume that the elimination rate is a random variable r_i depending on individual i, varying around a population mean $\bar{r}$. The term C_0e^{-rt} becomes

$$C_0e^{-[\bar{r}+(r_i-\bar{r})]t} = C_0e^{-(\beta+b_i)t},$$

where $\beta = \bar{r}$ is a fixed effect and $b_i = r_i - \bar{r}$ is a random effect.

Random effects are useful when data falls into natural groups. In the drug elimination model, the groups are simply the individuals under study. More sophisticated models might group data by an individual's age, weight, diet, etc. Although the groups are not the focus of the study, adding random effects to a model extends the reliability of inferences beyond the specific sample of individuals.

Mixed-effects models account for both fixed and random effects. As with all regression models, their purpose is to describe a response variable as a function of the predictor variables. Mixed-effects models, however, recognize correlations within sample subgroups. In this way, they provide a compromise between ignoring data groups entirely and fitting each group with a separate model.

Mixed-Effects Model Hierarchy

Suppose data for a nonlinear regression model falls into one of m distinct groups $i = 1, ..., m$. To account for the groups in a model, write response j in group i as:

$$y_{ij} = f(\varphi, x_{ij}) + \varepsilon_{ij}$$

y_{ij} is the response, x_{ij} is a vector of predictors, φ is a vector of model parameters, and ε_{ij} is the measurement or process error. The index j ranges from 1 to n_i, where n_i is the number of observations in group i. The function f specifies the form of the model. Often, x_{ij} is simply an observation time t_{ij}.

The errors are usually assumed to be independent and identically, normally distributed, with constant variance.

Estimates of the parameters in φ describe the population, assuming those estimates are the same for all groups. If, however, the estimates vary by group, the model becomes

$$y_{ij} = f(\varphi_i, x_{ij}) + \varepsilon_{ij}$$

In a mixed-effects model, φ_i may be a combination of a fixed and a random effect:

$$\varphi_i = \beta + b_i$$

The random effects b_i are usually described as multivariate normally distributed, with mean zero and covariance Ψ. Estimating the fixed effects β and the covariance of the random effects Ψ provides a description of the population that does not assume the parameters φ_i are the same across groups. Estimating the random effects b_i also gives a description of specific groups within the data.

Model parameters do not have to be identified with individual effects. In general, *design matrices* A and B are used to identify parameters with linear combinations of fixed and random effects:

$$\varphi_i = A\beta + Bb_i$$

If the design matrices differ among groups, the model becomes

$$\varphi_i = A_i\beta + B_ib_i$$

If the design matrices also differ among observations, the model becomes

$$\varphi_{ij} = A_{ij}\beta + B_{ij}b_i$$
$$y_{ij} = f(\varphi_{ij}, x_{ij}) + \varepsilon_{ij}$$

Some of the group-specific predictors in x_{ij} may not change with observation j. Calling those v_i, the model becomes

$$y_{ij} = f(\varphi_{ij}, x_{ij}, v_i) + \varepsilon_{ij}$$

Specifying Mixed-Effects Models

Suppose data for a nonlinear regression model falls into one of m distinct groups $i = 1, ..., m$. (Specifically, suppose that the groups are not nested.) To specify a general nonlinear mixed-effects model for this data:

1. Define group-specific model parameters φ_i as linear combinations of fixed effects β and random effects b_i.
2. Define response values y_i as a nonlinear function f of the parameters and group-specific predictor variables X_i.

The model is:

$$\varphi_i = A_i\beta + B_i b_i$$
$$y_i = f(\varphi_i, X_i) + \varepsilon_i$$
$$b_i \sim N(0, \Psi)$$
$$\varepsilon_i \sim N(0, \sigma^2)$$

This formulation of the nonlinear mixed-effects model uses the following notation:

φ_i	A vector of group-specific model parameters
β	A vector of fixed effects, modeling population parameters
b_i	A vector of multivariate normally distributed group-specific random effects
A_i	A group-specific design matrix for combining fixed effects
B_i	A group-specific design matrix for combining random effects
X_i	A data matrix of group-specific predictor values
y_i	A data vector of group-specific response values

f	A general, real-valued function of φ_i and X_i
ε_i	A vector of group-specific errors, assumed to be independent, identically, normally distributed, and independent of b_i
Ψ	A covariance matrix for the random effects
σ^2	The error variance, assumed to be constant across observations

For example, consider a model of the elimination of a drug from the bloodstream. The model incorporates two overlapping phases:

- An initial phase p during which drug concentrations reach equilibrium with surrounding tissues
- A second phase q during which the drug is eliminated from the bloodstream

For data on multiple individuals i, the model is

$$y_{ij} = C_{pi}e^{-r_{pi}t_{ij}} + C_{qi}e^{-r_{qi}t_{ij}} + \varepsilon_{ij},$$

where y_{ij} is the observed concentration in individual i at time t_{ij}. The model allows for different sampling times and different numbers of observations for different individuals.

The elimination rates r_{pi} and r_{qi} must be positive to be physically meaningful. Enforce this by introducing the log rates $R_{pi} = \log(r_{pi})$ and $R_{qi} = \log(r_{qi})$ and reparametrizing the model:

$$y_{ij} = C_{pi}e^{-\exp(R_{pi})t_{ij}} + C_{qi}e^{-\exp(R_{qi})t_{ij}} + \varepsilon_{ij}$$

Choosing which parameters to model with random effects is an important consideration when building a mixed-effects model. One technique is to add random effects to all parameters, and use estimates of their variances to determine their significance in the model. An alternative is to fit the model separately to each group, without random effects, and look at the variation of the parameter estimates. If an estimate varies widely across groups, or if confidence intervals for each group have minimal overlap, the parameter is a good candidate for a random effect.

To introduce fixed effects β and random effects b_i for all model parameters, reexpress the model as follows:

$$\begin{aligned} y_{ij} &= [\bar{C}_p + (C_{pi} - \bar{C}_p)]e^{-\exp[\bar{R}_p + (R_{pi} - \bar{R}_p)]t_{ij}} + \\ &\quad [\bar{C}_q + (C_{qi} - \bar{C}_q)]e^{-\exp[\bar{R}_q + (R_{qi} - \bar{R}_q)]t_{ij}} + \varepsilon_{ij} \\ &= (\beta_1 + b_{1i})e^{-\exp(\beta_2 + b_{2i})t_{ij}} + \\ &\quad (\beta_3 + b_{3i})e^{-\exp(\beta_4 + b_{4i})t_{ij}} + \varepsilon_{ij} \end{aligned}$$

In the notation of the general model:

$$\beta = \begin{pmatrix} \beta_1 \\ \vdots \\ \beta_4 \end{pmatrix}, b_i = \begin{pmatrix} b_{i1} \\ \vdots \\ b_{i4} \end{pmatrix}, y_i = \begin{pmatrix} y_{i1} \\ \vdots \\ y_{in_i} \end{pmatrix}, X_i = \begin{pmatrix} t_{i1} \\ \vdots \\ t_{in_i} \end{pmatrix},$$

where n_i is the number of observations of individual i. In this case, the design matrices A_i and B_i are, at least initially, 4-by-4 identity matrices. Design matrices may be altered, as necessary, to introduce weighting of individual effects, or time dependency.

Fitting the model and estimating the covariance matrix Ψ often leads to further refinements. A relatively small estimate for the variance of a random effect suggests that it can be removed from the model. Likewise, relatively small estimates for covariances among certain random effects suggests that a full covariance matrix is unnecessary. Since random effects are unobserved, Ψ must be estimated indirectly. Specifying a diagonal or block-diagonal covariance pattern for Ψ can improve convergence and efficiency of the fitting algorithm.

Statistics Toolbox functions `nlmefit` and `nlmefitsa` fit the general nonlinear mixed-effects model to data, estimating the fixed and random effects. The functions also estimate the covariance matrix Ψ for the random effects. Additional diagnostic outputs allow you to assess tradeoffs between the number of model parameters and the goodness of fit.

Specifying Covariate Models

If the model in "Specifying Mixed-Effects Models" on page 9-81 assumes a group-dependent covariate such as weight (w) the model becomes:

$$\begin{pmatrix}\varphi_1\\ \varphi_2\\ \varphi_3\end{pmatrix}=\begin{pmatrix}1 & 0 & 0 w_i\\ 0 & 1 & 0\ 0\\ 0 & 0 & 1\ 0\end{pmatrix}\begin{pmatrix}\beta_1\\ \beta_2\\ \beta_3\\ \beta_4\end{pmatrix}+\begin{pmatrix}1 & 0 & 0\\ 0 & 1 & 0\\ 0 & 0 & 1\end{pmatrix}\begin{pmatrix}b_1\\ b_2\\ b_3\end{pmatrix}$$

Thus, the parameter φ_i for any individual in the `i`th group is:

$$\begin{pmatrix}\varphi_{1_i}\\ \varphi_{2_i}\\ \varphi_{3_i}\end{pmatrix}=\begin{pmatrix}\beta_1 + \beta_4 * w_i\\ \beta_2\\ \beta_3\end{pmatrix}+\begin{pmatrix}b_{1_i}\\ b_{2_i}\\ b_{3_i}\end{pmatrix}$$

To specify a covariate model, use the `'FEGroupDesign'` option.

`'FEGroupDesign'` is a `p-by-q-by-m` array specifying a different `p-by-q` fixed-effects design matrix for each of the `m` groups. Using the previous example, the array resembles the following:

1 Create the array.

```
% Number of parameters in the model (Phi)
num_params = 3;
```

```
% Number of covariates
num_cov = 1;
% Assuming number of groups in the data set is 7
num_groups = 7;
% Array of covariate values
covariates = [75; 52; 66; 55; 70; 58; 62 ];
A = repmat(eye(num_params, num_params+num_cov),...
[1,1,num_groups]);
A(1,num_params+1,1:num_groups) = covariates(:,1)
```

2 Create a `struct` with the specified design matrix.

```
options.FEGroupDesign = A;
```

3 Specify the arguments for `nlmefit` (or `nlmefitsa`) as shown in "Example: Mixed-Effects Models Using nlmefit and nlmefitsa" on page 9-93.

Choosing nlmefit or nlmefitsa

Statistics Toolbox provides two functions, `nlmefit` and `nlmefitsa` for fitting non-linear mixed-effects models. Each function provides different capabilities, which may help you decide which to use.

Approximation Methods. `nlmefit` provides the following four approximation methods for fitting non-linear mixed-effects models:

- `'LME'` — Use the likelihood for the linear mixed-effects model at the current conditional estimates of `beta` and `B`. This is the default.
- `'RELME'` — Use the restricted likelihood for the linear mixed-effects model at the current conditional estimates of `beta` and `B`.
- `'FO'` — First-order Laplacian approximation without random effects.
- `'FOCE'` — First-order Laplacian approximation at the conditional estimates of `B`.

`nlmefitsa` provides an additional approximation method, Stochastic Approximation Expectation-Maximization (SAEM) [24] with three steps :

1. Simulation: Generate simulated values of the random effects b from the posterior density $p(b \mid \Sigma)$ given the current parameter estimates.
2. Stochastic approximation: Update the expected value of the log likelihood function by taking its value from the previous step, and moving part way toward the average value of the log likelihood calculated from the simulated random effects.
3. Maximization step: Choose new parameter estimates to maximize the log likelihood function given the simulated values of the random effects.

Both `nlmefit` and `nlmefitsa` attempt to find parameter estimates to maximize a likelihood function, which is difficult to compute. `nlmefit` deals with the problem by approximating the likelihood function in various ways, and maximizing the approximate function. It uses traditional optimization techniques that depend on things like convergence criteria and iteration limits.

`nlmefitsa`, on the other hand, simulates random values of the parameters in such a way that in the long run they converge to the values that maximize the exact likelihood function. The results are random, and traditional convergence tests don't apply. Therefore `nlmefitsa` provides options to plot the results as the simulation progresses, and to re-start the simulation multiple times. You can use these features to judge whether the results have converged to the accuracy you desire.

Parameters Specific to nlmefitsa. The following parameters are specific to `nlmefitsa`. Most control the stochastic algorithm.

- `CovO` — Initial value for the covariance matrix `PSI`. Must be an r-by-r positive definite matrix. If empty, the default value depends on the values of `BETAO`.
- `ComputeStdErrors` — `true` to compute standard errors for the coefficient estimates and store them in the output `STATS` structure, or `false` (default) to omit this computation.
- `LogLikMethod` — Specifies the method for approximating the log likelihood.

- `NBurnIn` — Number of initial burn-in iterations during which the parameter estimates are not recomputed. Default is 5.
- `NIterations` — Controls how many iterations are performed for each of three phases of the algorithm.
- `NMCMCIterations` — Number of Markov Chain Monte Carlo (MCMC) iterations.

Model and Data Requirements. There are some differences in the capabilities of `nlmefit` and `nlmefitsa`. Therefore some data and models are usable with either function, but some may require you to choose just one of them.

- **Error models** — `nlmefitsa` supports a variety of error models. For example, the standard deviation of the response can be constant, proportional to the function value, or a combination of the two. `nlmefit` fits models under the assumption that the standard deviation of the response is constant. One of the error models, `'exponential'`, specifies that the log of the response has a constant standard deviation. You can fit such models using `nlmefit` by providing the log response as input, and by re-writing the model function to produce the log of the nonlinear function value.
- **Random effects** — Both functions fit data to a nonlinear function with parameters, and the parameters may be simple scalar values or linear functions of covariates. `nlmefit` allows any coefficients of the linear functions to have both fixed and random effects. `nlmefitsa` supports random effects only for the constant (intercept) coefficient of the linear functions, but not for slope coefficients. So in the example in "Specifying Covariate Models" on page 9-84, `nlmefitsa` can treat only the first three beta values as random effects.
- **Model form** — `nlmefit` supports a very general model specification, with few restrictions on the design matrices that relate the fixed coefficients and the random effects to the model parameters. `nlmefitsa` is more restrictive:
  - The fixed effect design must be constant in every group (for every individual), so an observation-dependent design is not supported.
  - The random effect design must be constant for the entire data set, so neither an observation-dependent design nor a group-dependent design is supported.

- As mentioned under **Random Effects**, the random effect design must not specify random effects for slope coefficients. This implies that the design must consist of zeros and ones.
- The random effect design must not use the same random effect for multiple coefficients, and cannot use more than one random effect for any single coefficient.
- The fixed effect design must not use the same coefficient for multiple parameters. This implies that it can have at most one non-zero value in each column.

If you want to use `nlmefitsa` for data in which the covariate effects are random, include the covariates directly in the nonlinear model expression. Don't include the covariates in the fixed or random effect design matrices.

- **Convergence** — As described in the **Model form**, `nlmefit` and `nlmefitsa` have different approaches to measuring convergence. `nlmefit` uses traditional optimization measures, and `nlmefitsa` provides diagnostics to help you judge the convergence of a random simulation.

In practice, `nlmefitsa` tends to be more robust, and less likely to fail on difficult problems. However, `nlmefit` may converge faster on problems where it converges at all. Some problems may benefit from a combined strategy, for example by running `nlmefitsa` for a while to get reasonable parameter estimates, and using those as a starting point for additional iterations using `nlmefit`.

Using Output Functions with Mixed-Effects Models

The `Outputfcn` field of the `options` structure specifies one or more functions that the solver calls after each iteration. Typically, you might use an output function to plot points at each iteration or to display optimization quantities from the algorithm. To set up an output function:

1. Write the output function as a MATLAB file function or subfunction.
2. Use `statset` to set the value of `Outputfcn` to be a function handle, that is, the name of the function preceded by the `@` sign. For example, if the output function is `outfun.m`, the command

```
options = statset('OutputFcn', @outfun);
```

specifies `OutputFcn` to be the handle to `outfun`. To specify multiple output functions, use the syntax:

```
options = statset('OutputFcn',{@outfun, @outfun2});
```

3 Call the optimization function with `options` as an input argument.

For an example of an output function, see "Sample Output Function" on page 9-93.

Structure of the Output Function. The function definition line of the output function has the following form:

```
stop = outfun(beta,status,state)
```

where

- *beta* is the current fixed effects.
- *status* is a structure containing data from the current iteration. "Fields in status" on page 9-89 describes the structure in detail.
- *state* is the current state of the algorithm. "States of the Algorithm" on page 9-90 lists the possible values.
- *stop* is a flag that is `true` or `false` depending on whether the optimization routine should quit or continue. See "Stop Flag" on page 9-91 for more information.

The solver passes the values of the input arguments to `outfun` at each iteration.

Fields in status. The following table lists the fields of the `status` structure:

Field	Description
`procedure`	• `'ALT'` — alternating algorithm for the optimization of the linear mixed effects or restricted linear mixed effects approximations • `'LAP'` — optimization of the Laplacian approximation for first order or first order conditional estimation
`iteration`	An integer starting from 0.

Field	Description

`inner`	A structure describing the status of the inner iterations within the `ALT` and `LAP` procedures, with the fields:
	• `procedure` — When `procedure` is `'ALT'`:
	  - `'PNLS'` (penalized non-linear least squares)
	  - `'LME'` (linear mixed-effects estimation)
	  - `'none'`
	When `procedure` is `'LAP'`,
	  - `'PNLS'` (penalized non-linear least squares)
	  - `'PLM'` (profiled likelihood maximization)
	  - `'none'`
	• `state` — one of the following:
	  - `'init'`
	  - `'iter'`
	  - `'done'`
	  - `'none'`
	• `iteration` — an integer starting from 0, or `NaN`. For `nlmefitsa` with burn-in iterations, the output function is called after each of those iterations with a negative value for `STATUS.iteration`.

`fval`	The current log likelihood
`Psi`	The current random-effects covariance matrix
`theta`	The current parameterization of `Psi`
`mse`	The current error variance

States of the Algorithm. The following table lists the possible values for `state`:

state	Description
'init'	The algorithm is in the initial state before the first iteration.
'iter'	The algorithm is at the end of an iteration.
'done'	The algorithm is in the final state after the last iteration.

The following code illustrates how the output function might use the value of `state` to decide which tasks to perform at the current iteration:

```
switch state
    case 'iter'
          % Make updates to plot or guis as needed
    case 'init'
          % Setup for plots or guis
    case 'done'
          % Cleanup of plots, guis, or final plot
otherwise
end
```

Stop Flag. The output argument `stop` is a flag that is `true` or `false`. The flag tells the solver whether it should quit or continue. The following examples show typical ways to use the `stop` flag.

Stopping an Optimization Based on Intermediate Results

The output function can stop the estimation at any iteration based on the values of arguments passed into it. For example, the following code sets stop to true based on the value of the log likelihood stored in the `'fval'` field of the status structure:

```
stop = outfun(beta,status,state)
stop = false;
% Check if loglikelihood is more than 132.
if status.fval > -132
    stop = true;
end
```

Stopping an Iteration Based on GUI Input

If you design a GUI to perform `nlmefit` iterations, you can make the output function stop when a user clicks a **Stop** button on the GUI. For example, the following code implements a dialog to cancel calculations:

```
function retval = stop_outfcn(beta,str,status)
persistent h stop;
if isequal(str.inner.state,'none')
    switch(status)
        case 'init'
            % Initialize dialog
            stop = false;
            h = msgbox('Press STOP to cancel calculations.',...
                'NLMEFIT: Iteration 0 ');
            button = findobj(h,'type','uicontrol');
            set(button,'String','STOP','Callback',@stopper)
            pos = get(h,'Position');
            pos(3) = 1.1 * pos(3);
            set(h,'Position',pos)
            drawnow
        case 'iter'
            % Display iteration number in the dialog title
            set(h,'Name',sprintf('NLMEFIT: Iteration %d',...
                str.iteration))
            drawnow;
        case 'done'
            % Delete dialog
            delete(h);
    end
end
if stop
    % Stop if the dialog button has been pressed
    delete(h)
end
retval = stop;

    function stopper(varargin)
        % Set flag to stop when button is pressed
        stop = true;
```

```
        disp('Calculation stopped.')
    end
end
```

Sample Output Function. `nmlefitoutputfcn` is the sample Statistics Toolbox output function for `nlmefit` and `nlmefitsa`. It initializes or updates a plot with the fixed-effects (`BETA`) and variance of the random effects (`diag(STATUS.Psi)`). For `nlmefit`, the plot also includes the log-likelihood (`STATUS.fval`).

`nlmefitoutputfcn` is the default output function for `nlmefitsa`. To use it with `nlmefit`, specify a function handle for it in the options structure:

```
opt = statset('OutputFcn', @nlmefitoutputfcn,  )
beta = nlmefit( , 'Options', opt,  )
```

To prevent `nlmefitsa` from using of this function, specify an empty value for the output function:

```
opt = statset('OutputFcn', [],  )
beta = nlmefitsa( , 'Options', opt,  )
```

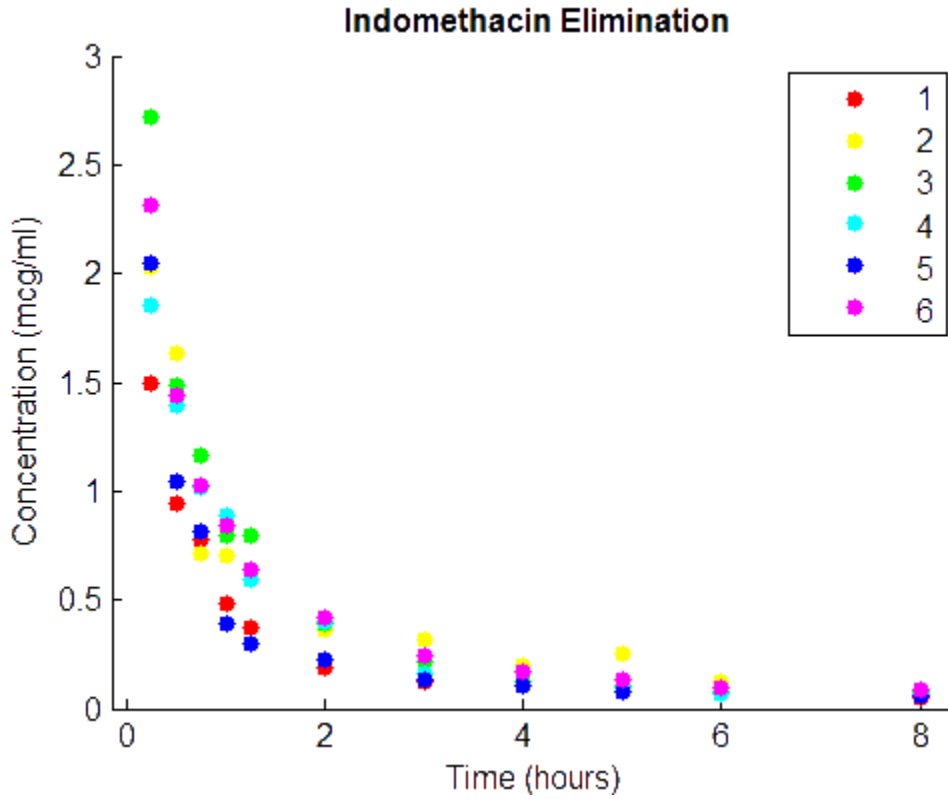
`nlmefitoutputfcn` stops `nlmefit` or `nlmefitsa` if you close the figure that it produces.

Example: Mixed-Effects Models Using nlmefit and nlmefitsa

The following example also works with `nlmefitsa` in place of `nlmefit`.

The data in `indomethacin.mat` records concentrations of the drug indomethacin in the bloodstream of six subjects over eight hours:

```
load indomethacin

gscatter(time,concentration,subject)
xlabel('Time (hours)')
ylabel('Concentration (mcg/ml)')
title('{\bf Indomethacin Elimination}')
hold on
```



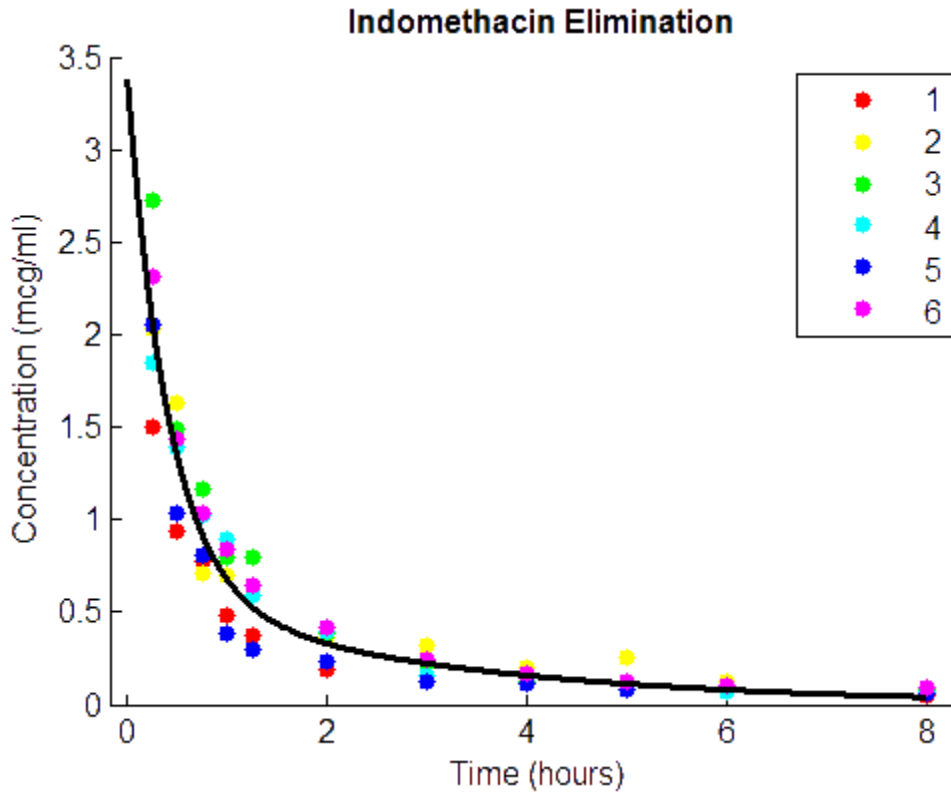
"Specifying Mixed-Effects Models" on page 9-81 discusses a useful model for this type of data. Construct the model via an anonymous function as follows:

```
model = @(phi,t)(phi(1)*exp(-exp(phi(2))*t) + ...
                 phi(3)*exp(-exp(phi(4))*t));
```

Use the `nlinfit` function to fit the model to all of the data, ignoring subject-specific effects:

```
phi0 = [1 2 1 1];
[phi,res] = nlinfit(time,concentration,model,phi0);

numObs = length(time);
numParams = 4;
df = numObs-numParams;
mse = (res'*res)/df
```

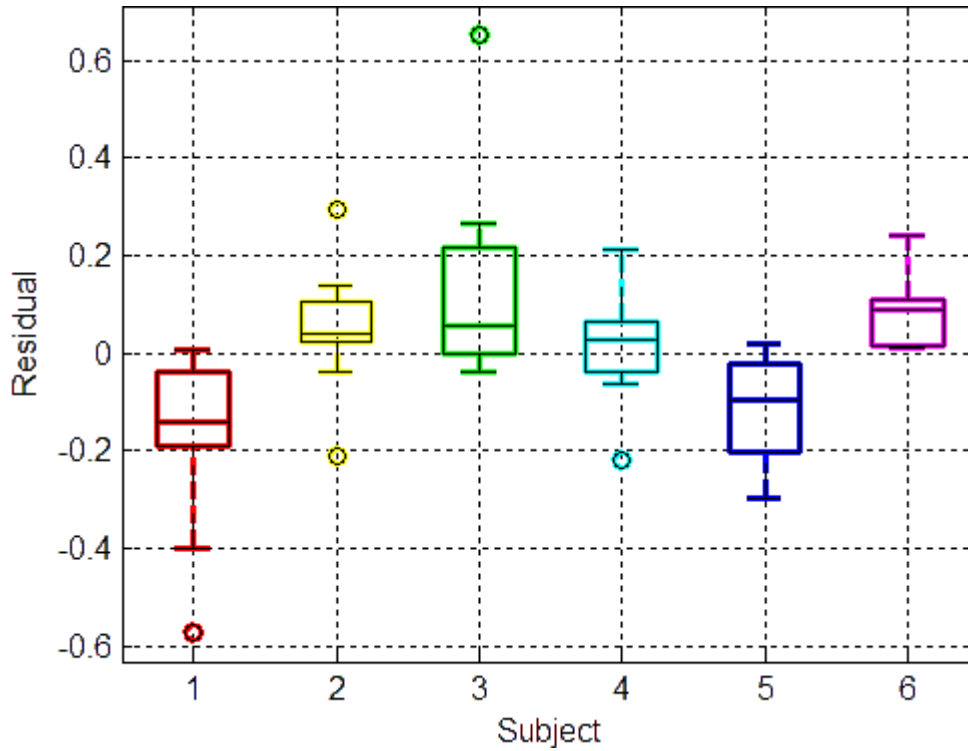
```
mse =
    0.0304

tplot = 0:0.01:8;
plot(tplot,model(phi,tplot),'k','LineWidth',2)
hold off
```



A box plot of residuals by subject shows that the boxes are mostly above or below zero, indicating that the model has failed to account for subject-specific effects:

```
colors = 'rygcbm';
h = boxplot(res,subject,'colors',colors,'symbol','o');
set(h(~isnan(h)),'LineWidth',2)
hold on
boxplot(res,subject,'colors','k','symbol','ko')
```

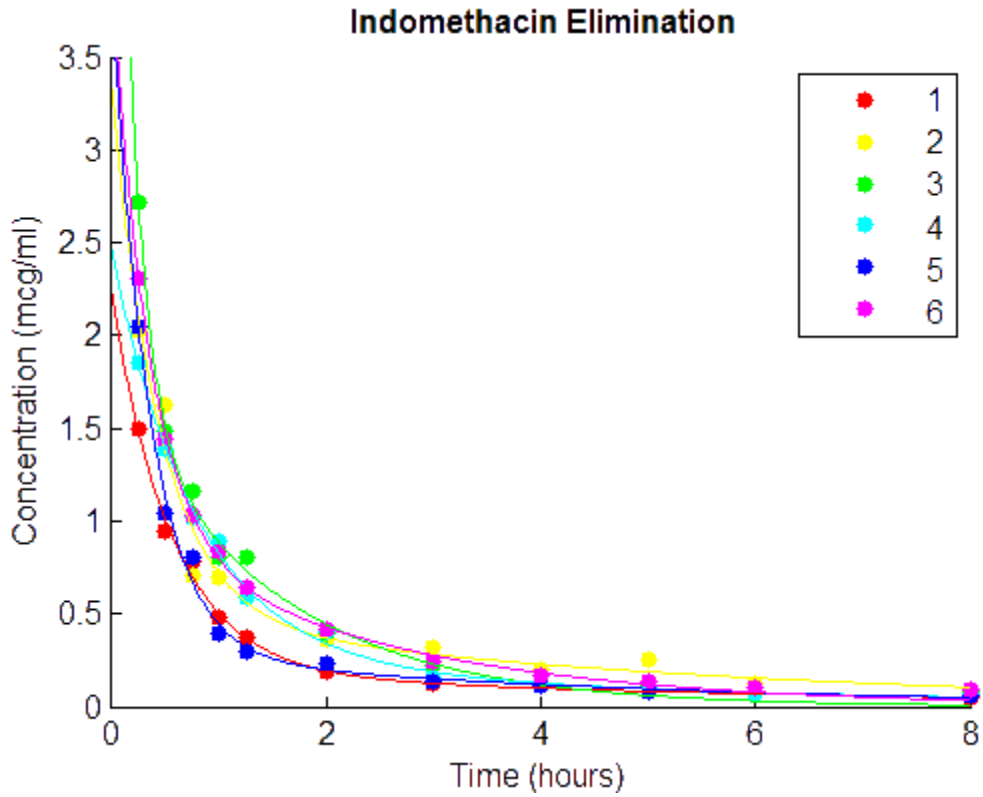
```
grid on
xlabel('Subject')
ylabel('Residual')
hold off
```



To account for subject-specific effects, fit the model separately to the data for each subject:

```
phi0 = [1 2 1 1];
PHI = zeros(4,6);
RES = zeros(11,6);
for I = 1:6
    tI = time(subject == I);
    cI = concentration(subject == I);
    [PHI(:,I),RES(:,I)] = nlinfit(tI,cI,model,phi0);
end
```

```
PHI
PHI =
    2.0293    2.8277    5.4683    2.1981    3.5661    3.0023
    0.5794    0.8013    1.7498    0.2423    1.0408    1.0882
    0.1915    0.4989    1.6757    0.2545    0.2915    0.9685
   -1.7878   -1.6354   -0.4122   -1.6026   -1.5069   -0.8731

numParams = 24;
df = numObs-numParams;
mse = (RES(:)'*RES(:))/df
mse =
    0.0057

gscatter(time,concentration,subject)
xlabel('Time (hours)')
ylabel('Concentration (mcg/ml)')
title('{\bf Indomethacin Elimination}')
hold on
for I = 1:6
    plot(tplot,model(PHI(:,I),tplot),'Color',colors(I))
end
axis([0 8 0 3.5])
hold off
```

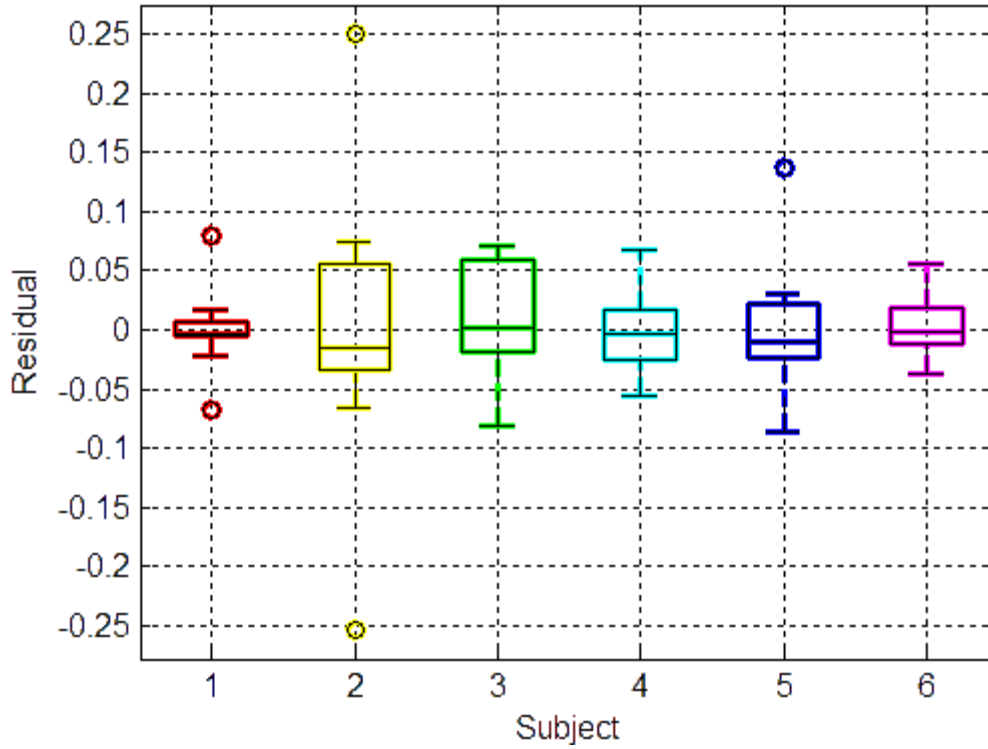


`PHI` gives estimates of the four model parameters for each of the six subjects. The estimates vary considerably, but taken as a 24-parameter model of the data, the mean-squared error of `0.0057` is a significant reduction from `0.0304` in the original four-parameter model.

A box plot of residuals by subject shows that the larger model accounts for most of the subject-specific effects:

```
h = boxplot(RES,'colors',colors,'symbol','o');
set(h(~isnan(h)),'LineWidth',2)
hold on
boxplot(RES,'colors','k','symbol','ko')
grid on
xlabel('Subject')
ylabel('Residual')
```

```
hold off
```



The spread of the residuals (the vertical scale of the box plot) is much smaller than in the previous box plot, and the boxes are now mostly centered on zero.

While the 24-parameter model successfully accounts for variations due to the specific subjects in the study, it does not consider the subjects as representatives of a larger population. The sampling distribution from which the subjects are drawn is likely more interesting than the sample itself. The purpose of mixed-effects models is to account for subject-specific variations more broadly, as random effects varying around population means.

Use the `nlmefit` function to fit a mixed-effects model to the data.

The following anonymous function, `nlme_model`, adapts the four-parameter `model` used by `nlinfit` to the calling syntax of `nlmefit` by allowing separate

parameters for each individual. By default, `nlmefit` assigns random effects to all the model parameters. Also by default, `nlmefit` assumes a diagonal covariance matrix (no covariance among the random effects) to avoid overparametrization and related convergence issues.

```
nlme_model = @(PHI,t)(PHI(:,1).*exp(-exp(PHI(:,2)).*t) + ...
                      PHI(:,3).*exp(-exp(PHI(:,4)).*t));

phi0 = [1 2 1 1];
[phi,PSI,stats] = nlmefit(time,concentration,subject, ...
                          [],nlme_model,phi0)
phi =
    2.8277
    0.7729
    0.4606
   -1.3459

PSI =
    0.3264         0         0         0
         0    0.0250         0         0
         0         0    0.0124         0
         0         0         0    0.0000

stats =
           dfe: 57
          logl: 54.5882
           mse: 0.0066
          rmse: 0.0787
    errorparam: 0.0815
           aic: -91.1765
           bic: -93.0506
          covb: [4x4 double]
        sebeta: [0.2558 0.1066 0.1092 0.2244]
          ires: [66x1 double]
          pres: [66x1 double]
         iwres: [66x1 double]
         pwres: [66x1 double]
         cwres: [66x1 double]
```

The mean-squared error of `0.0066` is comparable to the `0.0057` of the 24-parameter model without random effects, and significantly better than the `0.0304` of the four-parameter model without random effects.

The estimated covariance matrix `PSI` shows that the variance of the fourth random effect is essentially zero, suggesting that you can remove it to simplify the model. To do this, use the `REParamsSelect` parameter to specify the indices of the parameters to be modeled with random effects in `nlmefit`:

```
[phi,PSI,stats] = nlmefit(time,concentration,subject, ...
                          [],nlme_model,phi0, ...
                          'REParamsSelect',[1 2 3])
phi =
    2.8277
    0.7728
    0.4605
   -1.3460

PSI =
    0.3270         0         0
         0    0.0250         0
         0         0    0.0124

stats =
           dfe: 58
          logl: 54.5875
           mse: 0.0066
          rmse: 0.0780
    errorparam: 0.0815
           aic: -93.1750
           bic: -94.8410
          covb: [4x4 double]
        sebeta: [0.2560 0.1066 0.1092 0.2244]
          ires: [66x1 double]
          pres: [66x1 double]
         iwres: [66x1 double]
         pwres: [66x1 double]
         cwres: [66x1 double]
```

The log-likelihood `logl` is almost identical to what it was with random effects for all of the parameters, the Akaike information criterion `aic` is reduced from `-91.1765` to `-93.1750`, and the Bayesian information criterion `bic` is reduced from `-93.0506` to `-94.8410`. These measures support the decision to drop the fourth random effect.

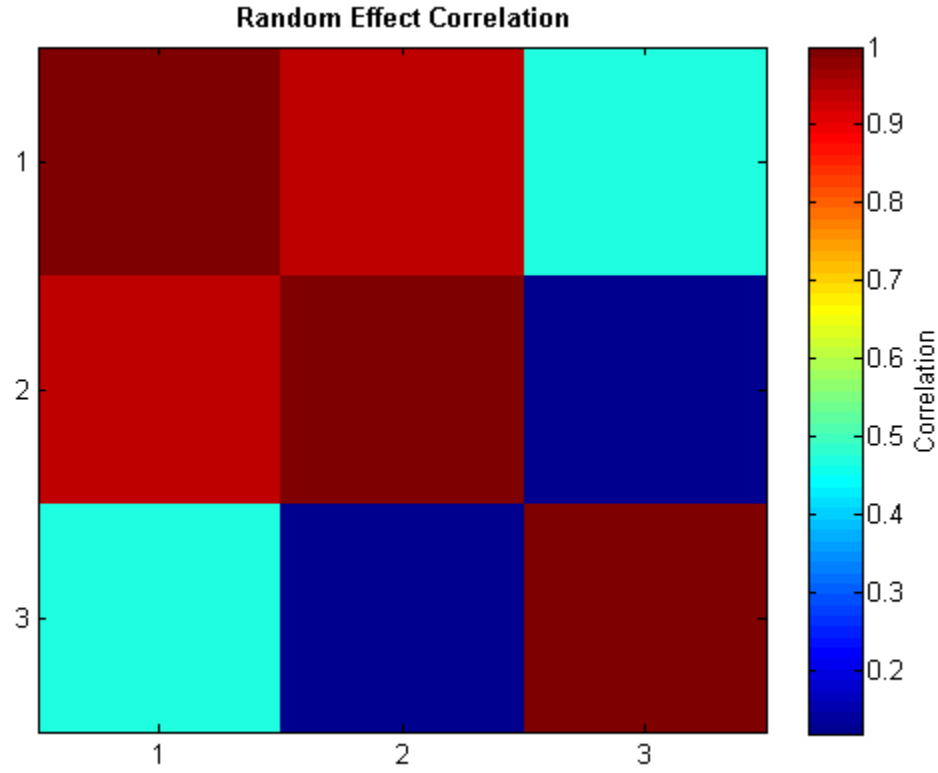
Refitting the simplified model with a full covariance matrix allows for identification of correlations among the random effects. To do this, use the `CovPattern` parameter to specify the pattern of nonzero elements in the covariance matrix:

```
[phi,PSI,stats] = nlmefit(time,concentration,subject, ...
                          [],nlme_model,phi0, ...
                          'REParamsSelect',[1 2 3], ...
                          'CovPattern',ones(3))
phi =
    2.8148
    0.8293
    0.5613
   -1.1407

PSI =
    0.4767    0.1152    0.0499
    0.1152    0.0321    0.0032
    0.0499    0.0032    0.0236

stats =
           dfe: 55
          logl: 58.4731
           mse: 0.0061
          rmse: 0.0782
    errorparam: 0.0781
           aic: -94.9462
           bic: -97.2369
          covb: [4x4 double]
        sebeta: [0.3028 0.1103 0.1179 0.1662]
          ires: [66x1 double]
          pres: [66x1 double]
         iwres: [66x1 double]
         pwres: [66x1 double]
```

```
            cwres: [66x1 double]
```

The estimated covariance matrix `PSI` shows that the random effects on the first two parameters have a relatively strong correlation, and both have a relatively weak correlation with the last random effect. This structure in the covariance matrix is more apparent if you convert `PSI` to a correlation matrix using `corrcov`:

```
RHO = corrcov(PSI)
RHO =
    1.0000    0.9316    0.4706
    0.9316    1.0000    0.1178
    0.4706    0.1178    1.0000

clf; imagesc(RHO)
set(gca,'XTick',[1 2 3],'YTick',[1 2 3])
title('{\bf Random Effect Correlation}')
h = colorbar;
set(get(h,'YLabel'),'String','Correlation');
```



Incorporate this structure into the model by changing the specification of the covariance pattern to block-diagonal:

```
P = [1 1 0;1 1 0;0 0 1] % Covariance pattern
P =
     1     1     0
     1     1     0
     0     0     1

[phi,PSI,stats,b] = nlmefit(time,concentration,subject, ...
                            [],nlme_model,phi0, ...
                            'REParamsSelect',[1 2 3], ...
                            'CovPattern',P)
```

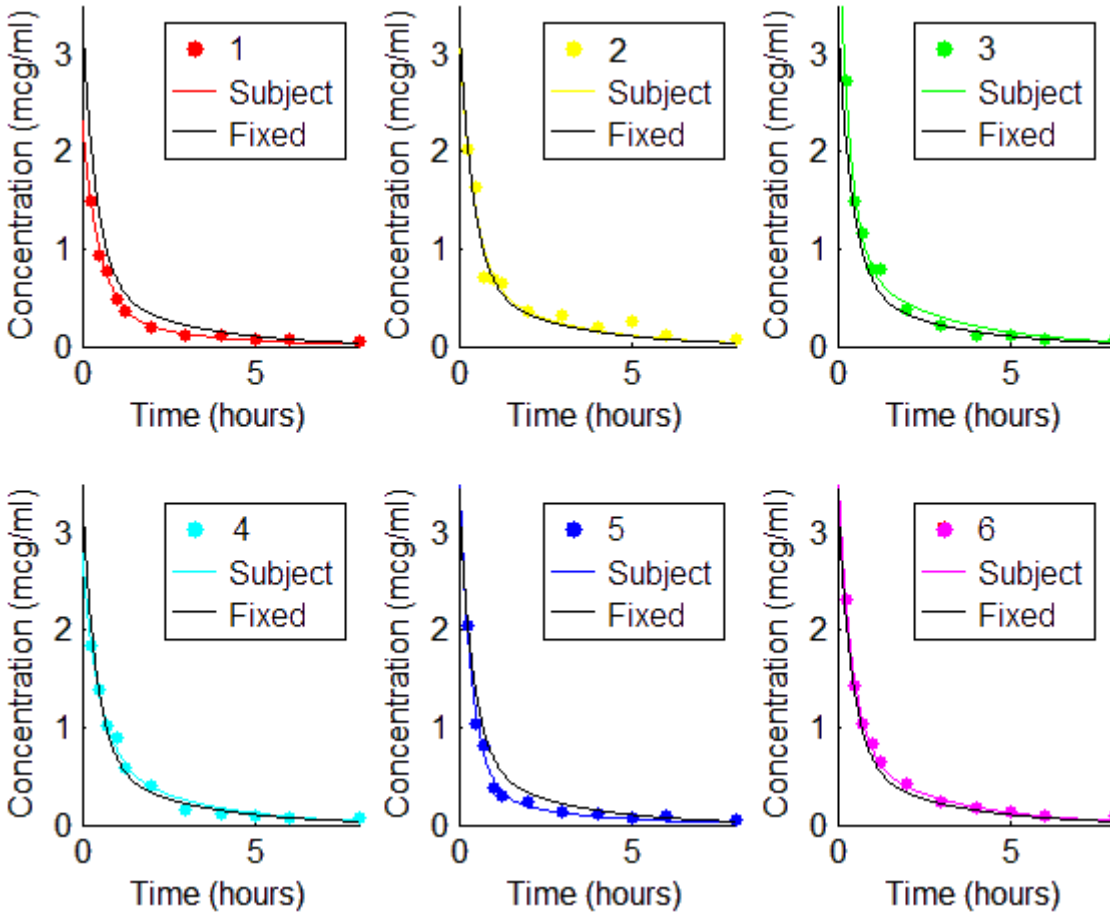
```
phi =
    2.7830
    0.8981
    0.6581
   -1.0000

PSI =
    0.5180    0.1069         0
    0.1069    0.0221         0
         0         0    0.0454

stats =
           dfe: 57
          logl: 58.0804
           mse: 0.0061
          rmse: 0.0768
    errorparam: 0.0782
           aic: -98.1608
           bic: -100.0350
          covb: [4x4 double]
        sebeta: [0.3171 0.1073 0.1384 0.1453]
          ires: [66x1 double]
          pres: [66x1 double]
         iwres: [66x1 double]
         pwres: [66x1 double]
         cwres: [66x1 double]

b =
   -0.8507   -0.1563    1.0427   -0.7559    0.5652    0.1550
   -0.1756   -0.0323    0.2152   -0.1560    0.1167    0.0320
   -0.2756    0.0519    0.2620    0.1064   -0.2835    0.1389
```

The block-diagonal covariance structure reduces `aic` from `-94.9462` to `-98.1608` and `bic` from `-97.2368` to `-100.0350` without significantly affecting the log-likelihood. These measures support the covariance structure used in the final model.

The output `b` gives predictions of the three random effects for each of the six subjects. These are combined with the estimates of the fixed effects in `phi` to produce the mixed-effects model.

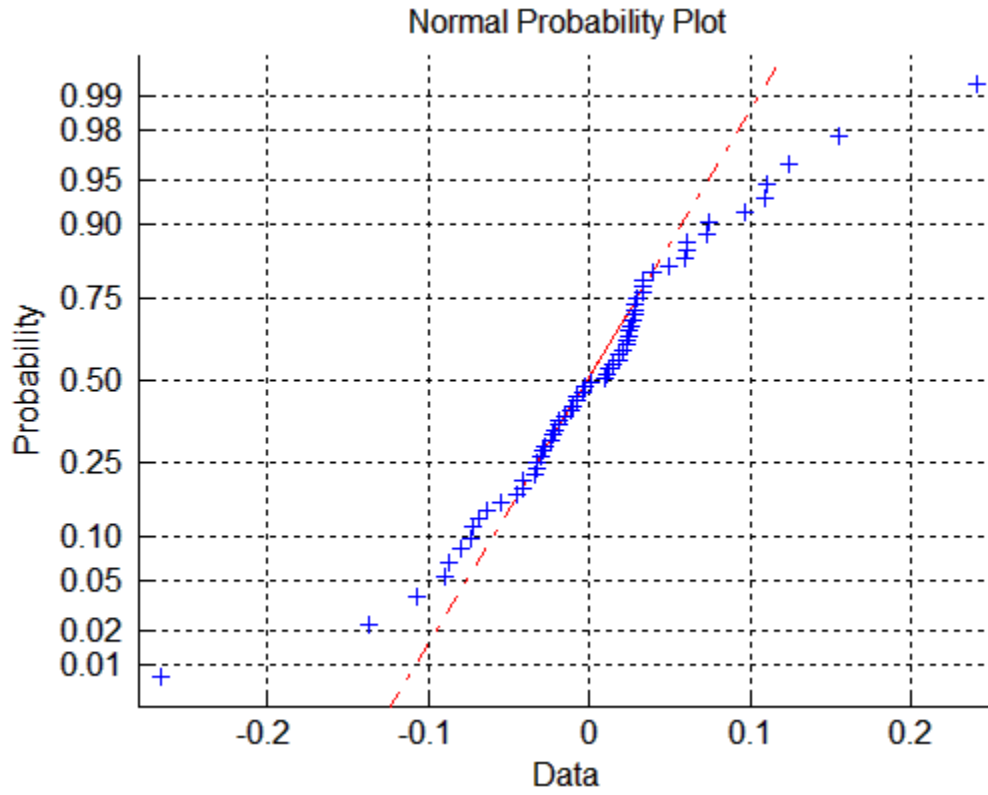
Use the following commands to plot the mixed-effects model for each of the six subjects. For comparison, the model without random effects is also shown.

```
PHI = repmat(phi,1,6) + ...                 % Fixed effects
      [b(1,:);b(2,:);b(3,:);zeros(1,6)];    % Random effects

RES = zeros(11,6); % Residuals
colors = 'rygcbm';
for I = 1:6
    fitted_model = @(t)(PHI(1,I)*exp(-exp(PHI(2,I))*t) + ...
                        PHI(3,I)*exp(-exp(PHI(4,I))*t));
    tI = time(subject == I);
    cI = concentration(subject == I);
    RES(:,I) = cI - fitted_model(tI);

    subplot(2,3,I)
    scatter(tI,cI,20,colors(I),'filled')
    hold on
    plot(tplot,fitted_model(tplot),'Color',colors(I))
    plot(tplot,model(phi,tplot),'k')
    axis([0 8 0 3.5])
    xlabel('Time (hours)')
    ylabel('Concentration (mcg/ml)')
    legend(num2str(I),'Subject','Fixed')
end
```



If obvious outliers in the data (visible in previous box plots) are ignored, a normal probability plot of the residuals shows reasonable agreement with model assumptions on the errors:

```
clf; normplot(RES(:))
```



Example: Examining Residuals for Model Verification

You can examine the `stats` structure, which is returned by both `nlmefit` and `nlmefitsa`, to determine the quality of your model. The `stats` structure contains fields with conditional weighted residuals (`cwres` field) and individual weighted residuals (`iwres` field). Since the model assumes that residuals are normally distributed, you can examine the residuals to see how well this assumption holds.

This example generates synthetic data using normal distributions. It shows how the fit statistics look:

- Good when testing against the same type of model as generates the data
- Poor when tested against incorrect data models

1 Initialize a 2-D model with 100 individuals:

```
nGroups = 100; % 100 Individuals
nlmefun = @(PHI,t)(PHI(:,1)*5 + PHI(:,2)^2.*t); % Regression fcn
REParamSelect = [1  2]; % Both Parameters have random effect
errorParam = .03;
beta0 = [ 1.5  5]; % Parameter means
psi = [ 0.35  0; ...  % Covariance Matrix
       0   0.51 ];
time =[0.25;0.5;0.75;1;1.25;2;3;4;5;6];
nParameters = 2;
rng(0,'twister') % for reproducibility
```

2 Generate the data for fitting with a proportional error model:

```
b_i = mvnrnd(zeros(1, numel(REParamSelect)), psi, nGroups);
individualParameters = zeros(nGroups,nParameters);
individualParameters(:, REParamSelect) = ...
     bsxfun(@plus,beta0(REParamSelect), b_i);

groups = repmat(1:nGroups,numel(time),1);
groups = vertcat(groups(:));

y = zeros(numel(time)*nGroups,1);
x = zeros(numel(time)*nGroups,1);
for i = 1:nGroups
    idx = groups == i;
    f = nlmefun(individualParameters(i,:), time);
    % Make a proportional error model for y:
    y(idx) = f + errorParam*f.*randn(numel(f),1);
    x(idx) = time;
end

P = [ 1 0 ; 0 1 ];
```

3 Fit the data using the same regression function and error model as the model generator:

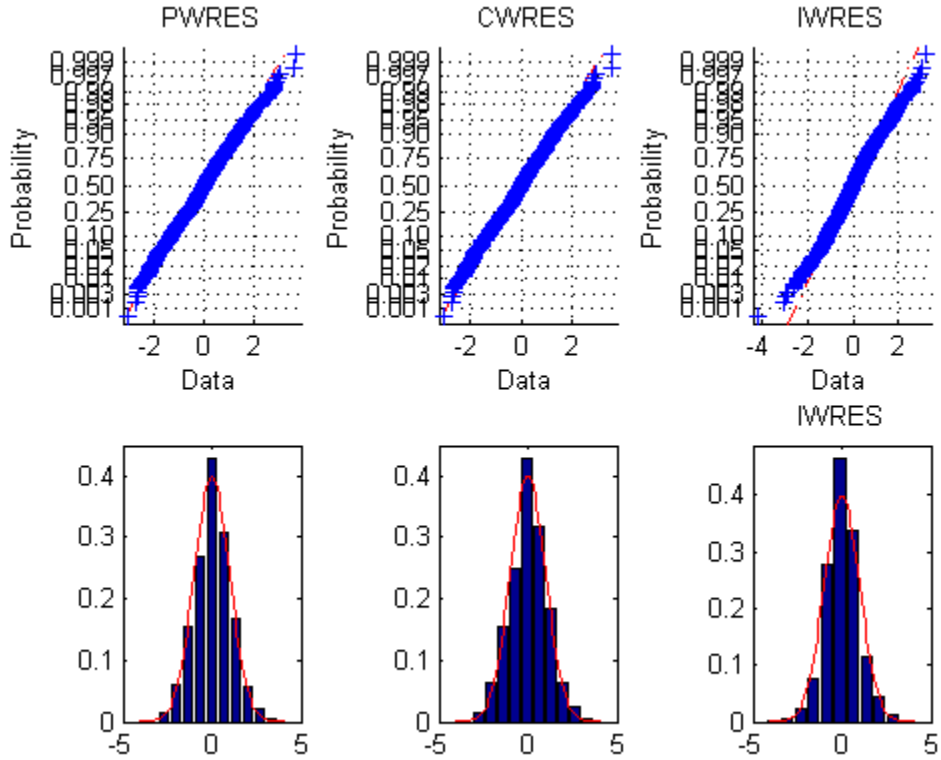
```
[~,~,stats] = nlmefit(x,y,groups, ...
    [],nlmefun,[1 1],'REParamsSelect',REParamSelect,...
    'ErrorModel','Proportional','CovPattern',P);
```

4 Create a plotting routine by copying the following function definition, and creating a file `plotResiduals.m` on your MATLAB path:

```
function plotResiduals(stats)
pwres = stats.pwres;
iwres = stats.iwres;
cwres = stats.cwres;
figure
subplot(2,3,1);
normplot(pwres); title('PWRES')
subplot(2,3,4);
createhistplot(pwres);

subplot(2,3,2);
normplot(cwres); title('CWRES')
subplot(2,3,5);
createhistplot(cwres);

subplot(2,3,3);
normplot(iwres); title('IWRES')
subplot(2,3,6);
createhistplot(iwres); title('IWRES')

function createhistplot(pwres)
[x, n] = hist(pwres);
d = n(2)- n(1);
x = x/sum(x*d);
bar(n,x);
ylim([0 max(x)*1.05]);
hold on;
x2 = -4:0.1:4;
f2 = normpdf(x2,0,1);
plot(x2,f2,'r');
end

end
```

5 Plot the residuals using the `plotResiduals` function:

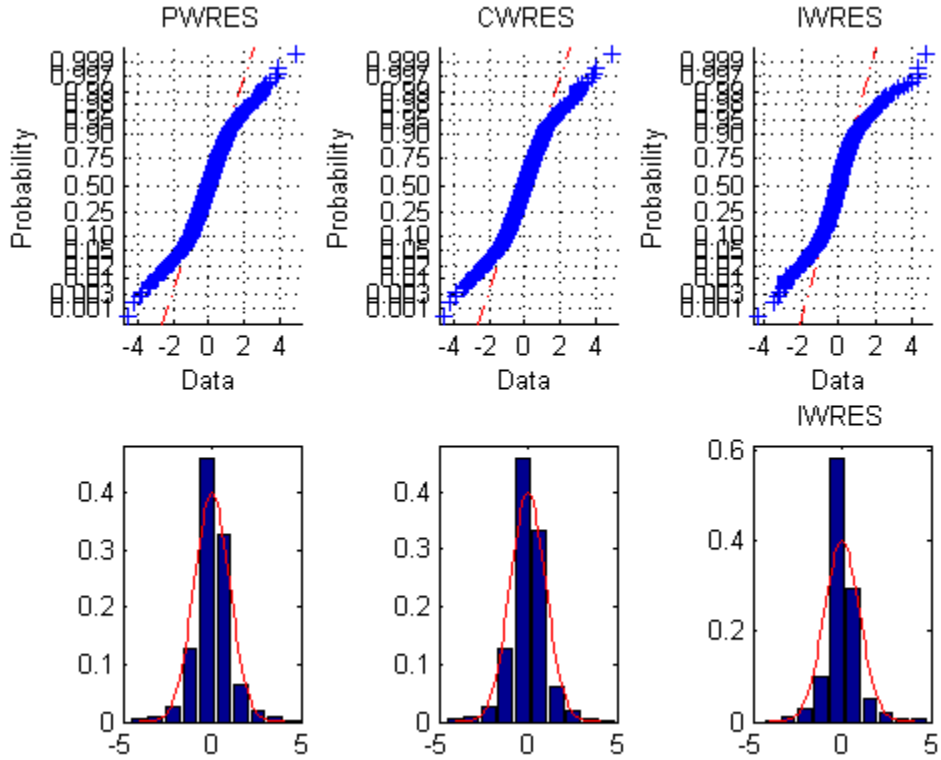
```
plotResiduals(stats);
```



The upper probability plots look straight, meaning the residuals are normally distributed. The bottom histogram plots match the superimposed normal density plot. So you can conclude that the error model matches the data.

6 For comparison, fit the data using a constant error model, instead of the proportional model that created the data:

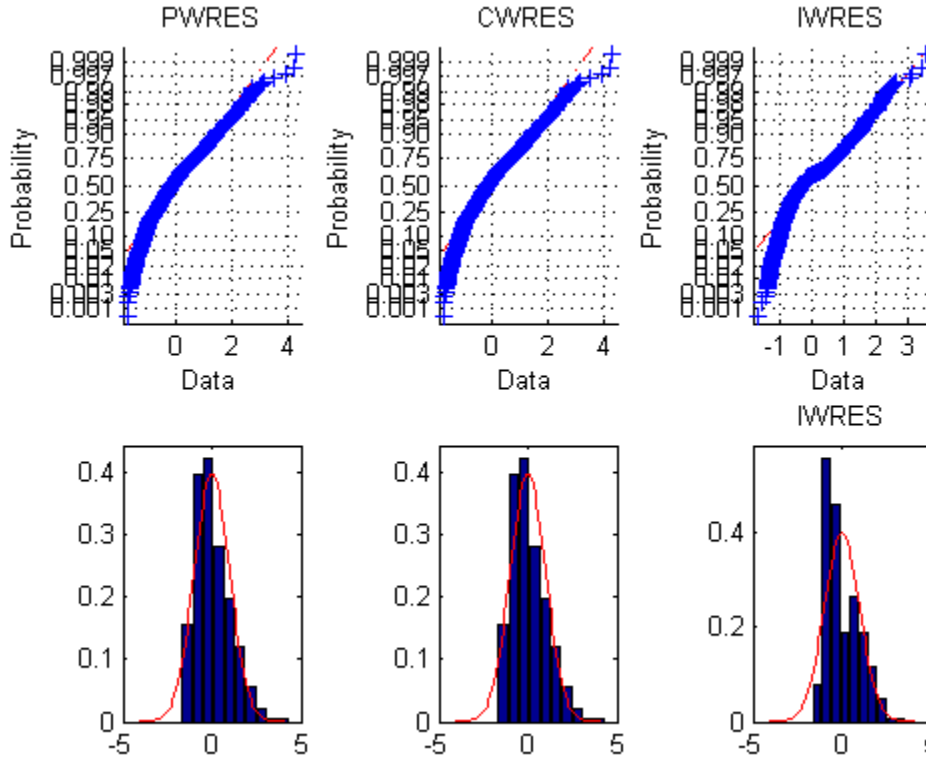
```
[~,~,stats] = nlmefit(x,y,groups, ...
    [],nlmefun,[0 0],'REParamsSelect',REParamSelect,...
    'ErrorModel','Constant','CovPattern',P);
plotResiduals(stats);
```



The upper probability plots are not straight, indicating the residuals are not normally distributed. The bottom histogram plots are fairly close to the superimposed normal density plots.

7 For another comparison, fit the data to a different structural model than created the data:

```
nlmefun2 = @(PHI,t)(PHI(:,1)*5 + PHI(:,2).*t.^4);
[~,~,stats] = nlmefit(x,y,groups, ...
    [],nlmefun2,[0 0],'REParamsSelect',REParamSelect,...
    'ErrorModel','constant', 'CovPattern',P);
plotResiduals(stats);
```



Not only are the upper probability plots not straight, but the histogram plot is quite skewed compared to the superimposed normal density. These residuals are not normally distributed, and do not match the model.

10

Multivariate Methods

Introduction to Multivariate Methods

Large, high-dimensional data sets are common in the modern era of computer-based instrumentation and electronic data storage. High-dimensional data present many challenges for statistical visualization, analysis, and modeling.

Data visualization, of course, is impossible beyond a few dimensions. As a result, pattern recognition, data preprocessing, and model selection must rely heavily on numerical methods.

A fundamental challenge in high-dimensional data analysis is the so-called *curse of dimensionality*. Observations in a high-dimensional space are necessarily sparser and less representative than those in a low-dimensional space. In higher dimensions, data over-represent the edges of a sampling distribution, because regions of higher-dimensional space contain the majority of their volume near the surface. (A d-dimensional spherical shell has a volume, relative to the total volume of the sphere, that approaches 1 as d approaches infinity.) In high dimensions, typical data points at the interior of a distribution are sampled less frequently.

Often, many of the dimensions in a data set—the measured features—are not useful in producing a model. Features may be irrelevant or redundant. Regression and classification algorithms may require large amounts of storage and computation time to process raw data, and even if the algorithms are successful the resulting models may contain an incomprehensible number of terms.

Because of these challenges, multivariate statistical methods often begin with some type of *dimension reduction*, in which data are approximated by points in a lower-dimensional space. Dimension reduction is the goal of the methods presented in this chapter. Dimension reduction often leads to simpler models and fewer measured variables, with consequent benefits when measurements are expensive and visualization is important.

Multidimensional Scaling

In this section...

Introduction to Multidimensional Scaling

One of the most important goals in visualizing data is to get a sense of how near or far points are from each other. Often, you can do this with a scatter plot. However, for some analyses, the data that you have might not be in the form of points at all, but rather in the form of pairwise similarities or dissimilarities between cases, observations, or subjects. There are no points to plot.

Even if your data are in the form of points rather than pairwise distances, a scatter plot of those data might not be useful. For some kinds of data, the relevant way to measure how near two points are might not be their Euclidean distance. While scatter plots of the raw data make it easy to compare Euclidean distances, they are not always useful when comparing other kinds of inter-point distances, city block distance for example, or even more general dissimilarities. Also, with a large number of variables, it is very difficult to visualize distances unless the data can be represented in a small number of dimensions. Some sort of dimension reduction is usually necessary.

Multidimensional scaling (MDS) is a set of methods that address all these problems. MDS allows you to visualize how near points are to each other for many kinds of distance or dissimilarity metrics and can produce a representation of your data in a small number of dimensions. MDS does not require raw data, but only a matrix of pairwise distances or dissimilarities.

Classical Multidimensional Scaling

Introduction to Classical Multidimensional Scaling

The function `cmdscale` performs classical (metric) multidimensional scaling, also known as *principal coordinates analysis*. `cmdscale` takes as an input a matrix of inter-point distances and creates a configuration of points. Ideally, those points are in two or three dimensions, and the Euclidean distances between them reproduce the original distance matrix. Thus, a scatter plot of the points created by `cmdscale` provides a visual representation of the original distances.

As a very simple example, you can reconstruct a set of points from only their inter-point distances. First, create some four dimensional points with a small component in their fourth coordinate, and reduce them to distances.

```
X = [ normrnd(0,1,10,3), normrnd(0,.1,10,1) ];
D = pdist(X,'euclidean');
```

Next, use `cmdscale` to find a configuration with those inter-point distances. `cmdscale` accepts distances as either a square matrix, or, as in this example, in the vector upper-triangular form produced by `pdist`.

```
[Y,eigvals] = cmdscale(D);
```

`cmdscale` produces two outputs. The first output, `Y`, is a matrix containing the reconstructed points. The second output, `eigvals`, is a vector containing the sorted eigenvalues of what is often referred to as the "scalar product matrix," which, in the simplest case, is equal to `Y*Y'`. The relative magnitudes of those eigenvalues indicate the relative contribution of the corresponding columns of `Y` in reproducing the original distance matrix `D` with the reconstructed points.

```
format short g
[eigvals eigvals/max(abs(eigvals))]
ans =
       12.623            1
       4.3699      0.34618
       1.9307      0.15295
     0.025884    0.0020505
  1.7192e-015  1.3619e-016
  6.8727e-016  5.4445e-017
```

```
  4.4367e-017  3.5147e-018
 -9.2731e-016 -7.3461e-017
  -1.327e-015 -1.0513e-016
 -1.9232e-015 -1.5236e-016
```

If `eigvals` contains only positive and zero (within round-off error) eigenvalues, the columns of `Y` corresponding to the positive eigenvalues provide an exact reconstruction of `D`, in the sense that their inter-point Euclidean distances, computed using `pdist`, for example, are identical (within round-off) to the values in `D`.

```
maxerr4 = max(abs(D - pdist(Y))) % exact reconstruction
maxerr4 =
  2.6645e-015
```

If two or three of the eigenvalues in `eigvals` are much larger than the rest, then the distance matrix based on the corresponding columns of `Y` nearly reproduces the original distance matrix `D`. In this sense, those columns form a lower-dimensional representation that adequately describes the data. However it is not always possible to find a good low-dimensional reconstruction.

```
% good reconstruction in 3D
maxerr3 = max(abs(D - pdist(Y(:,1:3))))
maxerr3 =
     0.029728

% poor reconstruction in 2D
maxerr2 = max(abs(D - pdist(Y(:,1:2))))
maxerr2 =
      0.91641
```

The reconstruction in three dimensions reproduces `D` very well, but the reconstruction in two dimensions has errors that are of the same order of magnitude as the largest values in `D`.

```
max(max(D))
ans =
       3.4686
```

Often, `eigvals` contains some negative eigenvalues, indicating that the distances in `D` cannot be reproduced exactly. That is, there might not be any configuration of points whose inter-point Euclidean distances are given by `D`. If the largest negative eigenvalue is small in magnitude relative to the largest positive eigenvalues, then the configuration returned by `cmdscale` might still reproduce `D` well.

Example: Multidimensional Scaling

Given only the distances between 10 US cities, `cmdscale` can construct a map of those cities. First, create the distance matrix and pass it to `cmdscale`. In this example,`D` is a full distance matrix: it is square and symmetric, has positive entries off the diagonal, and has zeros on the diagonal.

```
cities = ...
{'Atl','Chi','Den','Hou','LA','Mia','NYC','SF','Sea','WDC'};
D = [    0  587 1212  701 1936  604  748 2139 2182   543;
       587    0  920  940 1745 1188  713 1858 1737   597;
      1212  920    0  879  831 1726 1631  949 1021  1494;
       701  940  879    0 1374  968 1420 1645 1891  1220;
      1936 1745  831 1374    0 2339 2451  347  959  2300;
       604 1188 1726  968 2339    0 1092 2594 2734   923;
       748  713 1631 1420 2451 1092    0 2571 2408   205;
      2139 1858  949 1645  347 2594 2571    0  678  2442;
      2182 1737 1021 1891  959 2734 2408  678    0  2329;
       543  597 1494 1220 2300  923  205 2442 2329     0];
[Y,eigvals] = cmdscale(D);
```

Next, look at the eigenvalues returned by `cmdscale`. Some of these are negative, indicating that the original distances are not Euclidean. This is because of the curvature of the earth.

```
format short g
[eigvals eigvals/max(abs(eigvals))]
ans =
  9.5821e+006            1
  1.6868e+006      0.17604
       8157.3    0.0008513
       1432.9   0.00014954
       508.67  5.3085e-005
       25.143   2.624e-006
```

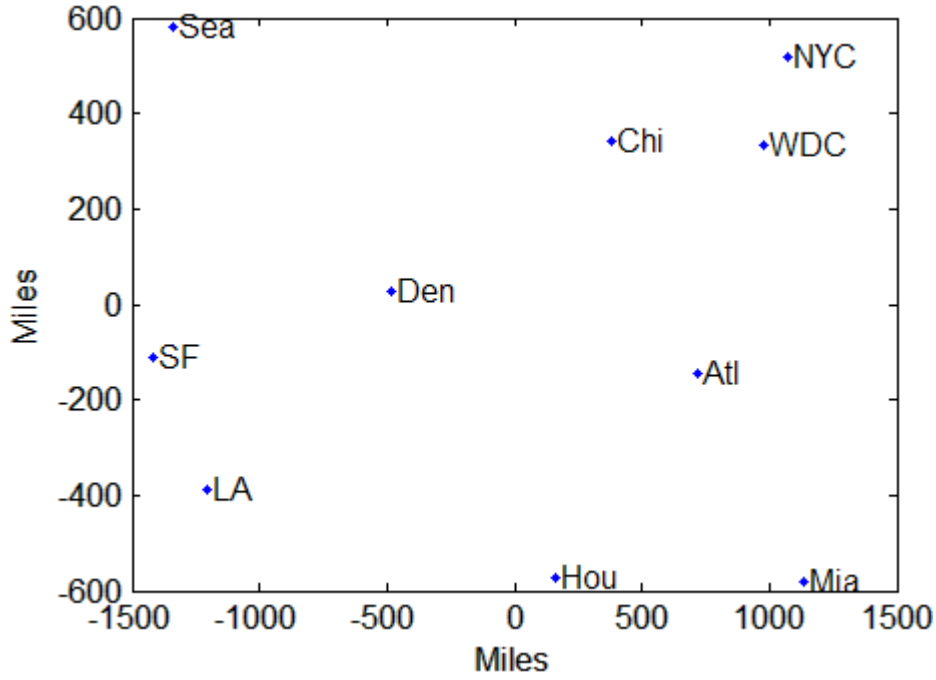
```
  5.3394e-010  5.5722e-017
       -897.7 -9.3685e-005
      -5467.6   -0.0005706
       -35479   -0.0037026
```

However, in this case, the two largest positive eigenvalues are much larger in magnitude than the remaining eigenvalues. So, despite the negative eigenvalues, the first two coordinates of `Y` are sufficient for a reasonable reproduction of `D`.

```
Dtriu = D(find(tril(ones(10),-1)))';
maxrelerr = max(abs(Dtriu-pdist(Y(:,1:2))))./max(Dtriu)
maxrelerr =
    0.0075371
```

Here is a plot of the reconstructed city locations as a map. The orientation of the reconstruction is arbitrary. In this case, it happens to be close to, although not exactly, the correct orientation.

```
plot(Y(:,1),Y(:,2),'.')
text(Y(:,1)+25,Y(:,2),cities)
xlabel('Miles')
ylabel('Miles')
```



Nonclassical Multidimensional Scaling

The function `mdscale` performs nonclassical multidimensional scaling. As with `cmdcale`, you use `mdscale` either to visualize dissimilarity data for which no "locations" exist, or to visualize high-dimensional data by reducing its dimensionality. Both functions take a matrix of dissimilarities as an input and produce a configuration of points. However, `mdscale` offers a choice of different criteria to construct the configuration, and allows missing data and weights.

For example, the cereal data include measurements on 10 variables describing breakfast cereals. You can use `mdscale` to visualize these data in two dimensions. First, load the data. For clarity, this example code selects a subset of 22 of the observations.

```
load cereal.mat
X = [Calories Protein Fat Sodium Fiber ...
    Carbo Sugars Shelf Potass Vitamins];
```

```
% Take a subset from a single manufacturer
mfg1 = strcmp('G',cellstr(Mfg));
X = X(mfg1,:);
size(X)
ans =
    22 10
```

Then use `pdist` to transform the 10-dimensional data into dissimilarities. The output from `pdist` is a symmetric dissimilarity matrix, stored as a vector containing only the (23*22/2) elements in its upper triangle.

```
dissimilarities = pdist(zscore(X),'cityblock');
size(dissimilarities)
ans =
     1   231
```

This example code first standardizes the cereal data, and then uses city block distance as a dissimilarity. The choice of transformation to dissimilarities is application-dependent, and the choice here is only for simplicity. In some applications, the original data are already in the form of dissimilarities.

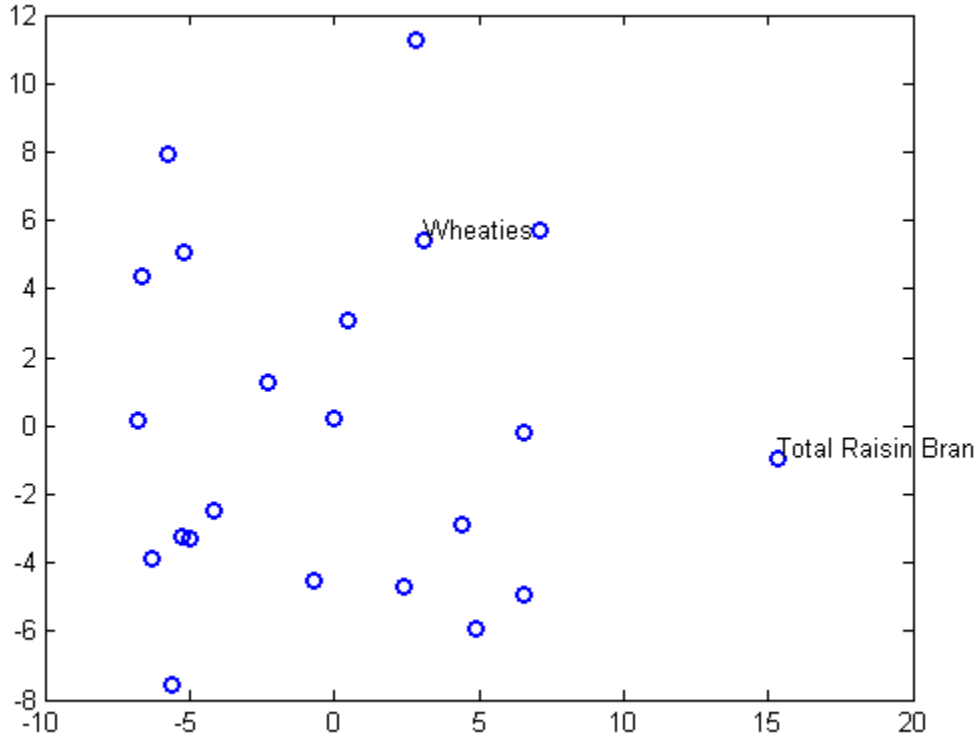
Next, use `mdscale` to perform metric MDS. Unlike `cmdscale`, you must specify the desired number of dimensions, and the method to use to construct the output configuration. For this example, use two dimensions. The metric STRESS criterion is a common method for computing the output; for other choices, see the `mdscale` reference page in the online documentation. The second output from `mdscale` is the value of that criterion evaluated for the output configuration. It measures the how well the inter-point distances of the output configuration approximate the original input dissimilarities:

```
[Y,stress] =...
mdscale(dissimilarities,2,'criterion','metricstress');
stress
stress =
    0.1856
```

A scatterplot of the output from `mdscale` represents the original 10-dimensional data in two dimensions, and you can use the `gname` function to label selected points:

```
plot(Y(:,1),Y(:,2),'o','LineWidth',2);
```

```
gname(Name(mfg1))
```



Nonmetric Multidimensional Scaling

Metric multidimensional scaling creates a configuration of points whose inter-point distances approximate the given dissimilarities. This is sometimes too strict a requirement, and non-metric scaling is designed to relax it a bit. Instead of trying to approximate the dissimilarities themselves, non-metric scaling approximates a nonlinear, but monotonic, transformation of them. Because of the monotonicity, larger or smaller distances on a plot of the output will correspond to larger or smaller dissimilarities, respectively. However, the nonlinearity implies that `mdscale` only attempts to preserve the

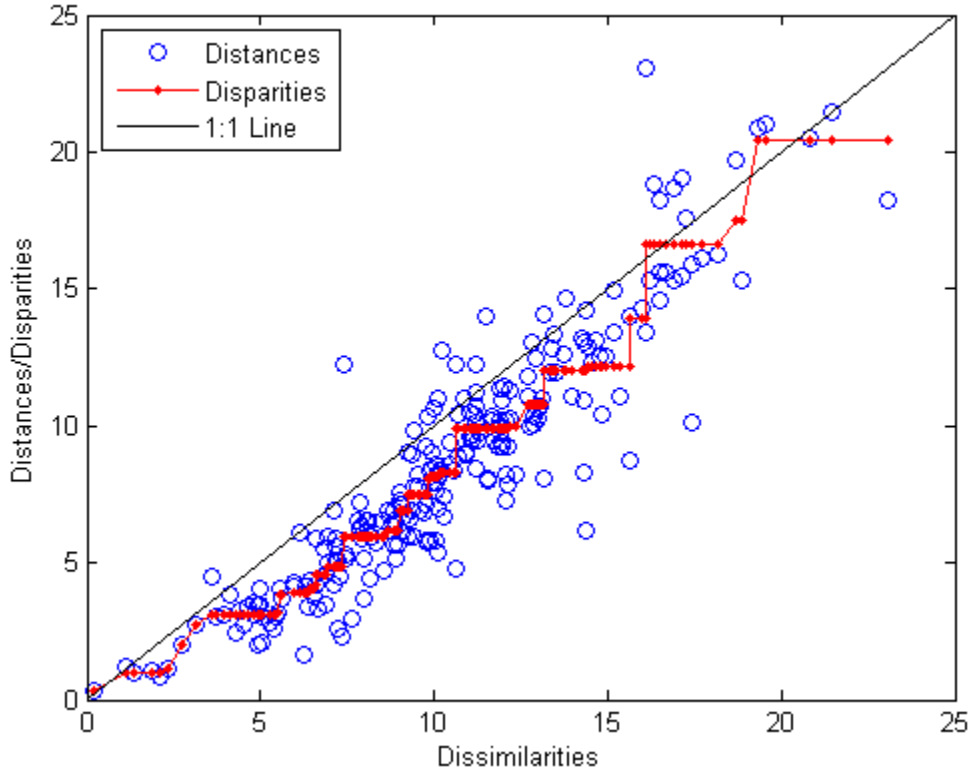
ordering of dissimilarities. Thus, there may be contractions or expansions of distances at different scales.

You use `mdscale` to perform nonmetric MDS in much the same way as for metric scaling. The nonmetric STRESS criterion is a common method for computing the output; for more choices, see the `mdscale` reference page in the online documentation. As with metric scaling, the second output from `mdscale` is the value of that criterion evaluated for the output configuration. For nonmetric scaling, however, it measures the how well the inter-point distances of the output configuration approximate the disparities. The disparities are returned in the third output. They are the transformed values of the original dissimilarities:

```
[Y,stress,disparities] = ...
mdscale(dissimilarities,2,'criterion','stress');
stress
stress =
    0.1562
```

To check the fit of the output configuration to the dissimilarities, and to understand the disparities, it helps to make a Shepard plot:

```
distances = pdist(Y);
[dum,ord] = sortrows([disparities(:) dissimilarities(:)]);
plot(dissimilarities,distances,'bo', ...
     dissimilarities(ord),disparities(ord),'r.-', ...
     [0 25],[0 25],'k-')
xlabel('Dissimilarities')
ylabel('Distances/Disparities')
legend({'Distances' 'Disparities' '1:1 Line'},...
       'Location','NorthWest');
```



This plot shows that `mdscale` has found a configuration of points in two dimensions whose inter-point distances approximates the disparities, which in turn are a nonlinear transformation of the original dissimilarities. The concave shape of the disparities as a function of the dissimilarities indicates that fit tends to contract small distances relative to the corresponding dissimilarities. This may be perfectly acceptable in practice.

`mdscale` uses an iterative algorithm to find the output configuration, and the results can often depend on the starting point. By default, `mdscale` uses `cmdscale` to construct an initial configuration, and this choice often leads to a globally best solution. However, it is possible for `mdscale` to stop at a configuration that is a local minimum of the criterion. Such

cases can be diagnosed and often overcome by running `mdscale` multiple times with different starting points. You can do this using the `'start'` and `'replicates'` parameters. The following code runs five replicates of MDS, each starting at a different randomly-chosen initial configuration. The criterion value is printed out for each replication; `mdscale` returns the configuration with the best fit.

```
opts = statset('Display','final');
[Y,stress] =...
mdscale(dissimilarities,2,'criterion','stress',...
'start','random','replicates',5,'Options',opts);

35 iterations, Final stress criterion = 0.156209
31 iterations, Final stress criterion = 0.156209
48 iterations, Final stress criterion = 0.171209
33 iterations, Final stress criterion = 0.175341
32 iterations, Final stress criterion = 0.185881
```

Notice that `mdscale` finds several different local solutions, some of which do not have as low a stress value as the solution found with the `cmdscale` starting point.

Procrustes Analysis

In this section...

Comparing Landmark Data

The `procrustes` function analyzes the distribution of a set of shapes using Procrustes analysis. This analysis method matches landmark data (geometric locations representing significant features in a given shape) to calculate the best shape-preserving Euclidian transformations. These transformations minimize the differences in location between compared landmark data.

Procrustes analysis is also useful in conjunction with multidimensional scaling. In "Example: Multidimensional Scaling" on page 10-6 there is an observation that the orientation of the reconstructed points is arbitrary. Two different applications of multidimensional scaling could produce reconstructed points that are very similar in principle, but that look different because they have different orientations. The `procrustes` function transforms one set of points to make them more comparable to the other.

Data Input

The `procrustes` function takes two matrices as input:

- The target shape matrix X has dimension $n \times p$, where n is the number of landmarks in the shape and p is the number of measurements per landmark.
- The comparison shape matrix Y has dimension $n \times q$ with $q \leq p$. If there are fewer measurements per landmark for the comparison shape than the target shape ($q < p$), the function adds columns of zeros to Y, yielding an $n \times p$ matrix.

The equation to obtain the transformed shape, Z, is

$$Z = bYT + c \qquad \textbf{(10-1)}$$

where:

- b is a scaling factor that stretches ($b > 1$) or shrinks ($b < 1$) the points.
- T is the orthogonal rotation and reflection matrix.
- c is a matrix with constant values in each column, used to shift the points.

The `procrustes` function chooses b, T, and c to minimize the distance between the target shape X and the transformed shape Z as measured by the least squares criterion:

$$\sum_{i=1}^{n}\sum_{j=1}^{p}(X_{ij} - Z_{ij})^2$$

Preprocessing Data for Accurate Results

Procrustes analysis is appropriate when all `p` measurement dimensions have similar scales. The analysis would be inaccurate, for example, if the columns of Z had different scales:

- The first column is measured in milliliters ranging from 2,000 to 6,000.
- The second column is measured in degrees Celsius ranging from 10 to 25.
- The third column is measured in kilograms ranging from 50 to 230.

In such cases, standardize your variables by:

1. Subtracting the sample mean from each variable.
2. Dividing each resultant variable by its sample standard deviation.

Use the `zscore` function to perform this standardization.

Example: Comparing Handwritten Shapes

In this example, use Procrustes analysis to compare two handwritten number threes. Visually and analytically explore the effects of forcing size and reflection changes as follows:

Step 1: Load and Display the Original Data

Input landmark data for two handwritten number threes:

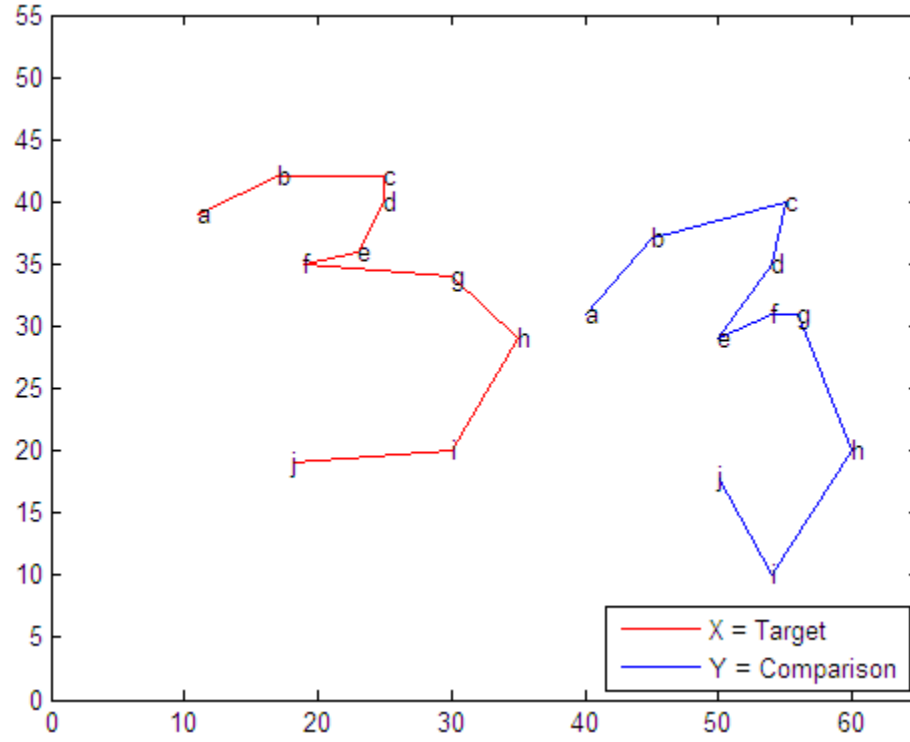
```
A = [11 39;17 42;25 42;25 40;23 36;19 35;30 34;35 29;...
30 20;18 19];
B = [15 31;20 37;30 40;29 35;25 29;29 31;31 31;35 20;...
29 10;25 18];
```

Create `X` and `Y` from `A` and `B`, moving `B` to the side to make each shape more visible:

```
X = A;
Y = B + repmat([25 0], 10,1);
```

Plot the shapes, using letters to designate the landmark points. Lines in the figure join the points to indicate the drawing path of each shape.

```
plot(X(:,1), X(:,2),'r-', Y(:,1), Y(:,2),'b-');
text(X(:,1), X(:,2),('abcdefghij')')
text(Y(:,1), Y(:,2),('abcdefghij')')
legend('X = Target','Y = Comparison','location','SE')
set(gca,'YLim',[0 55],'XLim',[0 65]);
```



Step 2: Calculate the Best Transformation

Use Procrustes analysis to find the transformation that minimizes distances between landmark data points.

Call `procrustes` as follows:

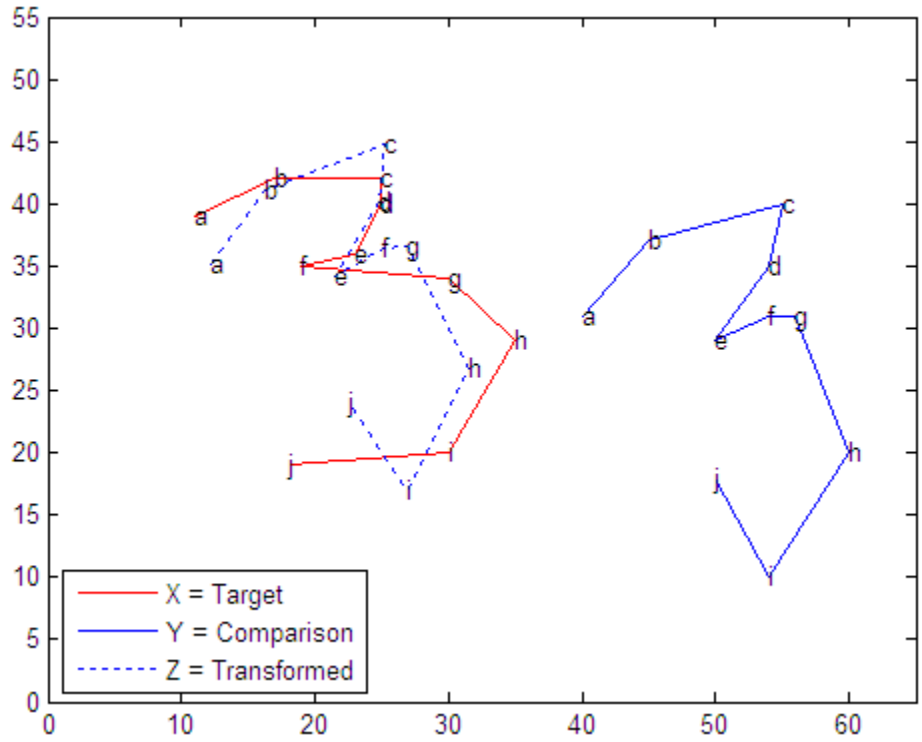
```
[d, Z, tr] = procrustes(X,Y);
```

The outputs of the function are:

- `d` – A standardized dissimilarity measure.)
- `Z` – A matrix of the transformed landmarks.
- `tr` – A structure array of the computed transformation with fields `T`, `b`, and `c` which correspond to the transformation equation, Equation 10-1.

Visualize the transformed shape, `Z`, using a dashed blue line:

```
plot(X(:,1), X(:,2),'r-', Y(:,1), Y(:,2),'b-',...
Z(:,1),Z(:,2),'b:');
text(X(:,1), X(:,2),('abcdefghij')')
text(Y(:,1), Y(:,2),('abcdefghij')')
text(Z(:,1), Z(:,2),('abcdefghij')')
legend('X = Target','Y = Comparison',...
'Z = Transformed','location','SW')
set(gca,'YLim',[0 55],'XLim',[0 65]);
```



Step 3: Examine the Similarity of the Two Shapes

Use two different numerical values to assess the similarity of the target shape and the transformed shape.

Dissimilarity Measure d. The dissimilarity measure `d` gives a number between 0 and 1 describing the difference between the target shape and the transformed shape. Values near 0 imply more similar shapes, while values near 1 imply dissimilarity. For this example:

```
d =
     0.1502
```

The small value of `d` in this case shows that the two shapes are similar.

`procrustes` calculates `d` by comparing the sum of squared deviations between the set of points with the sum of squared deviations of the original points from their column means:

```
numerator = sum(sum((X-Z).^2))
numerator =

  166.5321

denominator = sum(sum(bsxfun(@minus,X,mean(X)).^2))
denominator =

  1.1085e+003

ratio = numerator/denominator
ratio =

    0.1502
```

Note The resulting measure `d` is independent of the scale of the size of the shapes and takes into account only the similarity of landmark data. "Examining the Scaling Measure b" on page 10-19 shows how to examine the size similarity of the shapes.

Examining the Scaling Measure b. The target and comparison threes in the previous figure visually show that the two numbers are of a similar size. The closeness of calculated value of the scaling factor `b` to 1 supports this observation as well:

```
tr.b
ans =
    0.9291
```

The sizes of the target and comparison shapes appear similar. This visual impression is reinforced by the value of `b` = 0.93, which implies that the best transformation results in shrinking the comparison shape by a factor .93 (only 7%).

Step 4: Restrict the Form of the Transformations

Explore the effects of manually adjusting the scaling and reflection coefficients.

Fixing the Scaling Factor `b = 1`. Force `b` to equal 1 (set `'Scaling'` to `false`) to examine the amount of dissimilarity in size of the target and transformed figures:

```
ds = procrustes(X,Y,'Scaling',false)
ds =
    0.1552
```

In this case, setting `'Scaling'` to `false` increases the calculated value of `d` only 0.0049, which further supports the similarity in the size of the two number threes. A larger increase in `d` would have indicated a greater size discrepancy.

Forcing a Reflection in the Transformation. This example requires only a rotation, not a reflection, to align the shapes. You can show this by observing that the determinant of the matrix `T` is 1 in this analysis:

```
det(tr.T)
ans =
    1.0000
```

If you need a reflection in the transformation, the determinant of `T` is -1. You can force a reflection into the transformation as follows:

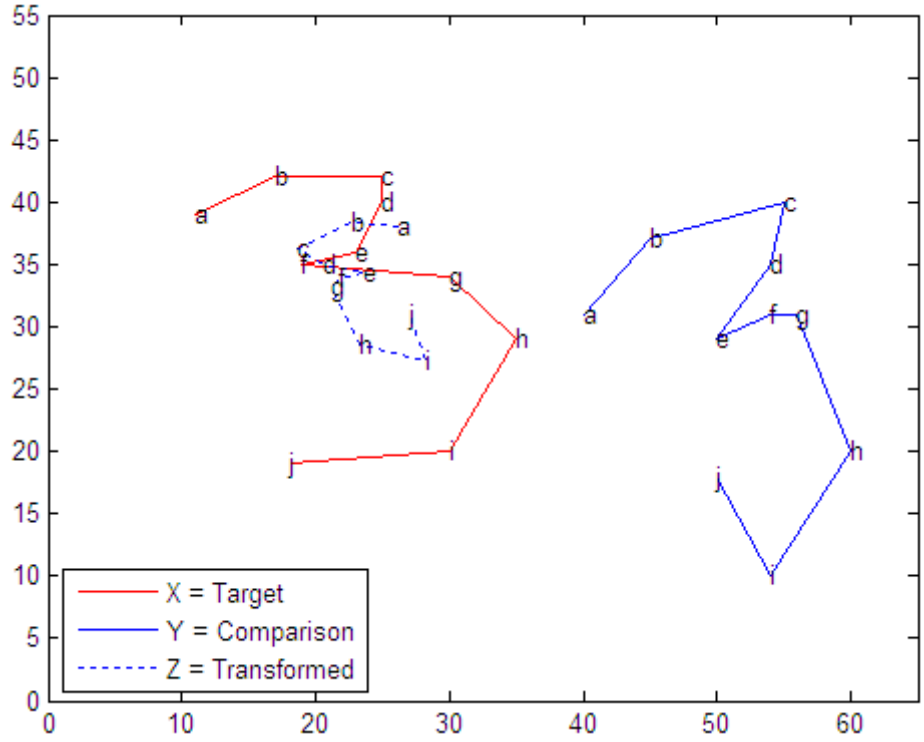
```
[dr,Zr,trr] = procrustes(X,Y,'Reflection',true);
dr
dr =
```

```
    0.8130
```

The `d` value increases dramatically, indicating that a forced reflection leads to a poor transformation of the landmark points. A plot of the transformed shape shows a similar result:

- The landmark data points are now further away from their target counterparts.
- The transformed three is now an undesirable mirror image of the target three.

```
plot(X(:,1), X(:,2),'r-', Y(:,1), Y(:,2),'b-',...
Zr(:,1),Zr(:,2),'b:');
text(X(:,1), X(:,2),('abcdefghij')')
text(Y(:,1), Y(:,2),('abcdefghij')')
text(Zr(:,1), Zr(:,2),('abcdefghij')')
legend('X = Target','Y = Comparison',...
'Z = Transformed','location','SW')
set(gca,'YLim',[0 55],'XLim',[0 65]);
```



It appears that the shapes might be better matched if you flipped the transformed shape upside down. Flipping the shapes would make the transformation even worse, however, because the landmark data points would be further away from their target counterparts. From this example, it is clear that manually adjusting the scaling and reflection parameters is generally not optimal.

Feature Selection

In this section...

Introduction to Feature Selection

Feature selection reduces the dimensionality of data by selecting only a subset of measured features (predictor variables) to create a model. Selection criteria usually involve the minimization of a specific measure of predictive error for models fit to different subsets. Algorithms search for a subset of predictors that optimally model measured responses, subject to constraints such as required or excluded features and the size of the subset.

Feature selection is preferable to feature transformation when the original units and meaning of features are important and the modeling goal is to identify an influential subset. When categorical features are present, and numerical transformations are inappropriate, feature selection becomes the primary means of dimension reduction.

Sequential Feature Selection

Introduction to Sequential Feature Selection

A common method of feature selection is *sequential feature selection*. This method has two components:

- An objective function, called the *criterion*, which the method seeks to minimize over all feasible feature subsets. Common criteria are mean squared error (for regression models) and misclassification rate (for classification models).
- A sequential search algorithm, which adds or removes features from a candidate subset while evaluating the criterion. Since an exhaustive

comparison of the criterion value at all 2^n subsets of an n-feature data set is typically infeasible (depending on the size of n and the cost of objective calls), sequential searches move in only one direction, always growing or always shrinking the candidate set.

The method has two variants:

- *Sequential forward selection* (*SFS*), in which features are sequentially added to an empty candidate set until the addition of further features does not decrease the criterion.
- *Sequential backward selection* (*SBS*), in which features are sequentially removed from a full candidate set until the removal of further features increase the criterion.

Stepwise regression is a sequential feature selection technique designed specifically for least-squares fitting. The functions `stepwise` and `stepwisefit` make use of optimizations that are only possible with least-squares criteria. Unlike generalized sequential feature selection, stepwise regression may remove features that have been added or add features that have been removed.

The Statistics Toolbox function `sequentialfs` carries out sequential feature selection. Input arguments include predictor and response data and a function handle to a file implementing the criterion function. Optional inputs allow you to specify SFS or SBS, required or excluded features, and the size of the feature subset. The function calls `cvpartition` and `crossval` to evaluate the criterion at different candidate sets.

Example: Sequential Feature Selection

For example, consider a data set with 100 observations of 10 predictors. As described in "Example: Generalized Linear Models" on page 9-67, the following generates random data from a logistic model, with a binomial distribution of responses at each set of values for the predictors. Some coefficients are set to zero so that not all of the predictors affect the response:

```
n = 100;
m = 10;
X = rand(n,m);
b = [1 0 0 2 .5 0 0 0.1 0 1];
Xb = X*b';
```

```
p = 1./(1+exp(-Xb));
N = 50;
y = binornd(N,p);
```

The `glmfit` function fits a logistic model to the data:

```
Y = [y N*ones(size(y))];
[b0,dev0,stats0] = glmfit(X,Y,'binomial');

% Display coefficient estimates and their standard errors:
model0 = [b0 stats0.se]
model0 =
    0.3115    0.2596
    0.9614    0.1656
   -0.1100    0.1651
   -0.2165    0.1683
    1.9519    0.1809
    0.5683    0.2018
   -0.0062    0.1740
    0.0651    0.1641
   -0.1034    0.1685
    0.0017    0.1815
    0.7979    0.1806

% Display the deviance of the fit:
dev0
dev0 =
  101.2594
```

This is the full model, using all of the features (and an initial constant term). Sequential feature selection searches for a subset of the features in the full model with comparative predictive power.

First, you must specify a criterion for selecting the features. The following function, which calls `glmfit` and returns the deviance of the fit (a generalization of the residual sum of squares) is a useful criterion in this case:

```
function dev = critfun(X,Y)

[b,dev] = glmfit(X,Y,'binomial');
```

You should create this function as a file on the MATLAB path.

The function `sequentialfs` performs feature selection, calling the criterion function via a function handle:

```
maxdev = chi2inv(.95,1);
opt = statset('display','iter',...
              'TolFun',maxdev,...
              'TolTypeFun','abs');

inmodel = sequentialfs(@critfun,X,Y,...
                       'cv','none',...
                       'nullmodel',true,...
                       'options',opt,...
                       'direction','forward');

Start forward sequential feature selection:
Initial columns included:  none
Columns that can not be included:  none
Step 1, used initial columns, criterion value 309.118
Step 2, added column 4, criterion value 180.732
Step 3, added column 1, criterion value 138.862
Step 4, added column 10, criterion value 114.238
Step 5, added column 5, criterion value 103.503
Final columns included:  1 4 5 10
```

The iterative display shows a decrease in the criterion value as each new feature is added to the model. The final result is a reduced model with only four of the original ten features: columns `1`, `4`, `5`, and `10` of `X`. These features are indicated in the logical vector `inmodel` returned by `sequentialfs`.

The deviance of the reduced model is higher than for the full model, but the addition of any other single feature would not decrease the criterion by more than the absolute tolerance, `maxdev`, set in the options structure. Adding a feature with no effect reduces the deviance by an amount that has a chi-square distribution with one degree of freedom. Adding a significant feature results in a larger change. By setting `maxdev` to `chi2inv(.95,1)`, you instruct `sequentialfs` to continue adding features so long as the change in deviance is more than would be expected by random chance.

The reduced model (also with an initial constant term) is:

```
[b,dev,stats] = glmfit(X(:,inmodel),Y,'binomial');

% Display coefficient estimates and their standard errors:
model = [b stats.se]
model =
    0.0784    0.1642
    1.0040    0.1592
    1.9459    0.1789
    0.6134    0.1872
    0.8245    0.1730
```

Feature Transformation

In this section...

Introduction to Feature Transformation

Feature transformation is a group of methods that create new features (predictor variables). The methods are useful for dimension reduction when the transformed features have a descriptive power that is more easily ordered than the original features. In this case, less descriptive features can be dropped from consideration when building models.

Feature transformation methods are contrasted with the methods presented in "Feature Selection" on page 10-23, where dimension reduction is achieved by computing an optimal subset of predictive features measured in the original data.

The methods presented in this section share some common methodology. Their goals, however, are essentially different:

- Nonnegative matrix factorization is used when model terms must represent nonnegative quantities, such as physical quantities.
- Principal component analysis is used to summarize data in fewer dimensions, for example, to visualize it.
- Factor analysis is used to build explanatory models of data correlations.

Nonnegative Matrix Factorization

Introduction to Nonnegative Matrix Factorization

Nonnegative matrix factorization (*NMF*) is a dimension-reduction technique based on a low-rank approximation of the feature space. Besides providing a reduction in the number of features, NMF guarantees that the features are nonnegative, producing additive models that respect, for example, the nonnegativity of physical quantities.

Given a nonnegative m-by-n matrix X and a positive integer $k < \min(m,n)$, NMF finds nonnegative m-by-k and k-by-n matrices W and H, respectively, that minimize the norm of the difference $X - WH$. W and H are thus approximate nonnegative factors of X.

The k columns of W represent transformations of the variables in X; the k rows of H represent the coefficients of the linear combinations of the original n variables in X that produce the transformed variables in W. Since k is generally smaller than the rank of X, the product WH provides a compressed approximation of the data in X. A range of possible values for k is often suggested by the modeling context.

The Statistics Toolbox function `nnmf` carries out nonnegative matrix factorization. `nnmf` uses one of two iterative algorithms that begin with random initial values for W and H. Because the norm of the residual $X - WH$ may have local minima, repeated calls to `nnmf` may yield different factorizations. Sometimes the algorithm converges to a solution of lower rank than k, which may indicate that the result is not optimal.

Example: Nonnegative Matrix Factorization

For example, consider the five predictors of biochemical oxygen demand in the data set `moore.mat`:

```
load moore
X = moore(:,1:5);
```

The following uses `nnmf` to compute a rank-two approximation of `X` with a multiplicative update algorithm that begins from five random initial values for `W` and `H`:

```
opt = statset('MaxIter',10,'Display','final');
[W0,H0] = nnmf(X,2,'replicates',5,...
                   'options',opt,...
```

```
                  'algorithm','mult');
    rep iteration    rms resid    |delta x|
      1       10      358.296   0.00190554
      2       10      78.3556  0.000351747
      3       10      230.962    0.0172839
      4       10      326.347   0.00739552
      5       10      361.547   0.00705539
Final root mean square residual = 78.3556
```

The 'mult' algorithm is sensitive to initial values, which makes it a good choice when using 'replicates' to find W and H from multiple random starting values.

Now perform the factorization using an alternating least-squares algorithm, which converges faster and more consistently. Run 100 times more iterations, beginning from the initial W0 and H0 identified above:

```
opt = statset('Maxiter',1000,'Display','final');
[W,H] = nnmf(X,2,'w0',W0,'h0',H0,...
                 'options',opt,...
                 'algorithm','als');
    rep iteration    rms resid    |delta x|
      1        3      77.5315 3.52673e-005
Final root mean square residual = 77.5315
```

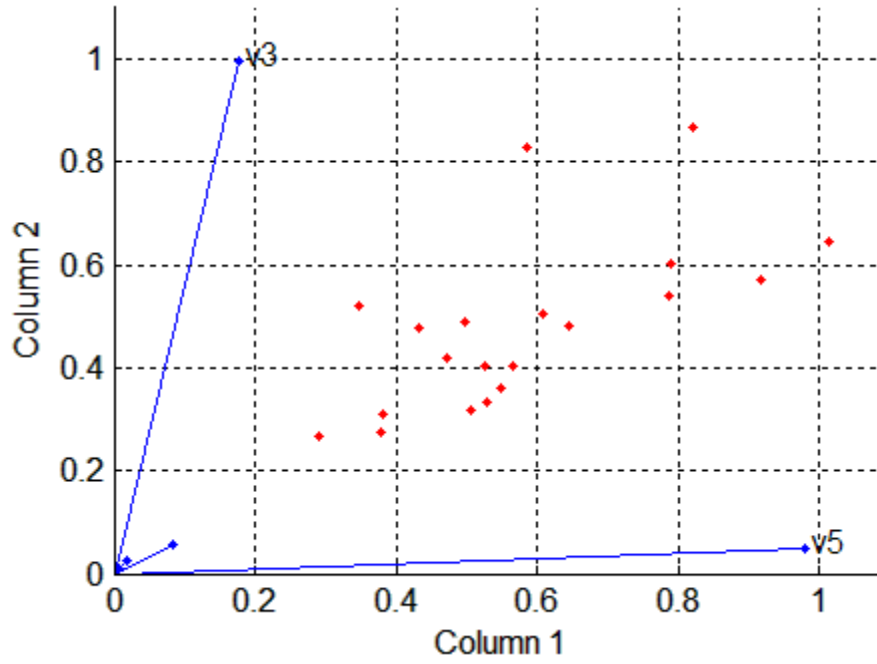
The two columns of W are the transformed predictors. The two rows of H give the relative contributions of each of the five predictors in X to the predictors in W:

```
H
H =
    0.0835  0.0190  0.1782  0.0072  0.9802
    0.0558  0.0250  0.9969  0.0085  0.0497
```

The fifth predictor in X (weight 0.9802) strongly influences the first predictor in W. The third predictor in X (weight 0.9969) strongly influences the second predictor in W.

Visualize the relative contributions of the predictors in X with a biplot, showing the data and original variables in the column space of W:

```
biplot(H','scores',W,'varlabels',{'','','v3','','v5'});
axis([0 1.1 0 1.1])
xlabel('Column 1')
ylabel('Column 2')
```



Principal Component Analysis (PCA)

Introduction to Principal Component Analysis (PCA)

One of the difficulties inherent in multivariate statistics is the problem of visualizing data that has many variables. The MATLAB function `plot` displays a graph of the relationship between two variables. The `plot3` and `surf` commands display different three-dimensional views. But when

there are more than three variables, it is more difficult to visualize their relationships.

Fortunately, in data sets with many variables, groups of variables often move together. One reason for this is that more than one variable might be measuring the same driving principle governing the behavior of the system. In many systems there are only a few such driving forces. But an abundance of instrumentation enables you to measure dozens of system variables. When this happens, you can take advantage of this redundancy of information. You can simplify the problem by replacing a group of variables with a single new variable.

Principal component analysis is a quantitatively rigorous method for achieving this simplification. The method generates a new set of variables, called *principal components*. Each principal component is a linear combination of the original variables. All the principal components are orthogonal to each other, so there is no redundant information. The principal components as a whole form an orthogonal basis for the space of the data.

There are an infinite number of ways to construct an orthogonal basis for several columns of data. What is so special about the principal component basis?

The first principal component is a single axis in space. When you project each observation on that axis, the resulting values form a new variable. And the variance of this variable is the maximum among all possible choices of the first axis.

The second principal component is another axis in space, perpendicular to the first. Projecting the observations on this axis generates another new variable. The variance of this variable is the maximum among all possible choices of this second axis.

The full set of principal components is as large as the original set of variables. But it is commonplace for the sum of the variances of the first few principal components to exceed 80% of the total variance of the original data. By examining plots of these few new variables, researchers often develop a deeper understanding of the driving forces that generated the original data.

You can use the function `princomp` to find the principal components. To use `princomp`, you need to have the actual measured data you want to analyze. However, if you lack the actual data, but have the sample covariance or correlation matrix for the data, you can still use the function `pcacov` to perform a principal components analysis. See the reference page for `pcacov` for a description of its inputs and outputs.

Example: Principal Component Analysis

Computing Components. Consider a sample application that uses nine different indices of the quality of life in 329 U.S. cities. These are climate, housing, health, crime, transportation, education, arts, recreation, and economics. For each index, higher is better. For example, a higher index for crime means a lower crime rate.

Start by loading the data in `cities.mat`.

```
load cities
whos
  Name             Size         Bytes  Class
  categories       9x14           252  char array
  names          329x43         28294  char array
  ratings        329x9          23688  double array
```

The `whos` command generates a table of information about all the variables in the workspace.

The `cities` data set contains three variables:

- `categories`, a string matrix containing the names of the indices

- `names`, a string matrix containing the 329 city names
- `ratings`, the data matrix with 329 rows and 9columns

The `categories` variable has the following values:

```
categories
categories =
   climate
   housing
   health
   crime
   transportation
   education
   arts
   recreation
   economics
```

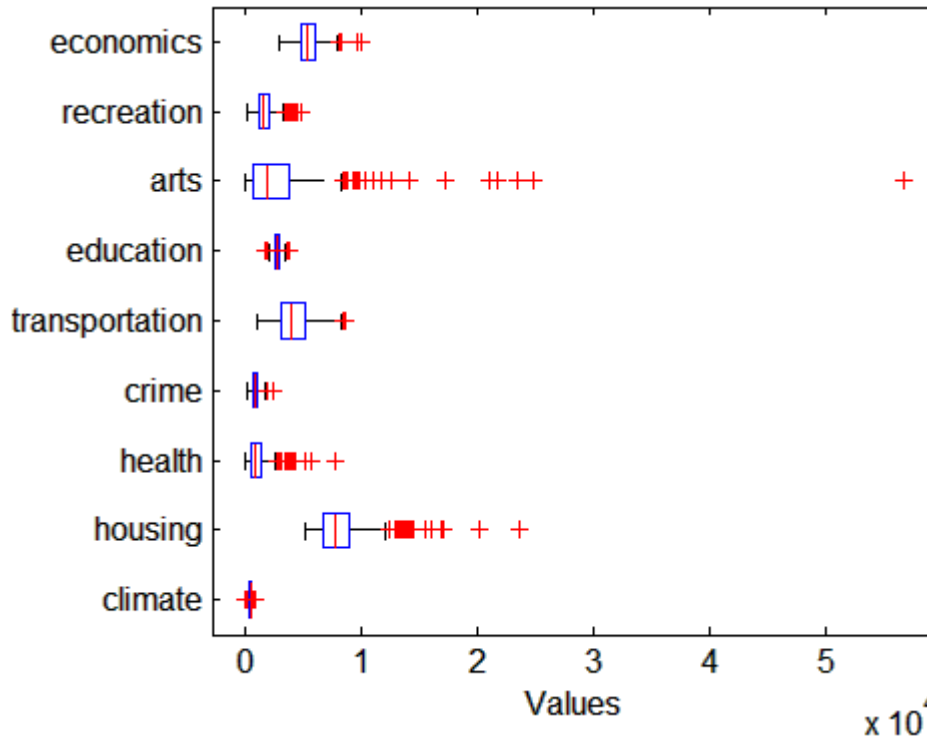
The first five rows of `names` are

```
first5 = names(1:5,:)
first5 =
   Abilene, TX
   Akron, OH
   Albany, GA
   Albany-Troy, NY
   Albuquerque, NM
```

To get a quick impression of the ratings data, make a box plot.

```
boxplot(ratings,'orientation','horizontal','labels',categories)
```

This command generates the plot below. Note that there is substantially more variability in the ratings of the arts and housing than in the ratings of crime and climate.



Ordinarily you might also graph pairs of the original variables, but there are 36two-variable plots. Perhaps principal components analysis can reduce the number of variables you need to consider.

Sometimes it makes sense to compute principal components for raw data. This is appropriate when all the variables are in the same units. Standardizing the data is often preferable when the variables are in different units or when the variance of the different columns is substantial (as in this case).

You can standardize the data by dividing each column by its standard deviation.

```
stdr = std(ratings);
sr = ratings./repmat(stdr,329,1);
```

Now you are ready to find the principal components.

```
[coefs,scores,variances,t2] = princomp(sr);
```

The following sections explain the four outputs from `princomp`.

Component Coefficients. The first output of the `princomp` function, `coefs`, contains the coefficients of the linear combinations of the original variables that generate the principal components. The coefficients are also known as *loadings*.

The first three principal component coefficient vectors are:

```
c3 = coefs(:,1:3)
c3 =
    0.2064    0.2178   -0.6900
    0.3565    0.2506   -0.2082
    0.4602   -0.2995   -0.0073
    0.2813    0.3553    0.1851
    0.3512   -0.1796    0.1464
    0.2753   -0.4834    0.2297
    0.4631   -0.1948   -0.0265
    0.3279    0.3845   -0.0509
    0.1354    0.4713    0.6073
```

The largest coefficients in the first column (first principal component) are the third and seventh elements, corresponding to the variables `health` and `arts`. All the coefficients of the first principal component have the same sign, making it a weighted average of all the original variables.

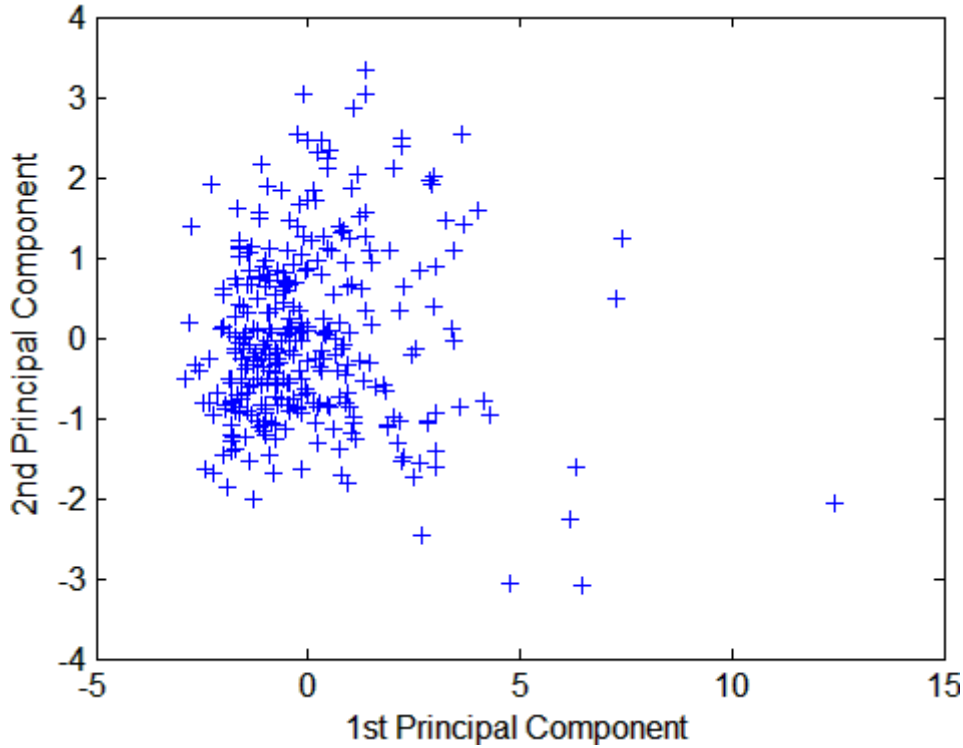
The principal components are unit length and orthogonal:

```
I = c3'*c3
I =
    1.0000   -0.0000   -0.0000
   -0.0000    1.0000   -0.0000
   -0.0000   -0.0000    1.0000
```

Component Scores. The second output, `scores`, contains the coordinates of the original data in the new coordinate system defined by the principal components. This output is the same size as the input data matrix.

A plot of the first two columns of `scores` shows the ratings data projected onto the first two principal components. `princomp` computes the scores to have mean zero.

```
plot(scores(:,1),scores(:,2),'+')
xlabel('1st Principal Component')
ylabel('2nd Principal Component')
```



Note the outlying points in the right half of the plot.

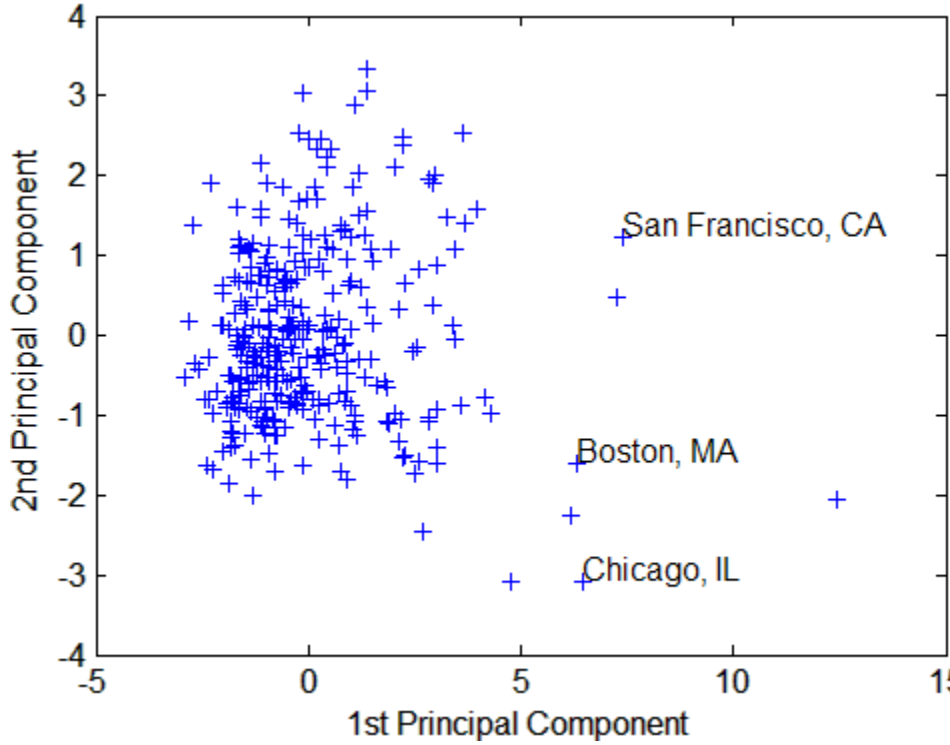
While it is possible to create a three-dimensional plot using three columns of `scores`, the examples in this section create two-dimensional plots, which are easier to describe.

The function `gname` is useful for graphically identifying a few points in a plot like this. You can call `gname` with a string matrix containing as many case

labels as points in the plot. The string matrix `names` works for labeling points with the city names.

```
gname(names)
```

Move your cursor over the plot and click once near each point in the right half. As you click each point, it is labeled with the proper row from the `names` string matrix. Here is the plot after a few clicks:



When you are finished labeling points, press the **Return** key.

The labeled cities are some of the biggest population centers in the United States. They are definitely different from the remainder of the data, so perhaps they should be considered separately. To remove the labeled cities from the data, first identify their corresponding row numbers as follows:

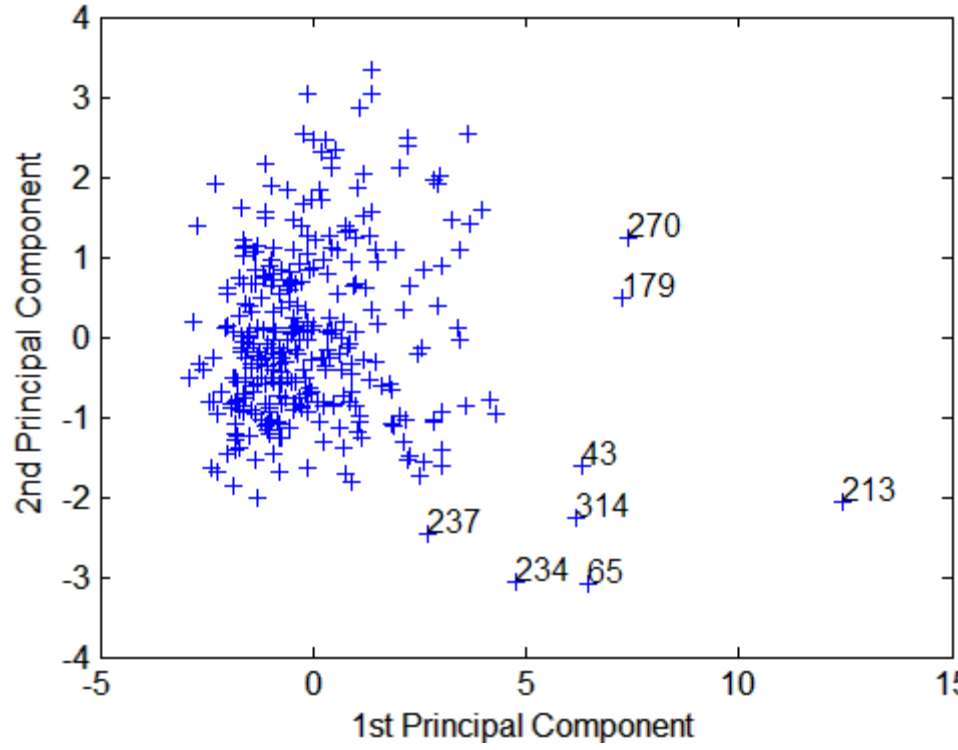
1. Close the plot window.

2. Redraw the plot by entering

```
plot(scores(:,1),scores(:,2),'+')
xlabel('1st Principal Component');
ylabel('2nd Principal Component');
```

3. Enter `gname` without any arguments.

4. Click near the points you labeled in the preceding figure. This labels the points by their row numbers, as shown in the following figure.



Then you can create an index variable containing the row numbers of all the metropolitan areas you choose.

```
metro = [43 65 179 213 234 270 314];
names(metro,:)
ans =
   Boston, MA
   Chicago, IL
   Los Angeles, Long Beach, CA
   New York, NY
   Philadelphia, PA-NJ
   San Francisco, CA
   Washington, DC-MD-VA
```

To remove these rows from the ratings matrix, enter the following.

```
rsubset = ratings;
nsubset = names;
nsubset(metro,:) = [];
rsubset(metro,:) = [];
size(rsubset)
ans =
   322     9
```

Component Variances. The third output, `variances`, is a vector containing the variance explained by the corresponding principal component. Each column of `scores` has a sample variance equal to the corresponding element of `variances`.

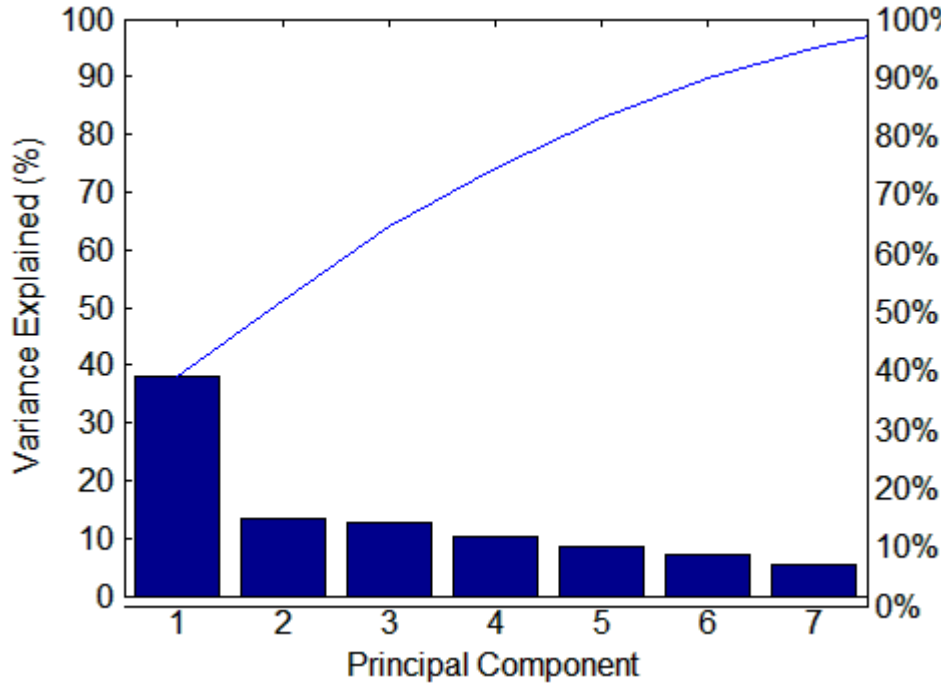
```
variances
variances =
    3.4083
    1.2140
    1.1415
    0.9209
    0.7533
    0.6306
    0.4930
    0.3180
    0.1204
```

You can easily calculate the percent of the total variability explained by each principal component.

```
percent_explained = 100*variances/sum(variances)
percent_explained =
   37.8699
   13.4886
   12.6831
   10.2324
    8.3698
    7.0062
    5.4783
    3.5338
    1.3378
```

Use the `pareto` function to make a *scree plot* of the percent variability explained by each principal component.

```
pareto(percent_explained)
xlabel('Principal Component')
ylabel('Variance Explained (%)')
```



The preceding figure shows that the only clear break in the amount of variance accounted for by each component is between the first and second components. However, that component by itself explains less than 40% of the variance, so more components are probably needed. You can see that the first three principal components explain roughly two-thirds of the total variability in the standardized ratings, so that might be a reasonable way to reduce the dimensions in order to visualize the data.

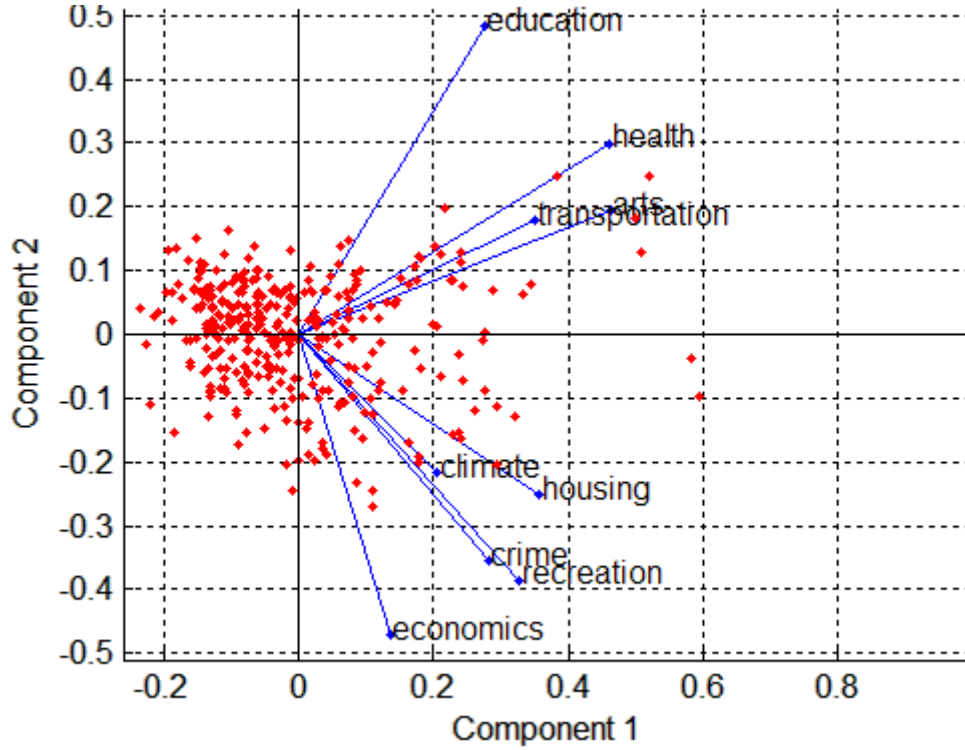
Hotelling's T2. The last output of the `princomp` function, `t2`, is Hotelling's T^2, a statistical measure of the multivariate distance of each observation from the center of the data set. This is an analytical way to find the most extreme points in the data.

```
[st2, index] = sort(t2,'descend'); % Sort in descending order.
extreme = index(1)
extreme =
   213
names(extreme,:)
ans =
   New York, NY
```

It is not surprising that the ratings for New York are the furthest from the average U.S. town.

Visualizing the Results. Use the `biplot` function to help visualize both the principal component coefficients for each variable and the principal component scores for each observation in a single plot. For example, the following command plots the results from the principal components analysis on the cities and labels each of the variables.

```
biplot(coefs(:,1:2), 'scores',scores(:,1:2),...
'varlabels',categories);
axis([-.26 1 -.51 .51]);
```



Each of the nine variables is represented in this plot by a vector, and the direction and length of the vector indicates how each variable contributes to the two principal components in the plot. For example, you have seen that the first principal component, represented in this biplot by the horizontal axis, has positive coefficients for all nine variables. That corresponds to the nine vectors directed into the right half of the plot. You have also seen that the second principal component, represented by the vertical axis, has positive coefficients for the variables education, health, arts, and transportation, and negative coefficients for the remaining five variables. That corresponds to vectors directed into the top and bottom halves of the plot, respectively. This indicates that this component distinguishes between cities that have high values for the first set of variables and low for the second, and cities that have the opposite.

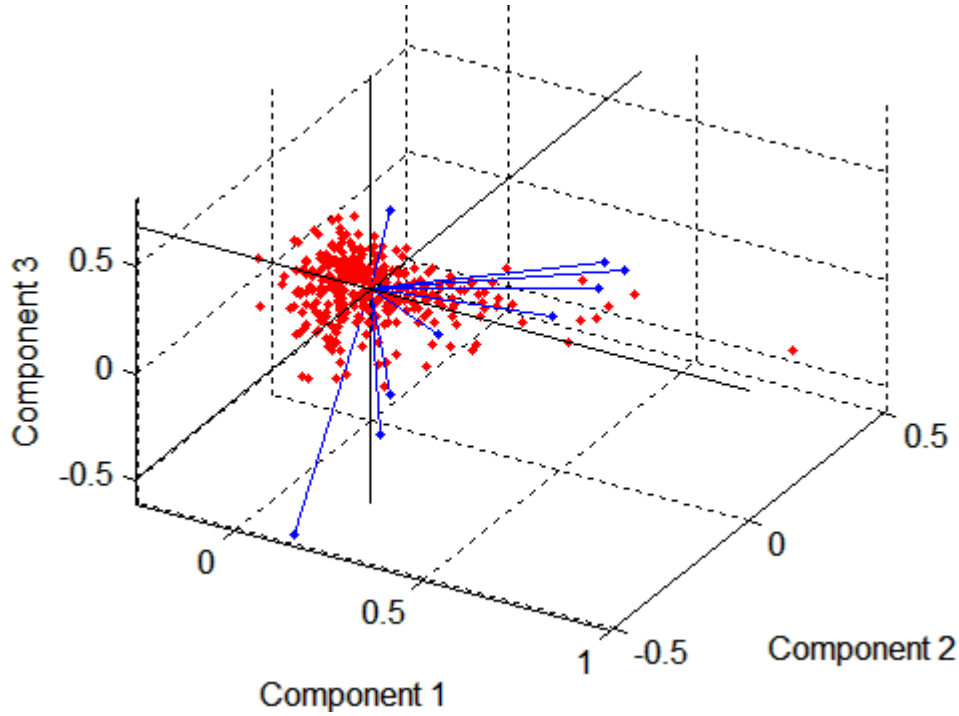
The variable labels in this figure are somewhat crowded. You could either leave out the `VarLabels` parameter when making the plot, or simply select and drag some of the labels to better positions using the Edit Plot tool from the figure window toolbar.

Each of the 329 observations is represented in this plot by a point, and their locations indicate the score of each observation for the two principal components in the plot. For example, points near the left edge of this plot have the lowest scores for the first principal component. The points are scaled to fit within the unit square, so only their relative locations may be determined from the plot.

You can use the `Data Cursor`, in the **Tools** menu in the figure window, to identify the items in this plot. By clicking on a variable (vector), you can read off that variable's coefficients for each principal component. By clicking on an observation (point), you can read off that observation's scores for each principal component.

You can also make a biplot in three dimensions. This can be useful if the first two principal coordinates do not explain enough of the variance in your data. Selecting `Rotate 3D` in the **Tools** menu enables you to rotate the figure to see it from different angles.

```
biplot(coefs(:,1:3), 'scores',scores(:,1:3),...
'obslabels',names);
axis([-.26 1 -.51 .51 -.61 .81]);
view([30 40]);
```



Factor Analysis

Introduction to Factor Analysis

Multivariate data often includes a large number of measured variables, and sometimes those variables overlap, in the sense that groups of them might be dependent. For example, in a decathlon, each athlete competes in 10 events, but several of them can be thought of as speed events, while others can be thought of as strength events, etc. Thus, you can think of a competitor's 10 event scores as largely dependent on a smaller set of three or four types of athletic ability.

Factor analysis is a way to fit a model to multivariate data to estimate just this sort of interdependence. In a factor analysis model, the measured variables depend on a smaller number of unobserved (latent) factors. Because each factor might affect several variables in common, they are known as *common factors*. Each variable is assumed to be dependent on a linear combination of the common factors, and the coefficients are known as *loadings*. Each measured variable also includes a component due to independent random variability, known as *specific variance* because it is specific to one variable.

Specifically, factor analysis assumes that the covariance matrix of your data is of the form

$$\sum_x = \Lambda\Lambda^T + \Psi$$

where Λ is the matrix of loadings, and the elements of the diagonal matrix Ψ are the specific variances. The function `factoran` fits the Factor Analysis model using maximum likelihood.

Example: Factor Analysis

Factor Loadings. Over the course of 100 weeks, the percent change in stock prices for ten companies has been recorded. Of the ten companies, the first four can be classified as primarily technology, the next three as financial, and the last three as retail. It seems reasonable that the stock prices for companies that are in the same sector might vary together as economic conditions change. Factor Analysis can provide quantitative evidence that companies within each sector do experience similar week-to-week changes in stock price.

In this example, you first load the data, and then call `factoran`, specifying a model fit with three common factors. By default, `factoran` computes rotated estimates of the loadings to try and make their interpretation simpler. But in this example, you specify an unrotated solution.

```
load stockreturns

[Loadings,specificVar,T,stats] = ...
  factoran(stocks,3,'rotate','none');
```

The first two `factoran` return arguments are the estimated loadings and the estimated specific variances. Each row of the loadings matrix represents one of the ten stocks, and each column corresponds to a common factor. With unrotated estimates, interpretation of the factors in this fit is difficult because most of the stocks contain fairly large coefficients for two or more factors.

```
Loadings
Loadings =
       0.8885    0.2367   -0.2354
       0.7126    0.3862    0.0034
       0.3351    0.2784   -0.0211
       0.3088    0.1113   -0.1905
       0.6277   -0.6643    0.1478
       0.4726   -0.6383    0.0133
       0.1133   -0.5416    0.0322
       0.6403    0.1669    0.4960
       0.2363    0.5293    0.5770
       0.1105    0.1680    0.5524
```

Note "Factor Rotation" on page 10-48 helps to simplify the structure in the `Loadings` matrix, to make it easier to assign meaningful interpretations to the factors.

From the estimated specific variances, you can see that the model indicates that a particular stock price varies quite a lot beyond the variation due to the common factors.

```
specificVar
specificVar =
       0.0991
       0.3431
       0.8097
       0.8559
       0.1429
```

```
    0.3691
    0.6928
    0.3162
    0.3311
    0.6544
```

A specific variance of 1 would indicate that there is *no* common factor component in that variable, while a specific variance of 0 would indicate that the variable is *entirely* determined by common factors. These data seem to fall somewhere in between.

The p value returned in the `stats` structure fails to reject the null hypothesis of three common factors, suggesting that this model provides a satisfactory explanation of the covariation in these data.

```
stats.p
ans =
       0.8144
```

To determine whether fewer than three factors can provide an acceptable fit, you can try a model with two common factors. The p value for this second fit is highly significant, and rejects the hypothesis of two factors, indicating that the simpler model is not sufficient to explain the pattern in these data.

```
[Loadings2,specificVar2,T2,stats2] = ...
  factoran(stocks, 2,'rotate','none');

stats2.p
ans =
      3.5610e-006
```

Factor Rotation. As the results illustrate, the estimated loadings from an unrotated factor analysis fit can have a complicated structure. The goal of factor rotation is to find a parameterization in which each variable has only a small number of large loadings. That is, each variable is affected by a small number of factors, preferably only one. This can often make it easier to interpret what the factors represent.

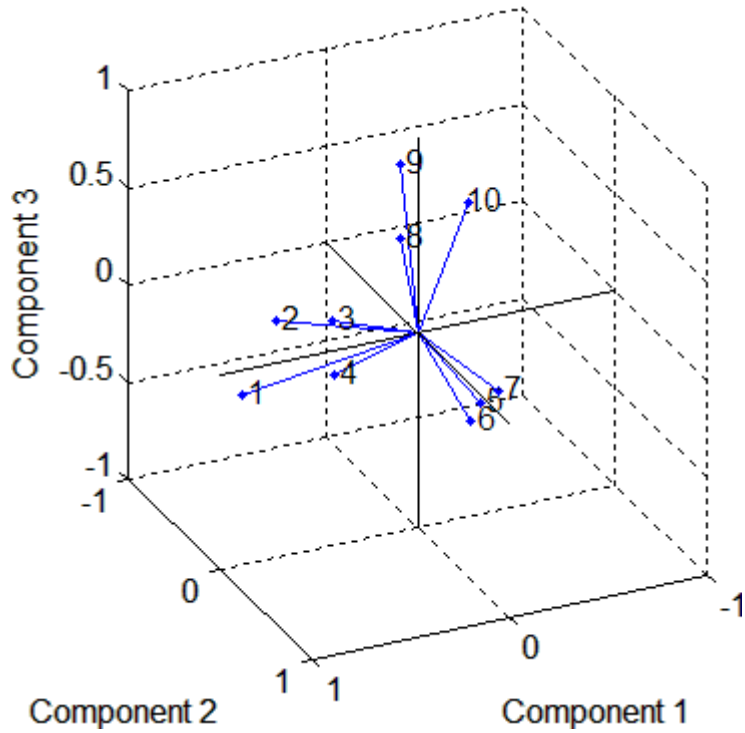
If you think of each row of the loadings matrix as coordinates of a point in M-dimensional space, then each factor corresponds to a coordinate axis. Factor rotation is equivalent to rotating those axes and computing new

loadings in the rotated coordinate system. There are various ways to do this. Some methods leave the axes orthogonal, while others are oblique methods that change the angles between them. For this example, you can rotate the estimated loadings by using the promax criterion, a common oblique method.

```
[LoadingsPM,specVarPM] = factoran(stocks,3,'rotate','promax');
LoadingsPM
LoadingsPM =
       0.9452    0.1214   -0.0617
       0.7064   -0.0178    0.2058
       0.3885   -0.0994    0.0975
       0.4162   -0.0148   -0.1298
       0.1021    0.9019    0.0768
       0.0873    0.7709   -0.0821
      -0.1616    0.5320   -0.0888
       0.2169    0.2844    0.6635
       0.0016   -0.1881    0.7849
      -0.2289    0.0636    0.6475
```

Promax rotation creates a simpler structure in the loadings, one in which most of the stocks have a large loading on only one factor. To see this structure more clearly, you can use the `biplot` function to plot each stock using its factor loadings as coordinates.

```
biplot(LoadingsPM,'varlabels',num2str((1:10)'));
axis square
view(155,27);
```



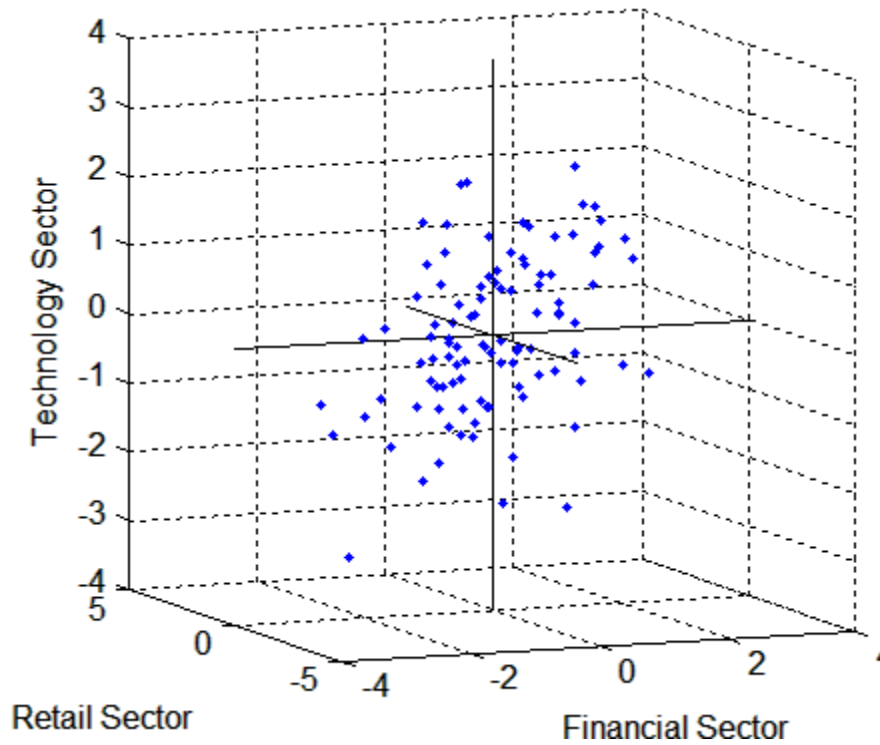
This plot shows that promax has rotated the factor loadings to a simpler structure. Each stock depends primarily on only one factor, and it is possible to describe each factor in terms of the stocks that it affects. Based on which companies are near which axes, you could reasonably conclude that the first factor axis represents the financial sector, the second retail, and the third technology. The original conjecture, that stocks vary primarily within sector, is apparently supported by the data.

Factor Scores. Sometimes, it is useful to be able to classify an observation based on its factor scores. For example, if you accepted the three-factor model and the interpretation of the rotated factors, you might want to categorize each week in terms of how favorable it was for each of the three stock sectors, based on the data from the 10 observed stocks.

Because the data in this example are the raw stock price changes, and not just their correlation matrix, you can have `factoran` return estimates of the

value of each of the three rotated common factors for each week. You can then plot the estimated scores to see how the different stock sectors were affected during each week.

```
[LoadingsPM,specVarPM,TPM,stats,F] = ...
  factoran(stocks, 3,'rotate','promax');

plot3(F(:,1),F(:,2),F(:,3),'b.')
line([-4 4 NaN 0 0 NaN 0 0], [0 0 NaN -4 4 NaN 0 0],...
     [0 0 NaN 0 0 NaN -4 4], 'Color','black')
xlabel('Financial Sector')
ylabel('Retail Sector')
zlabel('Technology Sector')
grid on
axis square
view(-22.5, 8)
```

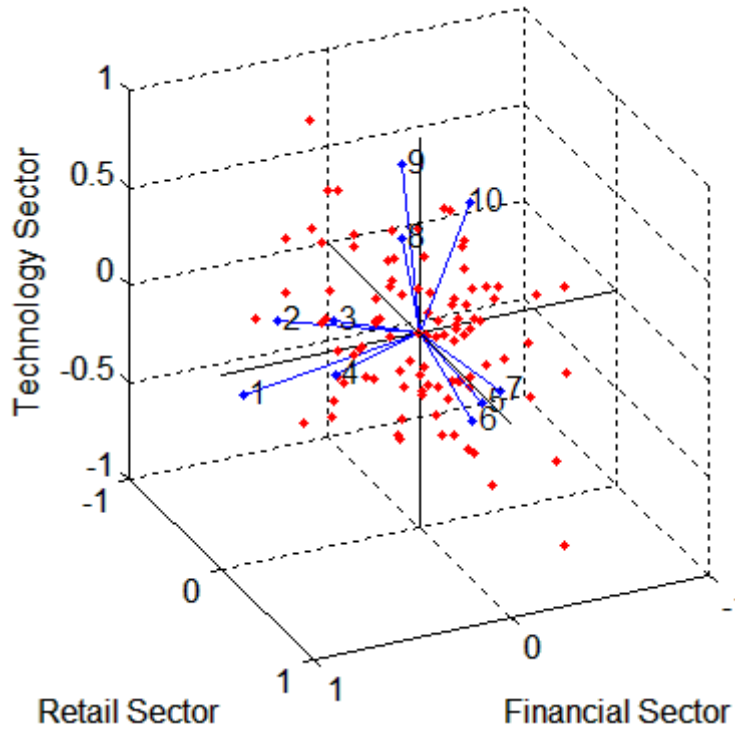


Oblique rotation often creates factors that are correlated. This plot shows some evidence of correlation between the first and third factors, and you can investigate further by computing the estimated factor correlation matrix.

```
inv(TPM'*TPM)
ans =
       1.0000    0.1559    0.4082
       0.1559    1.0000   -0.0559
       0.4082   -0.0559    1.0000
```

Visualizing the Results. You can use the `biplot` function to help visualize both the factor loadings for each variable and the factor scores for each observation in a single plot. For example, the following command plots the results from the factor analysis on the stock data and labels each of the 10 stocks.

```
biplot(LoadingsPM,'scores',F,'varlabels',num2str((1:10)'))
xlabel('Financial Sector')
ylabel('Retail Sector')
zlabel('Technology Sector')
axis square
view(155,27)
```



In this case, the factor analysis includes three factors, and so the biplot is three-dimensional. Each of the 10 stocks is represented in this plot by a vector, and the direction and length of the vector indicates how each stock depends on the underlying factors. For example, you have seen that after promax rotation, the first four stocks have positive loadings on the first factor, and unimportant loadings on the other two factors. That first factor, interpreted as a financial sector effect, is represented in this biplot as one of the horizontal axes. The dependence of those four stocks on that factor corresponds to the four vectors directed approximately along that axis. Similarly, the dependence of stocks 5, 6, and 7 primarily on the second factor, interpreted as a retail sector effect, is represented by vectors directed approximately along that axis.

Each of the 100 observations is represented in this plot by a point, and their locations indicate the score of each observation for the three factors. For example, points near the top of this plot have the highest scores for the

technology sector factor. The points are scaled to fit within the unit square, so only their relative locations can be determined from the plot.

You can use the **Data Cursor** tool from the **Tools** menu in the figure window to identify the items in this plot. By clicking a stock (vector), you can read off that stock's loadings for each factor. By clicking an observation (point), you can read off that observation's scores for each factor.

11

Cluster Analysis

Introduction to Cluster Analysis

Cluster analysis, also called *segmentation analysis* or *taxonomy analysis*, creates groups, or *clusters*, of data. Clusters are formed in such a way that objects in the same cluster are very similar and objects in different clusters are very distinct. Measures of similarity depend on the application.

"Hierarchical Clustering" on page 11-3 groups data over a variety of scales by creating a cluster tree or *dendrogram*. The tree is not a single set of clusters, but rather a multilevel hierarchy, where clusters at one level are joined as clusters at the next level. This allows you to decide the level or scale of clustering that is most appropriate for your application. The Statistics Toolbox function `clusterdata` performs all of the necessary steps for you. It incorporates the `pdist`, `linkage`, and `cluster` functions, which may be used separately for more detailed analysis. The `dendrogram` function plots the cluster tree.

"K-Means Clustering" on page 11-21 is a partitioning method. The function `kmeans` partitions data into k mutually exclusive clusters, and returns the index of the cluster to which it has assigned each observation. Unlike hierarchical clustering, k-means clustering operates on actual observations (rather than the larger set of dissimilarity measures), and creates a single level of clusters. The distinctions mean that k-means clustering is often more suitable than hierarchical clustering for large amounts of data.

"Gaussian Mixture Models" on page 11-28 form clusters by representing the probability density function of observed variables as a mixture of multivariate normal densities. Mixture models of the `gmdistribution` class use an expectation maximization (EM) algorithm to fit data, which assigns posterior probabilities to each component density with respect to each observation. Clusters are assigned by selecting the component that maximizes the posterior probability. Clustering using Gaussian mixture models is sometimes considered a soft clustering method. The posterior probabilities for each point indicate that each data point has some probability of belonging to each cluster. Like k-means clustering, Gaussian mixture modeling uses an iterative algorithm that converges to a local optimum. Gaussian mixture modeling may be more appropriate than k-means clustering when clusters have different sizes and correlation within them.

Hierarchical Clustering

In this section...

Introduction to Hierarchical Clustering

Hierarchical clustering groups data over a variety of scales by creating a cluster tree or *dendrogram*. The tree is not a single set of clusters, but rather a multilevel hierarchy, where clusters at one level are joined as clusters at the next level. This allows you to decide the level or scale of clustering that is most appropriate for your application. The Statistics Toolbox function `clusterdata` supports agglomerative clustering and performs all of the necessary steps for you. It incorporates the `pdist`, `linkage`, and `cluster` functions, which you can use separately for more detailed analysis. The `dendrogram` function plots the cluster tree.

Algorithm Description

To perform agglomerative hierarchical cluster analysis on a data set using Statistics Toolbox functions, follow this procedure:

1. **Find the similarity or dissimilarity between every pair of objects in the data set.** In this step, you calculate the *distance* between objects using the `pdist` function. The `pdist` function supports many different ways to compute this measurement. See "Similarity Measures" on page 11-4 for more information.

2. **Group the objects into a binary, hierarchical cluster tree.** In this step, you link pairs of objects that are in close proximity using the `linkage`

function. The `linkage` function uses the distance information generated in step 1 to determine the proximity of objects to each other. As objects are paired into binary clusters, the newly formed clusters are grouped into larger clusters until a hierarchical tree is formed. See "Linkages" on page 11-6 for more information.

3 **Determine where to cut the hierarchical tree into clusters.** In this step, you use the `cluster` function to prune branches off the bottom of the hierarchical tree, and assign all the objects below each cut to a single cluster. This creates a partition of the data. The `cluster` function can create these clusters by detecting natural groupings in the hierarchical tree or by cutting off the hierarchical tree at an arbitrary point.

The following sections provide more information about each of these steps.

Note The Statistics Toolbox function `clusterdata` performs all of the necessary steps for you. You do not need to execute the `pdist`, `linkage`, or `cluster` functions separately.

Similarity Measures

You use the `pdist` function to calculate the distance between every pair of objects in a data set. For a data set made up of m objects, there are $m*(m-1)/2$ pairs in the data set. The result of this computation is commonly known as a distance or dissimilarity matrix.

There are many ways to calculate this distance information. By default, the `pdist` function calculates the Euclidean distance between objects; however, you can specify one of several other options. See `pdist` for more information.

Note You can optionally normalize the values in the data set before calculating the distance information. In a real world data set, variables can be measured against different scales. For example, one variable can measure Intelligence Quotient (IQ) test scores and another variable can measure head circumference. These discrepancies can distort the proximity calculations. Using the `zscore` function, you can convert all the values in the data set to use the same proportional scale. See `zscore` for more information.

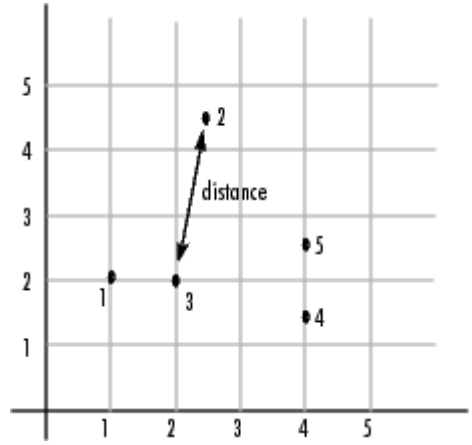
For example, consider a data set, `X`, made up of five objects where each object is a set of *x,y* coordinates.

- **Object 1**: 1, 2
- **Object 2**: 2.5, 4.5
- **Object 3**: 2, 2
- **Object 4**: 4, 1.5
- **Object 5**: 4, 2.5

You can define this data set as a matrix

```
X = [1 2;2.5 4.5;2 2;4 1.5;4 2.5]
```

and pass it to `pdist`. The `pdist` function calculates the distance between object 1 and object 2, object 1 and object 3, and so on until the distances between all the pairs have been calculated. The following figure plots these objects in a graph. The Euclidean distance between object 2 and object 3 is shown to illustrate one interpretation of distance.



Distance Information

The `pdist` function returns this distance information in a vector, `Y`, where each element contains the distance between a pair of objects.

```
Y = pdist(X)
Y =
  Columns 1 through 5
    2.9155    1.0000    3.0414    3.0414    2.5495
  Columns 6 through 10
    3.3541    2.5000    2.0616    2.0616    1.0000
```

To make it easier to see the relationship between the distance information generated by `pdist` and the objects in the original data set, you can reformat the distance vector into a matrix using the `squareform` function. In this matrix, element *i,j* corresponds to the distance between object *i* and object *j* in the original data set. In the following example, element 1,1 represents the distance between object 1 and itself (which is zero). Element 1,2 represents the distance between object 1 and object 2, and so on.

```
squareform(Y)
ans =
         0    2.9155    1.0000    3.0414    3.0414
    2.9155         0    2.5495    3.3541    2.5000
    1.0000    2.5495         0    2.0616    2.0616
    3.0414    3.3541    2.0616         0    1.0000
    3.0414    2.5000    2.0616    1.0000         0
```

Linkages

Once the proximity between objects in the data set has been computed, you can determine how objects in the data set should be grouped into clusters, using the `linkage` function. The `linkage` function takes the distance information generated by `pdist` and links pairs of objects that are close together into binary clusters (clusters made up of two objects). The `linkage` function then links these newly formed clusters to each other and to other objects to create bigger clusters until all the objects in the original data set are linked together in a hierarchical tree.

For example, given the distance vector `Y` generated by `pdist` from the sample data set of *x*- and *y*-coordinates, the `linkage` function generates a hierarchical cluster tree, returning the linkage information in a matrix, `Z`.

```
Z = linkage(Y)
Z =
    4.0000    5.0000    1.0000
```

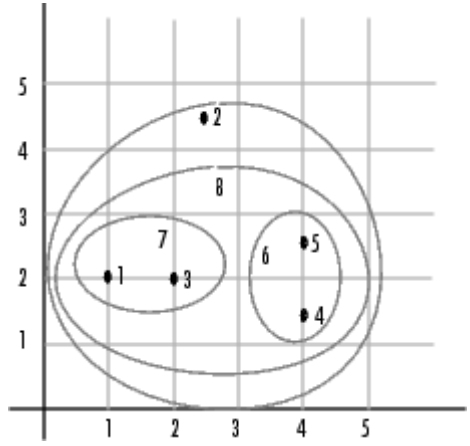
```
1.0000    3.0000    1.0000
6.0000    7.0000    2.0616
2.0000    8.0000    2.5000
```

In this output, each row identifies a link between objects or clusters. The first two columns identify the objects that have been linked. The third column contains the distance between these objects. For the sample data set of x- and y-coordinates, the `linkage` function begins by grouping objects 4 and 5, which have the closest proximity (distance value = 1.0000). The `linkage` function continues by grouping objects 1 and 3, which also have a distance value of 1.0000.

The third row indicates that the `linkage` function grouped objects 6 and 7. If the original sample data set contained only five objects, what are objects 6 and 7? Object 6 is the newly formed binary cluster created by the grouping of objects 4 and 5. When the `linkage` function groups two objects into a new cluster, it must assign the cluster a unique index value, starting with the value m+1, where m is the number of objects in the original data set. (Values 1 through m are already used by the original data set.) Similarly, object 7 is the cluster formed by grouping objects 1 and 3.

`linkage` uses distances to determine the order in which it clusters objects. The distance vector `Y` contains the distances between the original objects 1 through 5. But linkage must also be able to determine distances involving clusters that it creates, such as objects 6 and 7. By default, `linkage` uses a method known as single linkage. However, there are a number of different methods available. See the `linkage` reference page for more information.

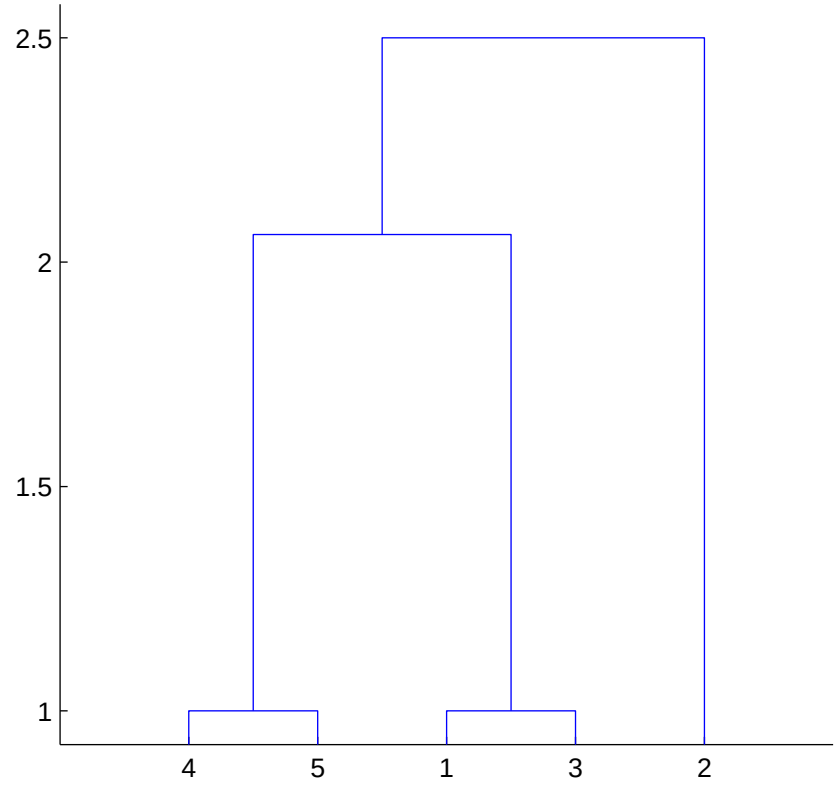
As the final cluster, the `linkage` function grouped object 8, the newly formed cluster made up of objects 6 and 7, with object 2 from the original data set. The following figure graphically illustrates the way `linkage` groups the objects into a hierarchy of clusters.



Dendrograms

The hierarchical, binary cluster tree created by the `linkage` function is most easily understood when viewed graphically. The Statistics Toolbox function `dendrogram` plots the tree, as follows:

```
dendrogram(Z)
```



In the figure, the numbers along the horizontal axis represent the indices of the objects in the original data set. The links between objects are represented as upside-down U-shaped lines. The height of the U indicates the distance between the objects. For example, the link representing the cluster containing objects 1 and 3 has a height of 1. The link representing the cluster that groups object 2 together with objects 1, 3, 4, and 5, (which are already clustered as object 8) has a height of 2.5. The height represents the distance `linkage` computes between objects 2 and 8. For more information about creating a dendrogram diagram, see the `dendrogram` reference page.

Verifying the Cluster Tree

After linking the objects in a data set into a hierarchical cluster tree, you might want to verify that the distances (that is, heights) in the tree reflect the original distances accurately. In addition, you might want to investigate natural divisions that exist among links between objects. Statistics Toolbox functions are available for both of these tasks, as described in the following sections:

- "Verifying Dissimilarity" on page 11-10
- "Verifying Consistency" on page 11-11

Verifying Dissimilarity

In a hierarchical cluster tree, any two objects in the original data set are eventually linked together at some level. The height of the link represents the distance between the two clusters that contain those two objects. This height is known as the *cophenetic distance* between the two objects. One way to measure how well the cluster tree generated by the `linkage` function reflects your data is to compare the cophenetic distances with the original distance data generated by the `pdist` function. If the clustering is valid, the linking of objects in the cluster tree should have a strong correlation with the distances between objects in the distance vector. The `cophenet` function compares these two sets of values and computes their correlation, returning a value called the *cophenetic correlation coefficient*. The closer the value of the cophenetic correlation coefficient is to 1, the more accurately the clustering solution reflects your data.

You can use the cophenetic correlation coefficient to compare the results of clustering the same data set using different distance calculation methods or clustering algorithms. For example, you can use the `cophenet` function to evaluate the clusters created for the sample data set

```
c = cophenet(Z,Y)
c =
    0.8615
```

where `Z` is the matrix output by the `linkage` function and `Y` is the distance vector output by the `pdist` function.

Execute `pdist` again on the same data set, this time specifying the city block metric. After running the `linkage` function on this new `pdist` output using the average linkage method, call `cophenet` to evaluate the clustering solution.

```
Y = pdist(X,'cityblock');
Z = linkage(Y,'average');
c = cophenet(Z,Y)
c =
    0.9047
```

The cophenetic correlation coefficient shows that using a different distance and linkage method creates a tree that represents the original distances slightly better.

Verifying Consistency

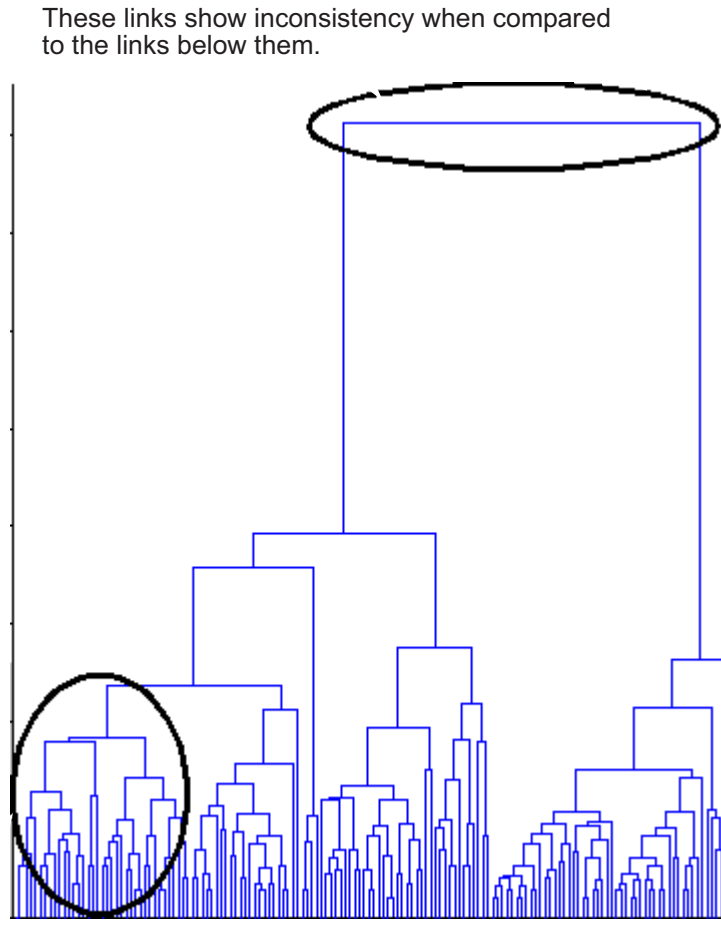
One way to determine the natural cluster divisions in a data set is to compare the height of each link in a cluster tree with the heights of neighboring links below it in the tree.

A link that is approximately the same height as the links below it indicates that there are no distinct divisions between the objects joined at this level of the hierarchy. These links are said to exhibit a high level of consistency, because the distance between the objects being joined is approximately the same as the distances between the objects they contain.

On the other hand, a link whose height differs noticeably from the height of the links below it indicates that the objects joined at this level in the cluster tree are much farther apart from each other than their components were when they were joined. This link is said to be inconsistent with the links below it.

In cluster analysis, inconsistent links can indicate the border of a natural division in a data set. The `cluster` function uses a quantitative measure of inconsistency to determine where to partition your data set into clusters.

The following dendrogram illustrates inconsistent links. Note how the objects in the dendrogram fall into two groups that are connected by links at a much higher level in the tree. These links are inconsistent when compared with the links below them in the hierarchy.



The relative consistency of each link in a hierarchical cluster tree can be quantified and expressed as the *inconsistency coefficient*. This value compares the height of a link in a cluster hierarchy with the average height of links below it. Links that join distinct clusters have a high inconsistency coefficient; links that join indistinct clusters have a low inconsistency coefficient.

To generate a listing of the inconsistency coefficient for each link in the cluster tree, use the `inconsistent` function. By default, the `inconsistent`

function compares each link in the cluster hierarchy with adjacent links that are less than two levels below it in the cluster hierarchy. This is called the *depth* of the comparison. You can also specify other depths. The objects at the bottom of the cluster tree, called leaf nodes, that have no further objects below them, have an inconsistency coefficient of zero. Clusters that join two leaves also have a zero inconsistency coefficient.

For example, you can use the `inconsistent` function to calculate the inconsistency values for the links created by the `linkage` function in "Linkages" on page 11-6.

```
I = inconsistent(Z)
I =
    1.0000         0    1.0000         0
    1.0000         0    1.0000         0
    1.3539    0.6129    3.0000    1.1547
    2.2808    0.3100    2.0000    0.7071
```

The `inconsistent` function returns data about the links in an (m-1)-by-4 matrix, whose columns are described in the following table.

Column	Description
1	Mean of the heights of all the links included in the calculation
2	Standard deviation of all the links included in the calculation
3	Number of links included in the calculation
4	Inconsistency coefficient

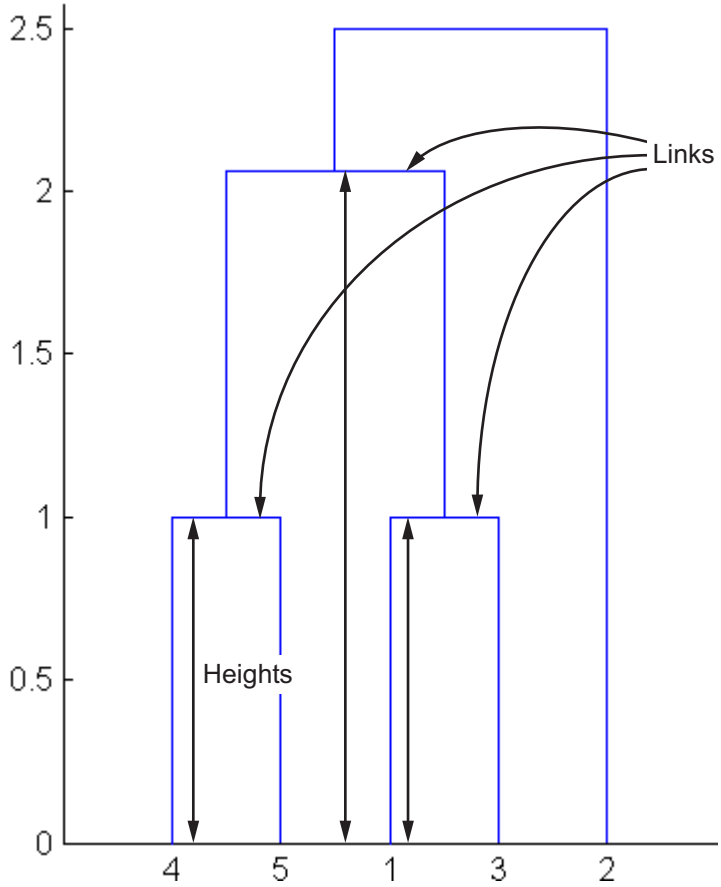
In the sample output, the first row represents the link between objects 4 and 5. This cluster is assigned the index 6 by the `linkage` function. Because both 4 and 5 are leaf nodes, the inconsistency coefficient for the cluster is zero. The second row represents the link between objects 1 and 3, both of which are also leaf nodes. This cluster is assigned the index 7 by the linkage function.

The third row evaluates the link that connects these two clusters, objects 6 and 7. (This new cluster is assigned index 8 in the `linkage` output). Column 3 indicates that three links are considered in the calculation: the link itself and the two links directly below it in the hierarchy. Column 1 represents the mean of the heights of these links. The `inconsistent` function uses the height

information output by the `linkage` function to calculate the mean. Column 2 represents the standard deviation between the links. The last column contains the inconsistency value for these links, 1.1547. It is the difference between the current link height and the mean, normalized by the standard deviation:

```
(2.0616 - 1.3539) / .6129
ans =
    1.1547
```

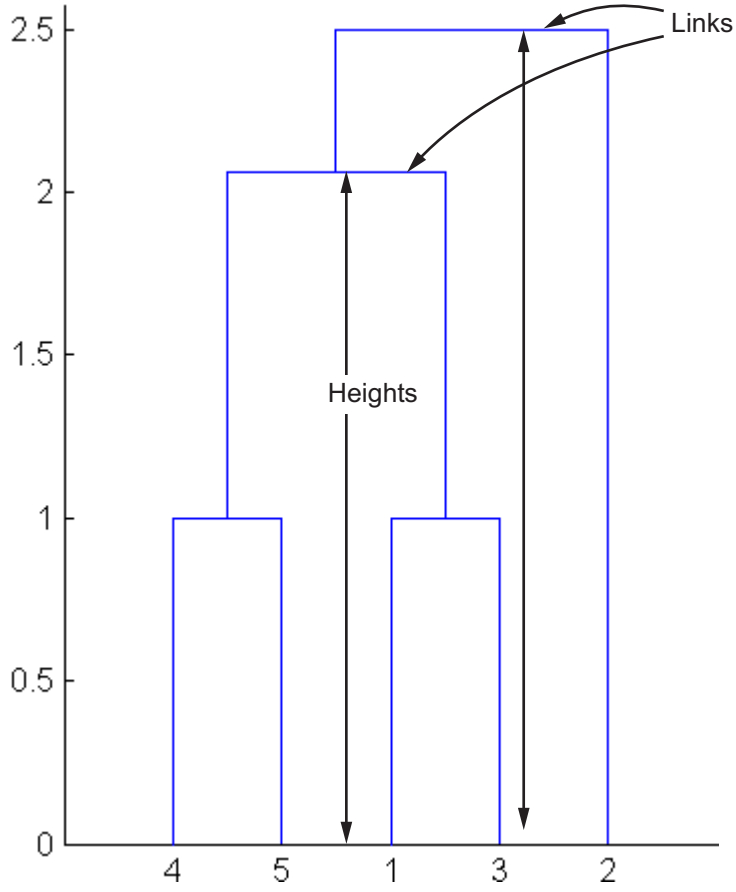
The following figure illustrates the links and heights included in this calculation.



Note In the preceding figure, the lower limit on the *y*-axis is set to `0` to show the heights of the links. To set the lower limit to `0`, select `Axes Properties` from the **Edit** menu, click the **Y Axis** tab, and enter `0` in the field immediately to the right of **Y Limits**.

Row 4 in the output matrix describes the link between object 8 and object 2. Column 3 indicates that two links are included in this calculation: the link itself and the link directly below it in the hierarchy. The inconsistency coefficient for this link is 0.7071.

The following figure illustrates the links and heights included in this calculation.



Creating Clusters

After you create the hierarchical tree of binary clusters, you can prune the tree to partition your data into clusters using the `cluster` function. The `cluster` function lets you create clusters in two ways, as discussed in the following sections:

- "Finding Natural Divisions in Data" on page 11-17
- "Specifying Arbitrary Clusters" on page 11-18

Finding Natural Divisions in Data

The hierarchical cluster tree may naturally divide the data into distinct, well-separated clusters. This can be particularly evident in a dendrogram diagram created from data where groups of objects are densely packed in certain areas and not in others. The inconsistency coefficient of the links in the cluster tree can identify these divisions where the similarities between objects change abruptly. (See "Verifying the Cluster Tree" on page 11-10 for more information about the inconsistency coefficient.) You can use this value to determine where the `cluster` function creates cluster boundaries.

For example, if you use the `cluster` function to group the sample data set into clusters, specifying an inconsistency coefficient threshold of `1.2` as the value of the `cutoff` argument, the `cluster` function groups all the objects in the sample data set into one cluster. In this case, none of the links in the cluster hierarchy had an inconsistency coefficient greater than `1.2`.

```
T = cluster(Z,'cutoff',1.2)
T =
     1
     1
     1
     1
     1
```

The `cluster` function outputs a vector, `T`, that is the same size as the original data set. Each element in this vector contains the number of the cluster into which the corresponding object from the original data set was placed.

If you lower the inconsistency coefficient threshold to `0.8`, the `cluster` function divides the sample data set into three separate clusters.

```
T = cluster(Z,'cutoff',0.8)
T =
    3
    2
    3
    1
    1
```

This output indicates that objects 1 and 3 were placed in cluster 1, objects 4 and 5 were placed in cluster 2, and object 2 was placed in cluster 3.

When clusters are formed in this way, the cutoff value is applied to the inconsistency coefficient. These clusters may, but do not necessarily, correspond to a horizontal slice across the dendrogram at a certain height. If you want clusters corresponding to a horizontal slice of the dendrogram, you can either use the `criterion` option to specify that the cutoff should be based on distance rather than inconsistency, or you can specify the number of clusters directly as described in the following section.

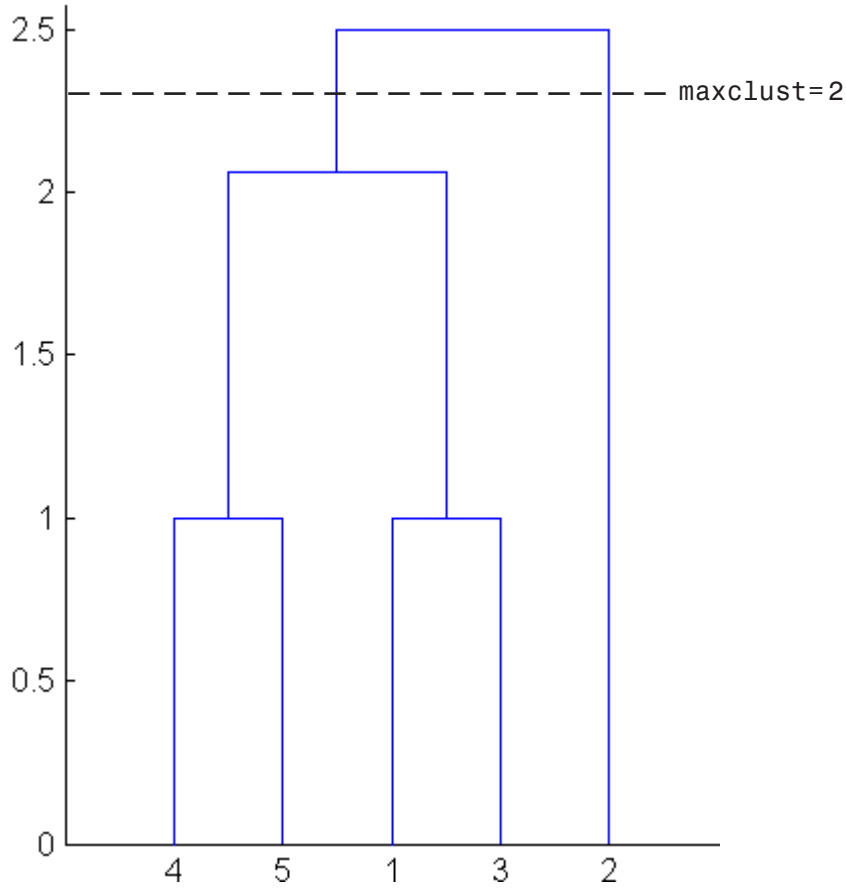
Specifying Arbitrary Clusters

Instead of letting the `cluster` function create clusters determined by the natural divisions in the data set, you can specify the number of clusters you want created.

For example, you can specify that you want the `cluster` function to partition the sample data set into two clusters. In this case, the `cluster` function creates one cluster containing objects 1, 3, 4, and 5 and another cluster containing object 2.

```
T = cluster(Z,'maxclust',2)
T =
     2
     1
     2
     2
     2
```

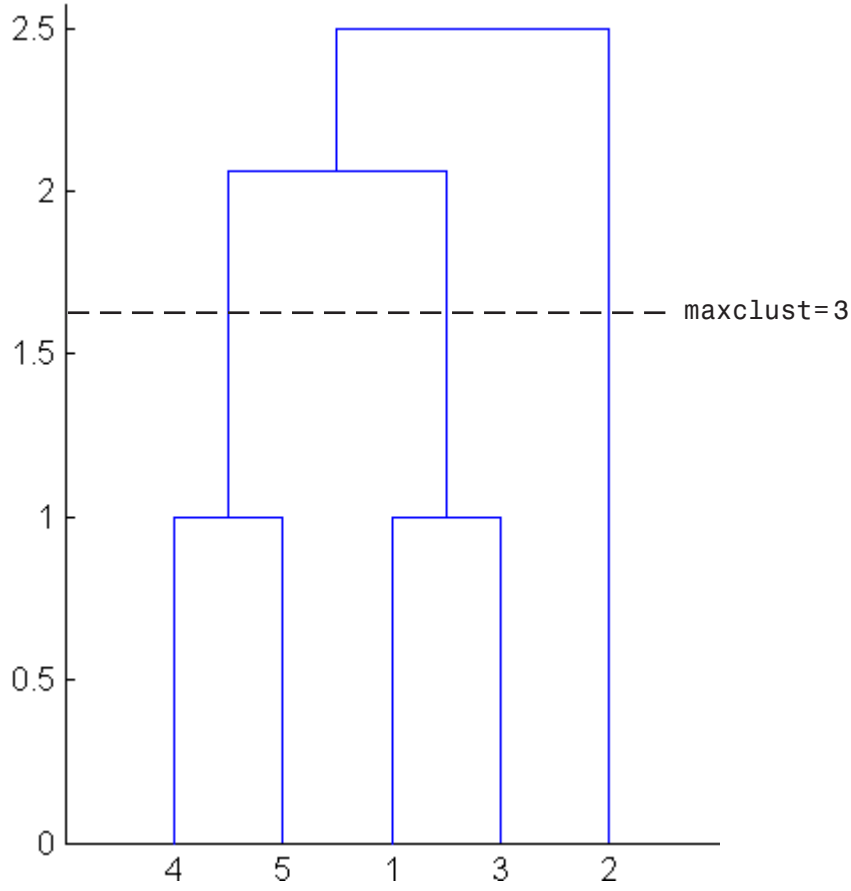
To help you visualize how the `cluster` function determines these clusters, the following figure shows the dendrogram of the hierarchical cluster tree. The horizontal dashed line intersects two lines of the dendrogram, corresponding to setting `'maxclust'` to `2`. These two lines partition the objects into two clusters: the objects below the left-hand line, namely 1, 3, 4, and 5, belong to one cluster, while the object below the right-hand line, namely 2, belongs to the other cluster.



On the other hand, if you set `'maxclust'` to `3`, the cluster function groups objects 4 and 5 in one cluster, objects 1 and 3 in a second cluster, and object 2 in a third cluster. The following command illustrates this.

```
T = cluster(Z,'maxclust',3)
T =
     1
     3
     1
     2
     2
```

This time, the `cluster` function cuts off the hierarchy at a lower point, corresponding to the horizontal line that intersects three lines of the dendrogram in the following figure.



K-Means Clustering

In this section...

Introduction to K-Means Clustering

K-means clustering is a partitioning method. The function `kmeans` partitions data into *k* mutually exclusive clusters, and returns the index of the cluster to which it has assigned each observation. Unlike hierarchical clustering, *k*-means clustering operates on actual observations (rather than the larger set of dissimilarity measures), and creates a single level of clusters. The distinctions mean that *k*-means clustering is often more suitable than hierarchical clustering for large amounts of data.

`kmeans` treats each observation in your data as an object having a location in space. It finds a partition in which objects within each cluster are as close to each other as possible, and as far from objects in other clusters as possible. You can choose from five different distance measures, depending on the kind of data you are clustering.

Each cluster in the partition is defined by its member objects and by its centroid, or center. The centroid for each cluster is the point to which the sum of distances from all objects in that cluster is minimized. `kmeans` computes cluster centroids differently for each distance measure, to minimize the sum with respect to the measure that you specify.

`kmeans` uses an iterative algorithm that minimizes the sum of distances from each object to its cluster centroid, over all clusters. This algorithm moves objects between clusters until the sum cannot be decreased further. The result is a set of clusters that are as compact and well-separated as possible. You can control the details of the minimization using several optional input parameters to `kmeans`, including ones for the initial values of the cluster centroids, and for the maximum number of iterations.

Creating Clusters and Determining Separation

The following example explores possible clustering in four-dimensional data by analyzing the results of partitioning the points into three, four, and five clusters.

Note Because each part of this example generates random numbers sequentially, i.e., without setting a new state, you must perform all steps in sequence to duplicate the results shown. If you perform the steps out of sequence, the answers will be essentially the same, but the intermediate results, number of iterations, or ordering of the silhouette plots may differ.

First, load some data:

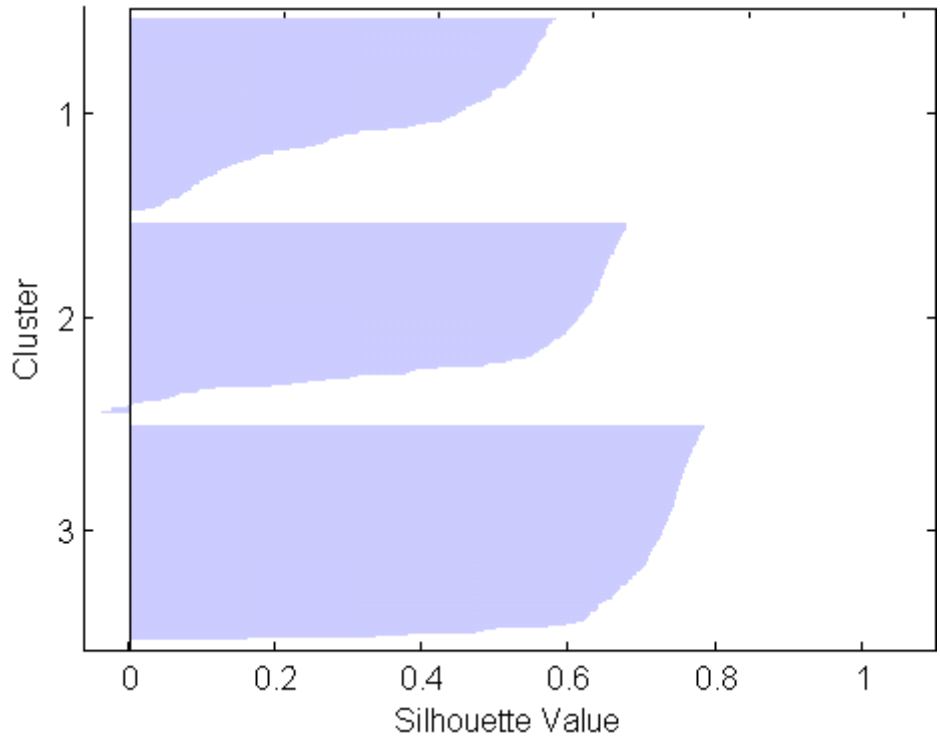
```
load kmeansdata;
size(X)
ans =
   560     4
```

Even though these data are four-dimensional, and cannot be easily visualized, `kmeans` enables you to investigate whether a group structure exists in them. Call `kmeans` with `k`, the desired number of clusters, equal to `3`. For this example, specify the city block distance measure, and use the default starting method of initializing centroids from randomly selected data points:

```
idx3 = kmeans(X,3,'distance','city');
```

To get an idea of how well-separated the resulting clusters are, you can make a silhouette plot using the cluster indices output from `kmeans`. The silhouette plot displays a measure of how close each point in one cluster is to points in the neighboring clusters. This measure ranges from +1, indicating points that are very distant from neighboring clusters, through 0, indicating points that are not distinctly in one cluster or another, to -1, indicating points that are probably assigned to the wrong cluster. `silhouette` returns these values in its first output:

```
[silh3,h] = silhouette(X,idx3,'city');
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
xlabel('Silhouette Value')
ylabel('Cluster')
```



From the silhouette plot, you can see that most points in the third cluster have a large silhouette value, greater than 0.6, indicating that the cluster is somewhat separated from neighboring clusters. However, the first cluster contains many points with low silhouette values, and the second contains a few points with negative values, indicating that those two clusters are not well separated.

Determining the Correct Number of Clusters

Increase the number of clusters to see if `kmeans` can find a better grouping of the data. This time, use the optional `'display'` parameter to print information about each iteration:

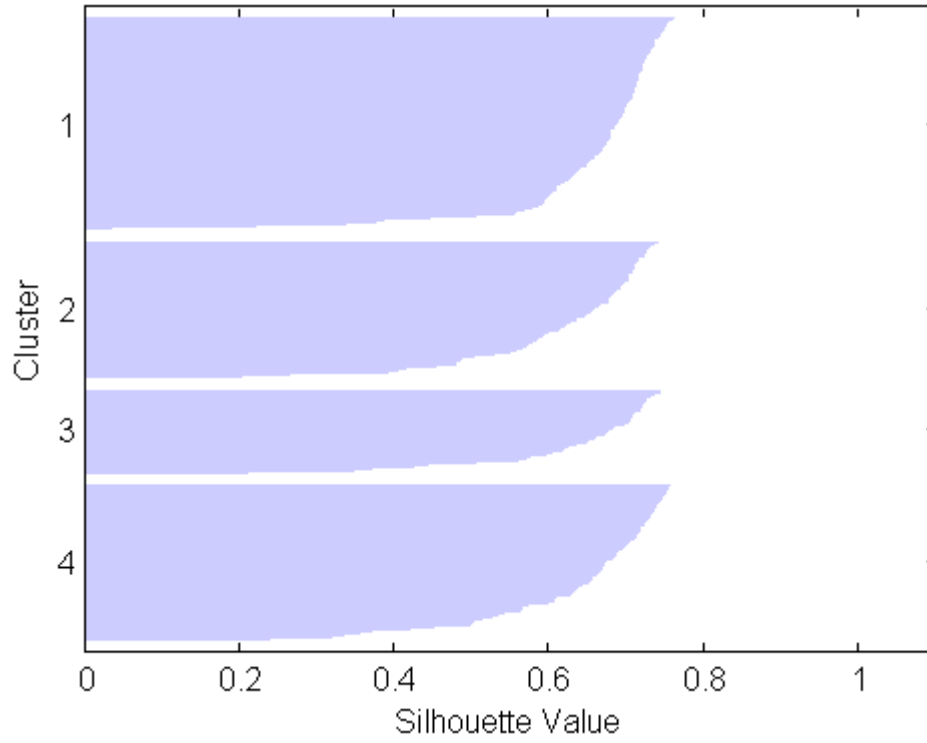
```
idx4 = kmeans(X,4, 'dist','city', 'display','iter');
  iter  phase      num          sum
     1      1      560      2897.56
```

```
     2      1       53      2736.67
     3      1       50      2476.78
     4      1      102      1779.68
     5      1        5       1771.1
     6      2        0       1771.1
6 iterations, total sum of distances = 1771.1
```

Notice that the total sum of distances decreases at each iteration as `kmeans` reassigns points between clusters and recomputes cluster centroids. In this case, the second phase of the algorithm did not make any reassignments, indicating that the first phase reached a minimum after five iterations. In some problems, the first phase might not reach a minimum, but the second phase always will.

A silhouette plot for this solution indicates that these four clusters are better separated than the three in the previous solution:

```
[silh4,h] = silhouette(X,idx4,'city');
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
xlabel('Silhouette Value')
ylabel('Cluster')
```



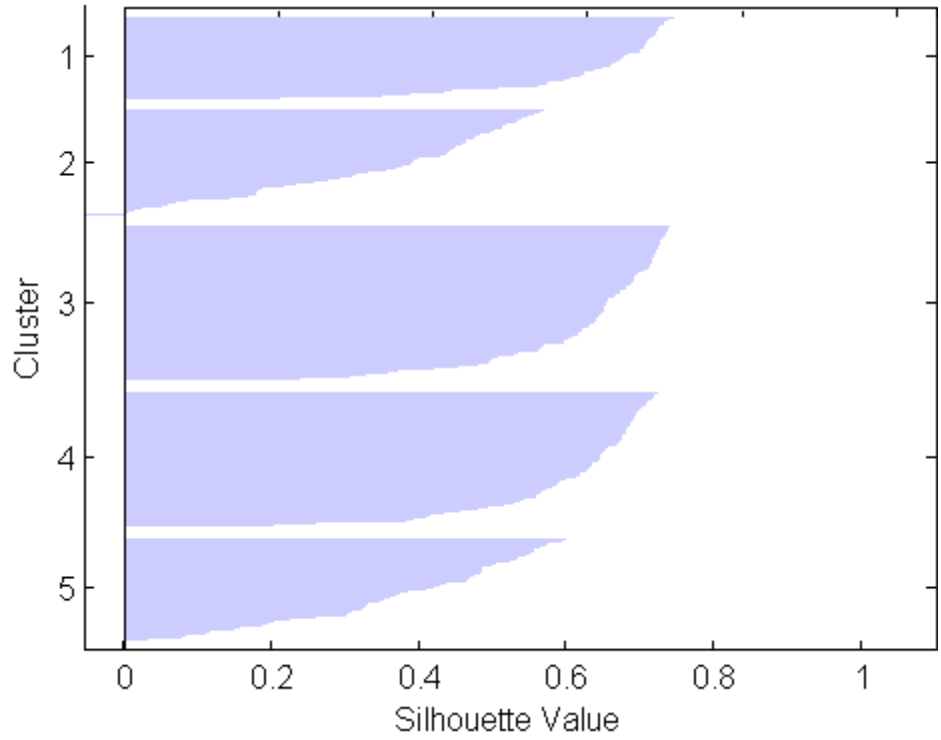
A more quantitative way to compare the two solutions is to look at the average silhouette values for the two cases:

```
mean(silh3)
ans =
      0.52594
mean(silh4)
ans =
      0.63997
```

Finally, try clustering the data using five clusters:

```
idx5 = kmeans(X,5,'dist','city','replicates',5);
[silh5,h] = silhouette(X,idx5,'city');
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
xlabel('Silhouette Value')
```

```
ylabel('Cluster')
mean(silh5)
ans =
      0.52657
```



This silhouette plot indicates that this is probably not the right number of clusters, since two of the clusters contain points with mostly low silhouette values. Without some knowledge of how many clusters are really in the data, it is a good idea to experiment with a range of values for `k`.

Avoiding Local Minima

Like many other types of numerical minimizations, the solution that `kmeans` reaches often depends on the starting points. It is possible for `kmeans` to reach a local minimum, where reassigning any one point to a new cluster would increase the total sum of point-to-centroid distances, but where a

better solution does exist. However, you can use the optional `'replicates'` parameter to overcome that problem.

For four clusters, specify five replicates, and use the `'display'` parameter to print out the final sum of distances for each of the solutions.

```
[idx4,cent4,sumdist] = kmeans(X,4,'dist','city',...
                      'display','final','replicates',5);
17 iterations, total sum of distances = 2303.36
 5 iterations, total sum of distances = 1771.1
 6 iterations, total sum of distances = 1771.1
 5 iterations, total sum of distances = 1771.1
 8 iterations, total sum of distances = 2303.36
```

The output shows that, even for this relatively simple problem, non-global minima do exist. Each of these five replicates began from a different randomly selected set of initial centroids, and `kmeans` found two different local minima. However, the final solution that `kmeans` returns is the one with the lowest total sum of distances, over all replicates.

```
sum(sumdist)
ans =
       1771.1
```

Gaussian Mixture Models

In this section...

Introduction to Gaussian Mixture Models

Gaussian mixture models are formed by combining multivariate normal density components. For information on individual multivariate normal densities, see "Multivariate Normal Distribution" on page B-58 and related distribution functions listed under "Multivariate Distributions" on page 5-8.

In Statistics Toolbox software, use the `gmdistribution` class to fit data using an expectation maximization (EM) algorithm, which assigns posterior probabilities to each component density with respect to each observation.

Gaussian mixture models are often used for data clustering. Clusters are assigned by selecting the component that maximizes the posterior probability. Like *k*-means clustering, Gaussian mixture modeling uses an iterative algorithm that converges to a local optimum. Gaussian mixture modeling may be more appropriate than *k*-means clustering when clusters have different sizes and correlation within them. Clustering using Gaussian mixture models is sometimes considered a soft clustering method. The posterior probabilities for each point indicate that each data point has some probability of belonging to each cluster.

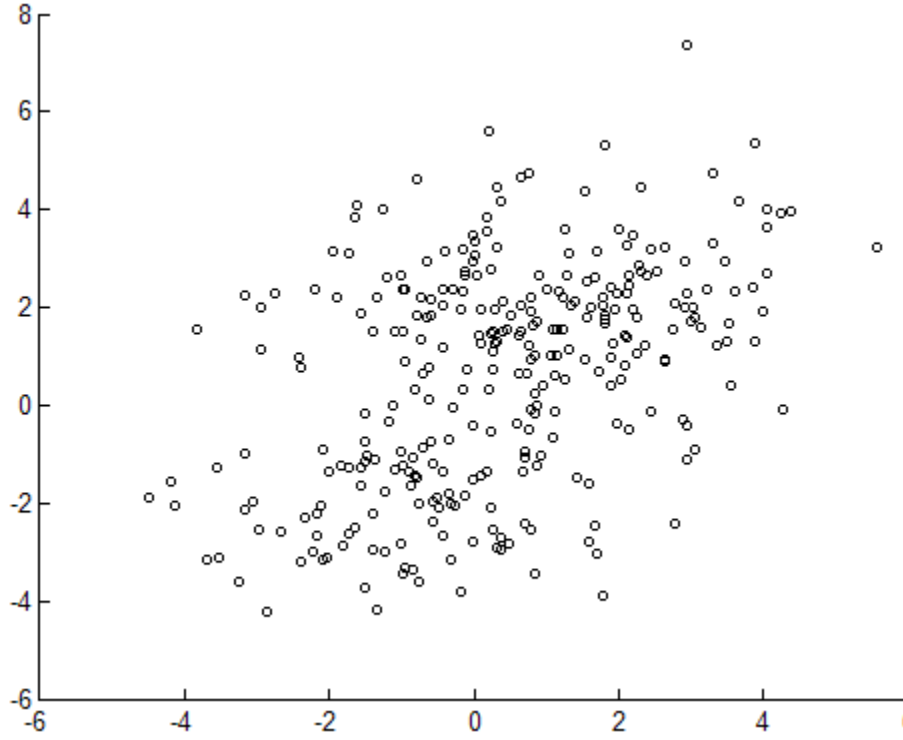
Creation of Gaussian mixture models is described in the "Gaussian Mixture Models" on page 5-99 section of Chapter 5, "Probability Distributions". This section describes their application in cluster analysis.

Clustering with Gaussian Mixtures

Gaussian mixture distributions can be used for clustering data, by realizing that the multivariate normal components of the fitted model can represent clusters.

1 To demonstrate the process, first generate some simulated data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function:

```
mu1 = [1 2];
sigma1 = [3 .2; .2 2];
mu2 = [-1 -2];
sigma2 = [2 0; 0 1];
X = [mvnrnd(mu1,sigma1,200);mvnrnd(mu2,sigma2,100)];

scatter(X(:,1),X(:,2),10,'ko')
```



2 Fit a two-component Gaussian mixture distribution. Here, you know the correct number of components to use. In practice, with real data, this decision would require comparing models with different numbers of components.

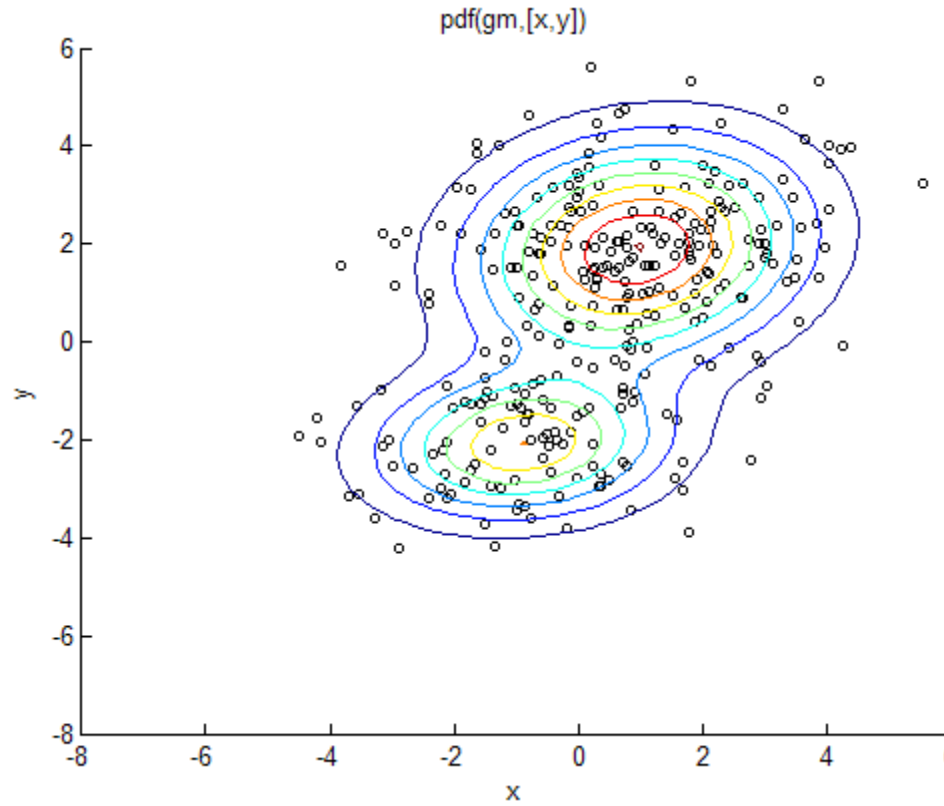
```
options = statset('Display','final');
gm = gmdistribution.fit(X,2,'Options',options);
```

This displays

```
 49 iterations, log-likelihood = -1207.91
```

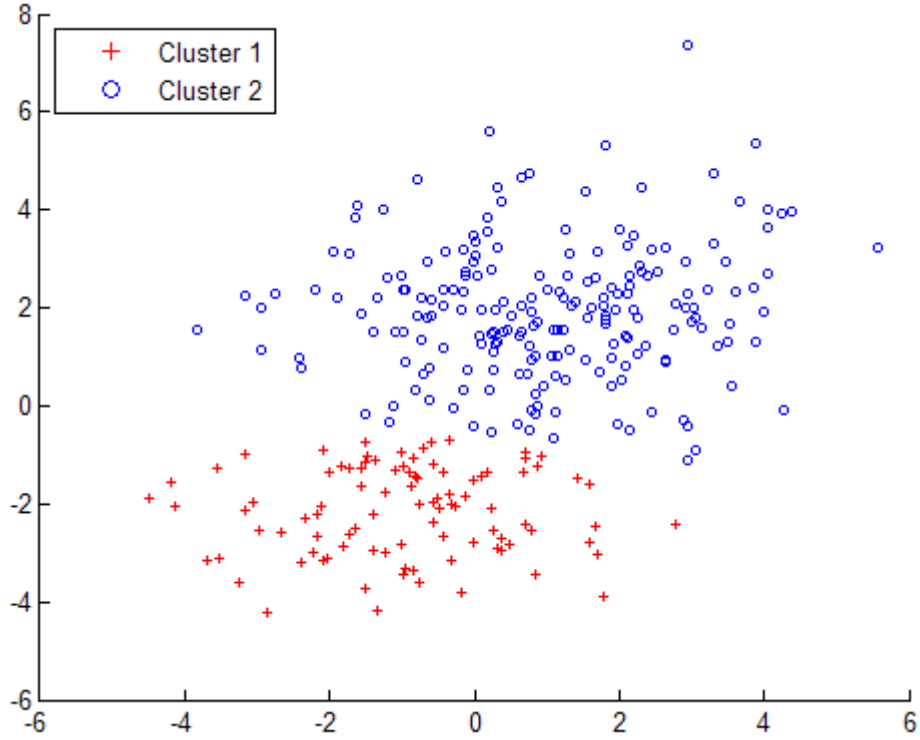
3 Plot the estimated probability density contours for the two-component mixture distribution. The two bivariate normal components overlap, but their peaks are distinct. This suggests that the data could reasonably be divided into two clusters:

```
hold on
ezcontour(@(x,y)pdf(gm,[x y]),[-8 6],[-8 6]);
hold off
```



4 Partition the data into clusters using the `cluster` method for the fitted mixture distribution. The `cluster` method assigns each point to one of the two components in the mixture distribution.

```
idx = cluster(gm,X);
cluster1 = (idx == 1);
cluster2 = (idx == 2);

scatter(X(cluster1,1),X(cluster1,2),10,'r+');
hold on
scatter(X(cluster2,1),X(cluster2,2),10,'bo');
hold off
legend('Cluster 1','Cluster 2','Location','NW')
```

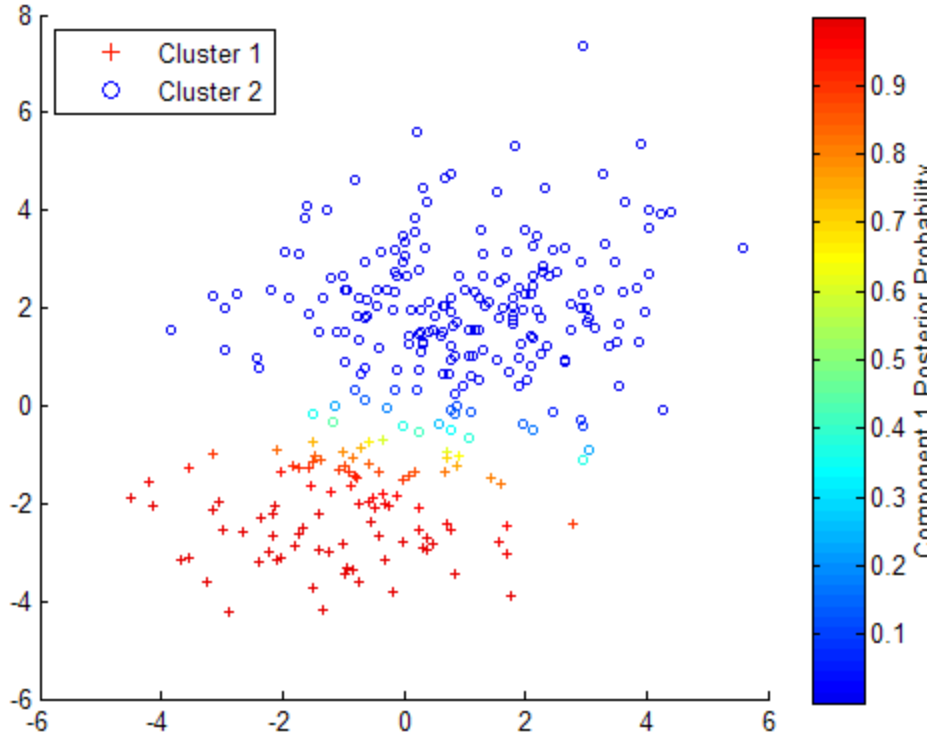


Each cluster corresponds to one of the bivariate normal components in the mixture distribution. `cluster` assigns points to clusters based on the estimated posterior probability that a point came from a component; each point is assigned to the cluster corresponding to the highest posterior probability. The posterior method returns those `posterior` probabilities.

For example, plot the posterior probability of the first component for each point:

```
P = posterior(gm,X);

scatter(X(cluster1,1),X(cluster1,2),10,P(cluster1,1),'+')
hold on
scatter(X(cluster2,1),X(cluster2,2),10,P(cluster2,1),'o')
hold off
legend('Cluster 1','Cluster 2','Location','NW')
clrmap = jet(80); colormap(clrmap(9:72,:))
```

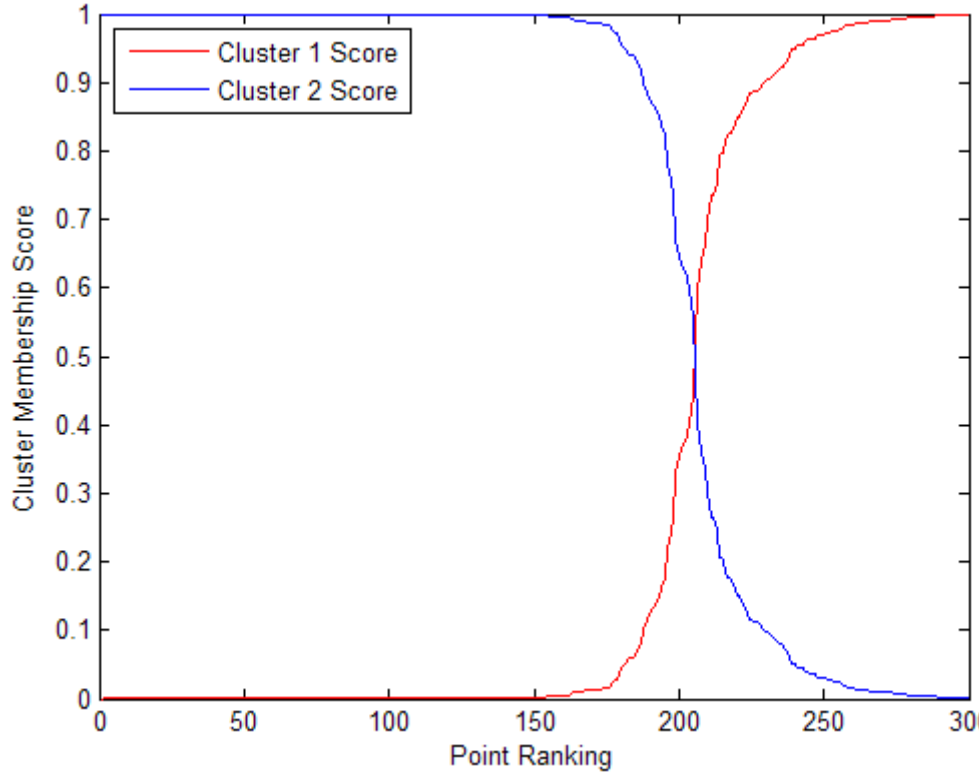
```
ylabel(colorbar,'Component 1 Posterior Probability')
```



Soft Clustering Using Gaussian Mixture Distributions

An alternative to the previous example is to use the posterior probabilities for "soft clustering". Each point is assigned a membership score to each cluster. Membership scores are simply the posterior probabilities, and describe how similar each point is to each cluster's archetype, i.e., the mean of the corresponding component. The points can be ranked by their membership score in a given cluster:

```
[~,order] = sort(P(:,1));
plot(1:size(X,1),P(order,1),'r-',1:size(X,1),P(order,2),'b-');
legend({'Cluster 1 Score' 'Cluster 2 Score'},'location','NW');
ylabel('Cluster Membership Score');
xlabel('Point Ranking');
```



Although a clear separation of the data is hard to see in a scatter plot of the data, plotting the membership scores indicates that the fitted distribution does a good job of separating the data into groups. Very few points have scores close to 0.5.

Soft clustering using a Gaussian mixture distribution is similar to fuzzy K-means clustering, which also assigns each point to each cluster with a membership score. The fuzzy K-means algorithm assumes that clusters are roughly spherical in shape, and all of roughly equal size. This is comparable to a Gaussian mixture distribution with a single covariance matrix that is shared across all components, and is a multiple of the identity matrix. In contrast, `gmdistribution` allows you to specify different covariance options. The default is to estimate a separate, unconstrained covariance matrix for

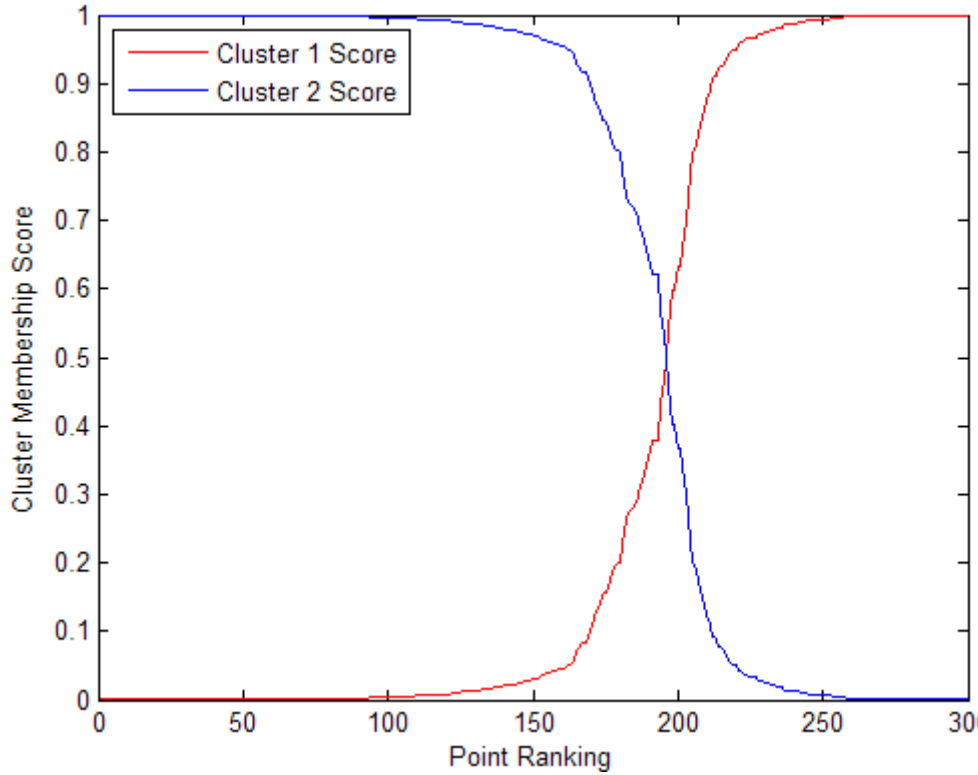
each component. A more restricted option, closer to K-means, would be to estimate a shared, diagonal covariance matrix:

```
gm2 = gmdistribution.fit(X,2,'CovType','Diagonal',...
  'SharedCov',true);
```

This covariance option is similar to fuzzy K-means clustering, but provides more flexibility by allowing unequal variances for different variables.

You can compute the soft cluster membership scores without computing hard cluster assignments, using `posterior`, or as part of hard clustering, as the second output from `cluster`:

```
P2 = posterior(gm2,X); % equivalently [idx,P2] = cluster(gm2,X)
[~,order] = sort(P2(:,1));
plot(1:size(X,1),P2(order,1),'r-',1:size(X,1),P2(order,2),'b-');
legend({'Cluster 1 Score' 'Cluster 2 Score'},'location','NW');
ylabel('Cluster Membership Score');
xlabel('Point Ranking');
```



Assigning New Data to Clusters

In the previous example, fitting the mixture distribution to data using `fit`, and clustering those data using `cluster`, are separate steps. However, the same data are used in both steps. You can also use the `cluster` method to assign new data points to the clusters (mixture components) found in the original data.

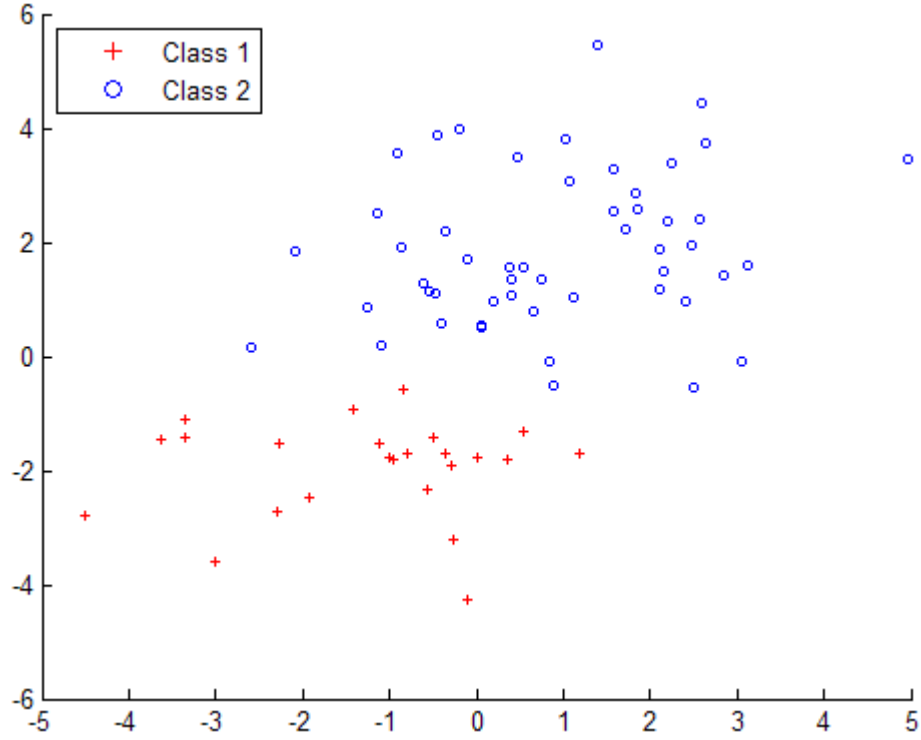
1. Given a data set `X`, first fit a Gaussian mixture distribution. The previous code has already done that.

```
gm

gm =
Gaussian mixture distribution with 2 components in 2 dimensions
```

```
Component 1:
Mixing proportion: 0.312592
Mean:    -0.9082   -2.1109

Component 2:
Mixing proportion: 0.687408
Mean:     0.9532    1.8940
```

2 You can then use `cluster` to assign each point in a new data set, `Y`, to one of the clusters defined for the original data:

```
Y = [mvnrnd(mu1,sigma1,50);mvnrnd(mu2,sigma2,25)];

idx = cluster(gm,Y);
cluster1 = (idx == 1);
cluster2 = (idx == 2);

scatter(Y(cluster1,1),Y(cluster1,2),10,'r+');
hold on
scatter(Y(cluster2,1),Y(cluster2,2),10,'bo');
hold off
legend('Class 1','Class 2','Location','NW')
```



As with the previous example, the posterior probabilities for each point can be treated as membership scores rather than determining "hard" cluster assignments.

For `cluster` to provide meaningful results with new data, `Y` should come from the same population as `X`, the original data used to create the mixture distribution. In particular, the estimated mixing probabilities for the Gaussian mixture distribution fitted to `X` are used when computing the posterior probabilities for `Y`.

12

Parametric Classification

Introduction to Parametric Classification

Models of data with a categorical response are called *classifiers*. A classifier is built from *training data*, for which classifications are known. The classifier assigns new *test data* to one of the categorical levels of the response.

Parametric methods, like "Discriminant Analysis" on page 12-3, fit a parametric model to the training data and interpolate to classify test data.

Nonparametric methods, like "Classification Trees and Regression Trees" on page 13-27, use other means to determine classifications. In this sense, classification methods are analogous to the methods discussed in "Nonlinear Regression" on page 9-72.

Discriminant Analysis

In this section...

About Discriminant Analysis

Discriminant analysis is a classification method. It assumes that different classes generate data based on different Gaussian distributions.

- To train (create) a classifier, the fitting function estimates the parameters of a Gaussian distribution for each class (see "How the ClassificationDiscriminant.fit Method Creates a Classifier" on page 12-4).
- To predict the classes of new data, the trained classifier by default finds the class with the largest posterior probability (see "How the predict Method Classifies" on page 12-6).

To learn how to prepare your data for discriminant analysis and create a classifier, see "Steps in Supervised Learning (Machine Learning)" on page 13-2.

Example: Create Discriminant Analysis Classifiers

To create the basic types of discriminant analysis classifiers for the Fisher iris data:

1 Load the data:

```
load fisheriris;
```

2 Create a default (linear) discriminant analysis classifier:

```
linclass = ClassificationDiscriminant.fit(meas,species);
```

To visualize the classification boundaries of a 2-D linear classification of the data, see Linear Discriminant Classification — Fisher Training Data on page 12-12.

3 Classify an iris with average measurements:

```
meanmeas = mean(meas);
meanclass = predict(linclass,meanmeas)

meanclass =
    'versicolor'
```

4 Create a quadratic classifier:

```
quadclass = ClassificationDiscriminant.fit(meas,species,...
    'discrimType','quadratic');
```

To visualize the classification boundaries of a 2-D quadratic classification of the data, see Quadratic Discriminant Classification — Fisher Training Data on page 12-14.

5 Classify an iris with average measurements using the quadratic classifier:

```
meanclass2 = predict(quadclass,meanmeas)

meanclass2 =
    'versicolor'
```

How the ClassificationDiscriminant.fit Method Creates a Classifier

The model for discriminant analysis is:

- Each class (`Y`) generates data (`X`) using a multivariate normal distribution. In other words, the model assumes `X` has a Gaussian mixture distribution (`gmdistribution`).
  - For linear discriminant analysis, the model has the same covariance matrix for each class; only the means vary.
  - For quadratic discriminant analysis, both means and covariances of each class vary.

Under this modeling assumption, `ClassificationDiscriminant.fit` infers the mean and covariance parameters of each class.

- For linear discriminant analysis, it computes the sample mean of each class. Then it computes the sample covariance by first subtracting the sample mean of each class from the observations of that class, and taking the empirical covariance matrix of the result.
- For quadratic discriminant analysis, it computes the sample mean of each class. Then it computes the sample covariances by first subtracting the sample mean of each class from the observations of that class, and taking the empirical covariance matrix of each class.

The `fit` method does not use prior probabilities or costs for fitting.

Weighted Observations

The `fit` method constructs weighted classifiers using the following scheme. Suppose M is an N-by-K class membership matrix:

$M_{nk} = 1$ if observation n is from class k
$M_{nk} = 0$ otherwise.

The estimate of the class mean for unweighted data is

$$\hat{\mu}_k = \frac{\sum_{n=1}^{N} M_{nk} x_n}{\sum_{n=1}^{N} M_{nk}}.$$

For weighted data with positive weights w_n, the natural generalization is

$$\hat{\mu}_k = \frac{\sum_{n=1}^{N} M_{nk} w_n x_n}{\sum_{n=1}^{N} M_{nk} w_n}.$$

The unbiased estimate of the pooled-in covariance matrix for unweighted data is

$$\hat{\Sigma} = \frac{\sum_{n=1}^{N}\sum_{k=1}^{K} M_{nk}\left(x_n - \hat{\mu}_k\right)\left(x_n - \hat{\mu}_k\right)^T}{N - K}.$$

For quadratic discriminant analysis, the `fit` method uses $K = 1$.

For weighted data, assuming the weights sum to 1, the unbiased estimate of the pooled-in covariance matrix is

$$\hat{\Sigma} = \frac{\sum_{n=1}^{N}\sum_{k=1}^{K} M_{nk} w_n \left(x_n - \hat{\mu}_k\right)\left(x_n - \hat{\mu}_k\right)^T}{1 - \sum_{k=1}^{K} \frac{W_k^{(2)}}{W_k}},$$

where

- $W_k = \sum_{n=1}^{N} M_{nk} w_n$ is the sum of the weights for class k.
- $W_k^{(2)} = \sum_{n=1}^{N} M_{nk} w_n^2$ is the sum of squared weights per class.

How the predict Method Classifies

There are three elements in the `predict` classification algorithm:

- "Posterior Probability" on page 12-7
- "Prior Probability" on page 12-8
- "Cost" on page 12-8

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \arg\min_{y=1,\ldots,K} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

The space of `X` values divides into regions where a classification `Y` is a particular value. The regions are separated by straight lines for linear discriminant analysis, and by conic sections (ellipses, hyperbolas, or parabolas) for quadratic discriminant analysis. For a visualization of these regions, see "Example: Creating and Visualizing a Discriminant Analysis Classifier" on page 12-9.

Posterior Probability

The posterior probability that a point x belongs to class k is the product of the prior probability and the multivariate normal density. The density function of the multivariate normal with mean μ_k and covariance Σ_k at a point x is

$$P(x \mid k) = \frac{1}{\left(2\pi |\Sigma_k|\right)^{1/2}} \exp\left(-\frac{1}{2} (x - \mu_k)^T \Sigma_k^{-1} (x - \mu_k) \right),$$

where $|\Sigma_k|$ is the determinant of Σ_k, and Σ_k^{-1} is the inverse matrix.

Let $P(k)$ represent the prior probability of class k. Then the posterior probability that an observation x is of class k is

$$\hat{P}(k \mid x) = \frac{P(x \mid k) P(k)}{P(x)},$$

where $P(x)$ is a normalization constant, namely, the sum over k of $P(x|k)P(k)$.

Prior Probability

The prior probability is one of three choices:

- `'uniform'` — The prior probability of class `k` is 1 over the total number of classes.
- `'empirical'` — The prior probability of class `k` is the number of training samples of class `k` divided by the total number of training samples.
- A numeric vector — The prior probability of class `k` is the `j`th element of the `prior` vector. See `ClassificationDiscriminant.fit`.

After creating a classifier `obj`, you can set the prior using dot addressing:

```
obj.Prior = v;
```

where `v` is a vector of positive elements representing the frequency with which each element occurs. You do not need to retrain the classifier when you set a new prior.

Cost

There are two costs associated with discriminant analysis classification: the true misclassification cost per class, and the expected misclassification cost per observation.

True Misclassification Cost per Class. `Cost(i,j)` is the cost of classifying an observation into class `j` if its true class is `i`. By default, `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`. In other words, the cost is `0` for correct classification, and `1` for incorrect classification.

You can set any cost matrix you like when creating a classifier. Pass the cost matrix in the `Cost` name-value pair in `ClassificationDiscriminant.fit`.

After you create a classifier `obj`, you can set a custom cost using dot addressing:

```
obj.Cost = B;
```

`B` is a square matrix of size `K`-by-`K` when there are `K` classes. You do not need to retrain the classifier when you set a new cost.

Expected Misclassification Cost per Observation. Suppose you have `Nobs` observations that you want to classify with a trained discriminant analysis classifier `obj`. Suppose you have `K` classes. You place the observations into a matrix `Xnew` with one observation per row. The command

```
[label,score,cost] = predict(obj,Xnew)
```

returns, among other outputs, a cost matrix of size `Nobs`-by-`K`. Each row of the cost matrix contains the expected (average) cost of classifying the observation into each of the `K` classes. `cost(n,k)` is

$$\sum_{i=1}^{K}\hat{P}(i\,|\,Xnew(n))C(k\,|\,i),$$

where

- K is the number of classes.
- $\hat{P}(i\,|\,Xnew(n))$ is the posterior probability of class i for observation $Xnew(n)$.
- $C(k\,|\,i)$ is the cost of classifying an observation as k when its true class is i.

Example: Creating and Visualizing a Discriminant Analysis Classifier

This example shows both linear and quadratic classification of the Fisher iris data. The example uses only two of the four predictors to enable simple plotting.

1 Load the data:

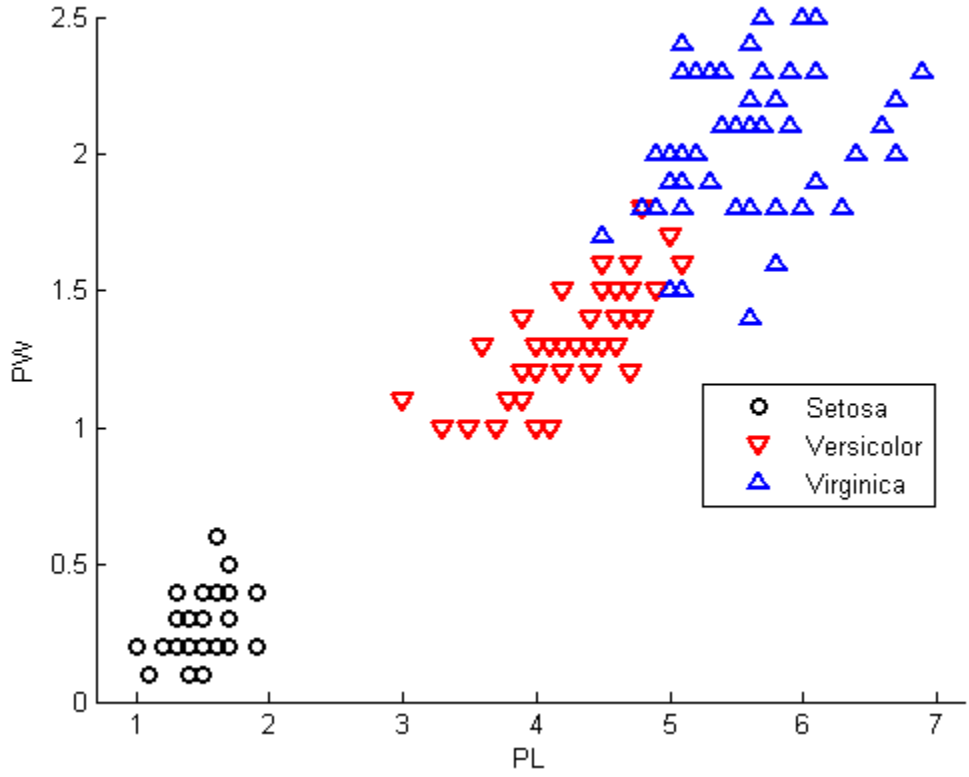
```
load fisheriris
```

2 Use the petal length (`PL`) and petal width (`PW`) measurements:

```
PL = meas(:,3);
PW = meas(:,4);
```

3 Plot the data, showing the classification:

```
h1 = gscatter(PL,PW,species,'krb','ov^',[],'off');
set(h1,'LineWidth',2)
legend('Setosa','Versicolor','Virginica',...
       'Location','best')
```

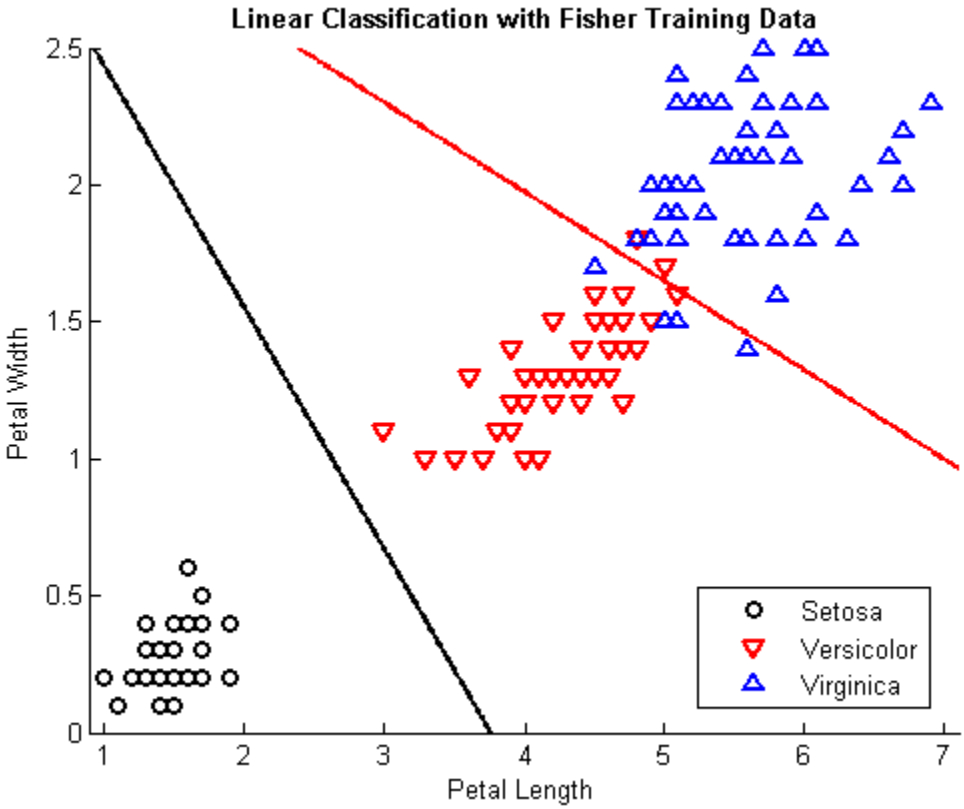


4 Create a linear classifier:

```
X = [PL,PW];
cls = ClassificationDiscriminant.fit(X,species);
```

5 Plot the classification boundaries:

```
hold on
K = cls.Coeffs(2,3).Const;
L = cls.Coeffs(2,3).Linear;
% Plot the curve K + [x,y]*L  = 0:
f = @(x1,x2) K + L(1)*x1 + L(2)*x2;
h2 = ezplot(f,[.9 7.1 0 2.5]);
set(h2,'Color','r','LineWidth',2)

K = cls.Coeffs(1,2).Const;
L = cls.Coeffs(1,2).Linear;
% Plot the curve K + [x1,x2]*L  = 0:
f = @(x1,x2) K + L(1)*x1 + L(2)*x2;
h3 = ezplot(f,[.9 7.1 0 2.5]);
set(h3,'Color','k','LineWidth',2)
axis([.9 7.1 0 2.5])
xlabel('Petal Length')
ylabel('Petal Width')
title('{\bf Linear Classification with Fisher Training Data}')
```



Linear Discriminant Classification — Fisher Training Data

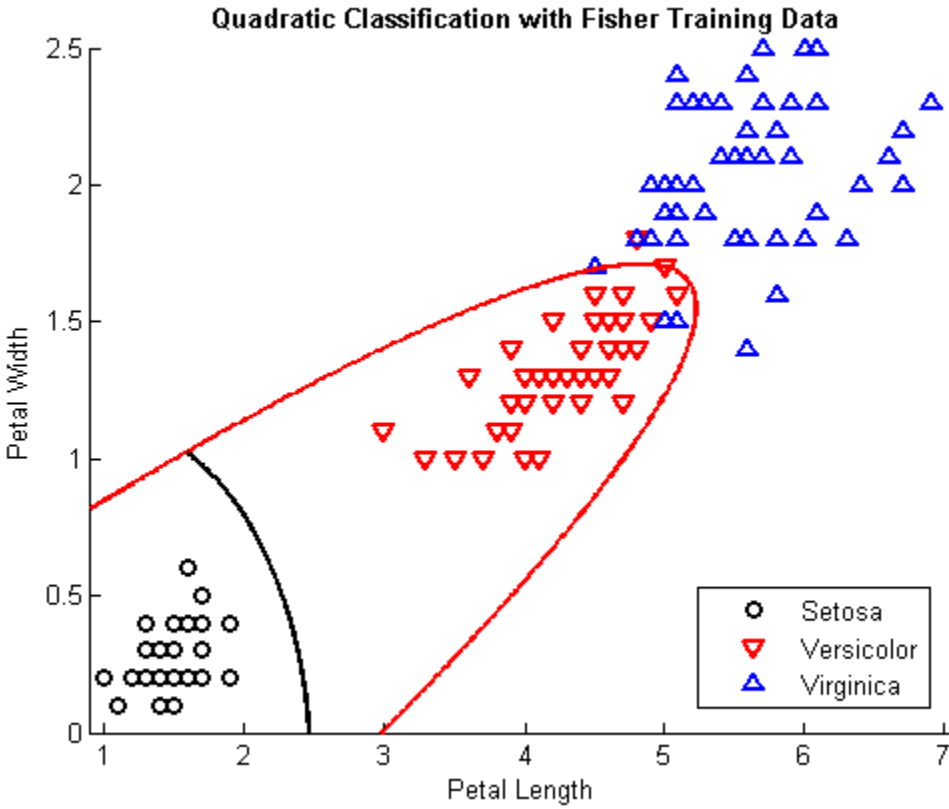
6 Create a quadratic discriminant classifier:

```
cqs = ClassificationDiscriminant.fit(X,species,...
    'DiscrimType','quadratic');
```

7 Plot the classification boundaries:

```
delete(h2); delete(h3) % remove the linear plots
K = cqs.Coeffs(2,3).Const;
L = cqs.Coeffs(2,3).Linear;
Q = cqs.Coeffs(2,3).Quadratic;
% Plot the curve K + [x1,x2]*L + [x1,x2]*Q*[x1,x2]'=0:
```

```
f = @(x1,x2) K + L(1)*x1 + L(2)*x2 + Q(1,1)*x1.^2 + ...
    (Q(1,2)+Q(2,1))*x1.*x2 + Q(2,2)*x2.^2;
h2 = ezplot(f,[.9 7.1 0 2.5]);
set(h2,'Color','r','LineWidth',2)

K = cqs.Coeffs(1,2).Const;
L = cqs.Coeffs(1,2).Linear;
Q = cqs.Coeffs(1,2).Quadratic;
% Plot the curve K + [x1,x2]*L + [x1,x2]*Q*[x1,x2]'=0:
f = @(x1,x2) K + L(1)*x1 + L(2)*x2 + Q(1,1)*x1.^2 + ...
    (Q(1,2)+Q(2,1))*x1.*x2 + Q(2,2)*x2.^2;
h3 = ezplot(f,[.9 7.1 0 1.02]); % plot the relevant
                                % portion of the curve
set(h3,'Color','k','LineWidth',2)
axis([.9 7.1 0 2.5])
xlabel('Petal Length')
ylabel('Petal Width')
title('{\bf Quadratic Classification with Fisher Training Data}')
hold off
```



Quadratic Discriminant Classification — Fisher Training Data

Improving a Discriminant Analysis Classifier

Deal with Singular Data

Discriminant analysis needs data sufficient to fit Gaussian models with invertible covariance matrices. If your data is not sufficient to fit such a model uniquely, `ClassificationDiscriminant.fit` fails. This section shows methods for handling failures.

Tip To obtain a discriminant analysis classifier without failure, set the `DiscrimType` name-value pair to `'pseudoLinear'` or `'pseudoQuadratic'` in `ClassificationDiscriminant.fit`.

"Pseudo" discriminants never fail, because they use the pseudoinverse of the covariance matrix Σ_k (see `pinv`).

Example: Singular Covariance Matrix. When the covariance matrix of the fitted classifier is singular, `ClassificationDiscriminant.fit` fails:

```
load popcorn
X = popcorn(:,[1 2]);
Y = popcorn(:,3);
ppcrn = ClassificationDiscriminant.fit(X,Y);

Error using
ClassificationDiscriminant>ClassificationDiscriminant.ClassificationDiscriminant
You cannot obtain discriminant coefficients because the pooled-in matrix is singular.
Set 'discrimType' to 'pseudoLinear' or 'diagLinear'.

Error in FitTemplate>FitTemplate.fit at 212
            obj = this.MakeFitObject(X,Y,W,this.ModelParams,fitArgs{:});

Error in ClassificationDiscriminant>ClassificationDiscriminant.fit at 43
            this = fit(temp,X,Y);
```

To proceed with linear discriminant analysis, use a `pseudoLinear` or `diagLinear` discriminant type:

```
ppcrn = ClassificationDiscriminant.fit(X,Y,...
    'discrimType','pseudoLinear');
meanpredict = predict(ppcrn,mean(X))
```

```
meanpredict =
     4
```

Choose a Discriminant Type

There are six types of discriminant analysis classifiers: linear and quadratic, with *diagonal* and *pseudo* variants of each type.

Tip To see if your covariance matrix is singular, set `discrimType` to `'linear'` or `'quadratic'`. If it is singular, the `ClassificationDiscriminant.fit` method fails.

To obtain a classifier even when your covariance matrix is singular, set `discrimType` to `'pseudoQuadratic'`, `'pseudoLinear'`, or either diagonal type.

```
obj = ClassificationDiscriminant.fit(X,Y,...
    'discrimType','pseudoQuadratic') % or 'pseudoLinear'
```

Choose a classifier type by setting the `discrimType` name-value pair to one of:

- `'linear'` (default) — Estimate one covariance matrix for all classes.
- `'quadratic'` — Estimate one covariance matrix for each class.
- `'diagLinear'` — Use the diagonal of the `'linear'` covariance matrix, and use its pseudoinverse if necessary.
- `'diagQuadratic'` — Use the diagonals of the `'quadratic'` covariance matrices, and use their pseudoinverses if necessary.
- `'pseudoLinear'` — Use the pseudoinverse of the `'linear'` covariance matrix if necessary.
- `'pseudoQuadratic'` — Use the pseudoinverses of the `'quadratic'` covariance matrices if necessary.

`ClassificationDiscriminant.fit` can fail for the `'linear'` and `'quadratic'` classifiers. When it fails, it returns an explanation, as shown in "Deal with Singular Data" on page 12-15.

`ClassificationDiscriminant.fit` always succeeds with the diagonal and pseudo variants. For information about pseudoinverses, see `pinv`.

You can set the discriminant type using dot addressing after constructing a classifier:

```
obj.DiscrimType = 'discrimType'
```

You can change between linear types or between quadratic types, but cannot change between a linear and a quadratic type.

Examine the Resubstitution Error and Confusion Matrix

The *resubstitution error* is the difference between the response training data and the predictions the classifier makes of the response based on the input training data. If the resubstitution error is high, you cannot expect the predictions of the classifier to be good. However, having low resubstitution error does not guarantee good predictions for new data. Resubstitution error is often an overly optimistic estimate of the predictive error on new data.

The *confusion matrix* shows how many errors, and which types, arise in resubstitution. When there are `K` classes, the confusion matrix `R` is a `K`-by-`K` matrix with

`R(i,j)` = the number of observations of class `i` that the classifier predicts to be of class `j`.

Example: Resubstitution Error of a Discriminant Analysis Classifier.

Examine the resubstitution error of the default discriminant analysis classifier for the Fisher iris data:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species);
resuberror = resubLoss(obj)

resuberror =
    0.0200
```

The resubstitution error is very low, meaning `obj` classifies nearly all the Fisher iris data correctly. The total number of misclassifications is:

```
resuberror * obj.NObservations

ans =
    3.0000
```

To see the details of the three misclassifications, examine the confusion matrix:

```
R = confusionmat(obj.Y,resubPredict(obj))

R =
    50     0     0
     0    48     2
     0     1    49

obj.ClassNames

ans =
    'setosa'
    'versicolor'
    'virginica'
```

- `R(1,:) = [50 0 0]` means `obj` classifies all 50 setosa irises correctly.
- `R(2,:) = [0 48 2]` means `obj` classifies 48 versicolor irises correctly, and misclassifies two versicolor irises as virginica.
- `R(3,:) = [0 1 49]` means `obj` classifies 49 virginica irises correctly, and misclassifies one virginica iris as versicolor.

Cross Validation

Typically, discriminant analysis classifiers are robust and do not exhibit overtraining when the number of predictors is much less than the number of observations. Nevertheless, it is good practice to cross validate your classifier to ensure its stability.

Example: Cross Validating a Discriminant Analysis Classifier. Try five-fold cross validation of a quadratic discriminant analysis classifier:

1. Load the Fisher iris data:

```
load fisheriris
```

2. Create a quadratic discriminant analysis classifier for the data:

```
quadisc = ClassificationDiscriminant.fit(meas,species,...
    'DiscrimType','quadratic');
```

3. Find the resubstitution error of the classifier:

```
qerror = resubLoss(quadisc)

qerror =
    0.0200
```

The classifier does an excellent job. Nevertheless, resubstitution error can be an optimistic estimate of the error when classifying new data. So proceed to cross validation.

4. Create a cross-validation model:

```
cvmodel = crossval(quadisc,'kfold',5);
```

5. Find the cross-validation loss for the model, meaning the error of the out-of-fold observations:

```
cverror = kfoldLoss(cvmodel)

cverror =
    0.0333
```

The cross-validated loss is nearly as low as the original resubstitution loss. Therefore, you can have confidence that the classifier is reasonably accurate.

Change Costs and Priors

Sometimes you want to avoid certain misclassification errors more than others. For example, it might be better to have oversensitive cancer detection instead of undersensitive cancer detection. Oversensitive detection gives more false positives (unnecessary testing or treatment). Undersensitive detection gives more false negatives (preventable illnesses or deaths). The

consequences of underdetection can be high. Therefore, you might want to set costs to reflect the consequences.

Similarly, the training data `Y` can have a distribution of classes that does not represent their true frequency. If you have a better estimate of the true frequency, you can include this knowledge in the classification `prior` property.

Example: Setting Custom Misclassification Costs. Consider the Fisher iris data. Suppose that the cost of classifying a versicolor iris as virginica is 10 times as large as making any other classification error. Create a classifier from the data, then incorporate this cost and then view the resulting classifier.

1 Load the Fisher iris data and create a default (linear) classifier as in "Example: Resubstitution Error of a Discriminant Analysis Classifier" on page 12-17:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species);
resuberror = resubLoss(obj)

resuberror =
    0.0200

R = confusionmat(obj.Y,resubPredict(obj))

R =
    50     0     0
     0    48     2
     0     1    49

obj.ClassNames

ans =
    'setosa'
    'versicolor'
    'virginica'
```

`R(2,:) = [0 48 2]` means `obj` classifies 48 versicolor irises correctly, and misclassifies two versicolor irises as virginica.

2 Change the cost matrix to make fewer mistakes in classifying versicolor irises as virginica:

```
obj.Cost(2,3) = 10;
R2 = confusionmat(obj.Y,resubPredict(obj))

R2 =
    50     0     0
     0    50     0
     0     7    43
```

`obj` now classifies all versicolor irises correctly, at the expense of increasing the number of misclassifications of virginica irises from 1 to 7.

Example: Setting Alternative Priors. Consider the Fisher iris data. There are 50 irises of each kind in the data. Suppose that, in a particular region, you have historical data that shows virginica are five times as prevalent as the other kinds. Create a classifier that incorporates this information.

1 Load the Fisher iris data and make a default (linear) classifier as in "Example: Resubstitution Error of a Discriminant Analysis Classifier" on page 12-17:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species);
resuberror = resubLoss(obj)

resuberror =
    0.0200

R = confusionmat(obj.Y,resubPredict(obj))

R =
    50     0     0
     0    48     2
     0     1    49

obj.ClassNames

ans =
    'setosa'
    'versicolor'
```

```
'virginica'
```

`R(3,:) = [0 1 49]` means `obj` classifies 49 virginica irises correctly, and misclassifies one virginica iris as versicolor.

2 Change the prior to match your historical data, and examine the confusion matrix of the new classifier:

```
obj.Prior = [1 1 5];
R2 = confusionmat(obj.Y,resubPredict(obj))

R2 =
    50     0     0
     0    46     4
     0     0    50
```

The new classifier classifies all virginica irises correctly, at the expense of increasing the number of misclassifications of versicolor irises from 2 to 4.

Examining the Gaussian Mixture Assumption

Discriminant analysis assumes that the data comes from a Gaussian mixture model (see "How the ClassificationDiscriminant.fit Method Creates a Classifier" on page 12-4). If the data appears to come from a Gaussian mixture model, you can expect discriminant analysis to be a good classifier. Furthermore, the default linear discriminant analysis assumes that all class covariance matrices are equal. This section shows methods to check these assumptions:

- "Bartlett Test of Equal Covariance Matrices for Linear Discriminant Analysis" on page 12-22
- "Q-Q Plot" on page 12-24
- "Mardia Kurtosis Test of Multivariate Normality" on page 12-27

Bartlett Test of Equal Covariance Matrices for Linear Discriminant Analysis

The Bartlett test (see Box [1]) checks equality of the covariance matrices of the various classes. If the covariance matrices are equal, the test indicates that linear discriminant analysis is appropriate. If not, consider using

quadratic discriminant analysis, setting the `DiscrimType` name-value pair to `'quadratic'` in `ClassificationDiscriminant.fit`.

The Bartlett test assumes normal (Gaussian) samples, where neither the means nor covariance matrices are known. To determine whether the covariances are equal, compute the following quantities:

- Sample covariance matrices per class σ_i, $1 \le i \le k$, where k is the number of classes.
- Pooled-in covariance matrix σ.
- Test statistic V:

$$V = (n-k)\log(|\Sigma|) - \sum_{i=1}^{k}(n_i - 1)\log(|\Sigma_i|)$$

  where n is the total number of observations, and n_i is the number of observations in class i, and $|\Sigma|$ means the determinant of the matrix Σ.
- Asymptotically, as the number of observations in each class n_i become large, V is distributed approximately χ^2 with $kd(d+1)/2$ degrees of freedom, where d is the number of predictors (number of dimensions in the data).

The Bartlett test is to check whether V exceeds a given percentile of the χ^2 distribution with $kd(d+1)/2$ degrees of freedom. If it does, then reject the hypothesis that the covariances are equal.

Example: Bartlett Test for Equal Covariance Matrices. Check whether the Fisher iris data is well modeled by a single Gaussian covariance, or whether it would be better to model it as a Gaussian mixture.

```
load fisheriris;
prednames = {'SepalLength','SepalWidth',...
    'PetalLength','PetalWidth'};
L = ClassificationDiscriminant.fit(meas,species,...
    'PredictorNames',prednames);
Q = ClassificationDiscriminant.fit(meas,species,...
    'PredictorNames',prednames,'DiscrimType','quadratic');
D = 4; % Number of dimensions of X
Nclass = [50 50 50];
```

```
N = L.NObservations;
K = numel(L.ClassNames);
SigmaQ = Q.Sigma;
SigmaL = L.Sigma;
logV = (N-K)*log(det(SigmaL));
for k=1:K
    logV = logV - (Nclass(k)-1)*log(det(SigmaQ(:,:,k)));
end
nu = (K-1)*D*(D+1)/2;
pval = 1-chi2cdf(logV,nu)

pval =
     0
```

The Bartlett test emphatically rejects the hypothesis of equal covariance matrices. If `pval` had been greater than `0.05`, the test would not have rejected the hypothesis. The result indicates to use quadratic discriminant analysis, as opposed to linear discriminant analysis.

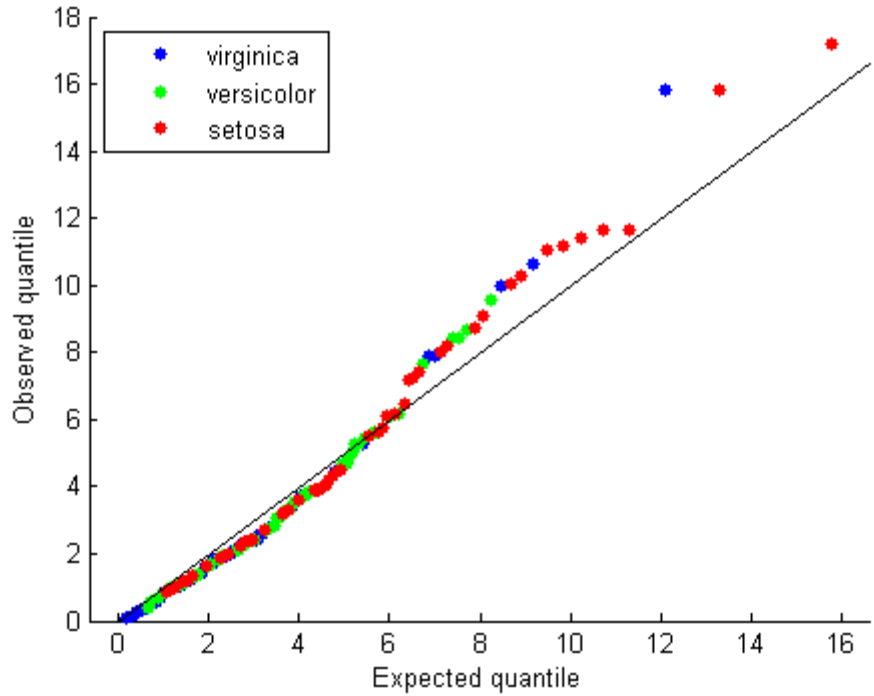
Q-Q Plot

A Q-Q plot graphically shows whether an empirical distribution is close to a theoretical distribution. If the two are equal, the Q-Q plot lies on a 45° line. If not, the Q-Q plot strays from the 45° line.

Check Q-Q Plots for Linear and Quadratic Discriminants. For linear discriminant analysis, use a single covariance matrix for all classes.

```
load fisheriris;
prednames = {'SepalLength','SepalWidth',...
    'PetalLength','PetalWidth'};
L = ClassificationDiscriminant.fit(meas,species,...
    'PredictorNames',prednames);
N = L.NObservations;
K = numel(L.ClassNames);
mahL = mahal(L,L.X,'ClassLabels',L.Y);
D = 4;
expQ = chi2inv(((1:N)-0.5)/N,D); % expected quantiles
[mahL,sorted] = sort(mahL); % sorted obbserved quantiles
figure;
gscatter(expQ,mahL,L.Y(sorted),'bgr',[],[],'off');
```

```
legend('virginica','versicolor','setosa','Location','NW');
xlabel('Expected quantile');
ylabel('Observed quantile');
line([0 20],[0 20],'color','k');
```

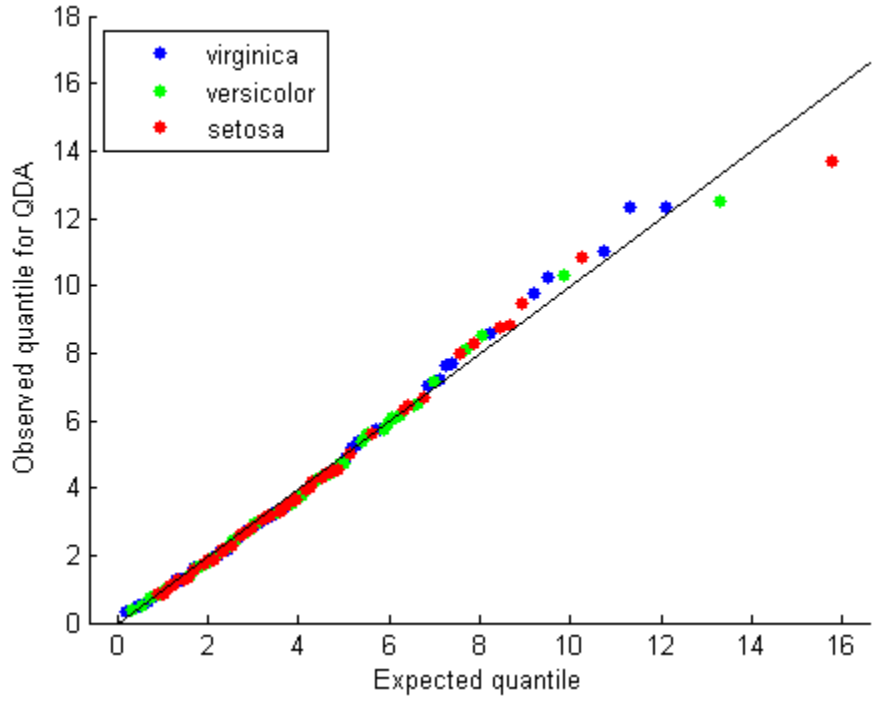


Overall, the agreement between the expected and observed quantiles is good. Look at the right half of the plot. The deviation of the plot from the 45° line upward indicates that the data has tails heavier than a normal distribution. There are three possible outliers on the right: two observations from class `'setosa'` and one observation from class `'virginica'`.

As shown in “Bartlett Test of Equal Covariance Matrices for Linear Discriminant Analysis” on page 12-22, the data does not match a single covariance matrix. Redo the calculations for a quadratic discriminant.

```
load fisheriris;
```

```
prednames = {'SepalLength','SepalWidth',...
    'PetalLength','PetalWidth'};
Q = ClassificationDiscriminant.fit(meas,species,...
    'PredictorNames',prednames,'DiscrimType','quadratic');
Nclass = [50 50 50];
N = L.NObservations;
K = numel(L.ClassNames);
mahQ = mahal(Q,Q.X,'ClassLabels',Q.Y);
expQ = chi2inv(((1:N)-0.5)/N,D);
[mahQ,sorted] = sort(mahQ);
figure;
gscatter(expQ,mahQ,Q.Y(sorted),'bgr',[],[],'off');
legend('virginica','versicolor','setosa','Location','NW');
xlabel('Expected quantile');
ylabel('Observed quantile for QDA');
line([0 20],[0 20],'color','k');
```



The Q-Q plot shows a better agreement between the observed and expected quantiles. There is only one outlier candidate, from class `'setosa'`.

Mardia Kurtosis Test of Multivariate Normality

The Mardia kurtosis test (see Mardia [2]) is an alternative to examining a Q-Q plot. It gives a numeric approach to deciding if data matches a Gaussian mixture model.

In the Mardia kurtosis test you compute M, the mean of the fourth power of the Mahalanobis distance of the data from the class means. If the data is normally distributed with constant covariance matrix (and is thus suitable for linear discriminant analysis), M is asymptotically distributed as normal with mean $d(d + 2)$ and variance $8d(d + 2)/n$, where

- d is the number of predictors (number of dimensions in the data).
- n is the total number of observations.

The Mardia test is two sided: check whether M is close enough to $d(d + 2)$ with respect to a normal distribution of variance $8d(d + 2)/n$.

Example: Mardia Kurtosis Test for Linear and Quadratic Discriminants. Check whether the Fisher iris data is approximately normally distributed for both linear and quadratic discriminant analysis. According to "Bartlett Test of Equal Covariance Matrices for Linear Discriminant Analysis" on page 12-22, the data is not normal for linear discriminant analysis (the covariance matrices are different). "Check Q-Q Plots for Linear and Quadratic Discriminants" on page 12-24 indicates that the data is well modeled by a Gaussian mixture model with different covariances per class. Check these conclusions with the Mardia kurtosis test:

```
load fisheriris;
prednames = {'SepalLength','SepalWidth',...
    'PetalLength','PetalWidth'};
L = ClassificationDiscriminant.fit(meas,species,...
    'PredictorNames',prednames);
mahL = mahal(L,L.X,'ClassLabels',L.Y);
D = 4;
N = L.NObservations;
obsKurt = mean(mahL.^2);
```

```
expKurt = D*(D+2);
varKurt = 8*D*(D+2)/N;
[~,pval] = ztest(obsKurt,expKurt,sqrt(varKurt))

pval =
    0.0208
```

The Mardia test indicates to reject the hypothesis that the data is normally distributed.

Continuing the example with quadratic discriminant analysis:

```
Q = ClassificationDiscriminant.fit(meas,species,...
    'PredictorNames',prednames,'DiscrimType','quadratic');
mahQ = mahal(Q,Q.X,'ClassLabels',Q.Y);
obsKurt = mean(mahQ.^2);
[~,pval] = ztest(obsKurt,expKurt,sqrt(varKurt))

pval =
    0.7230
```

Because `pval` is high, you conclude the data are consistent with the multivariate normal distribution.

Bibliography

[1] Box, G. E. P. *A General Distribution Theory for a Class of Likelihood Criteria.* Biometrika 36(3), pp. 317–346, 1949.

[2] Mardia, K. V. *Measures of multivariate skewness and kurtosis with applications.* Biometrika 57 (3), pp. 519–530, 1970.

Naive Bayes Classification

The Naive Bayes classifier is designed for use when features are independent of one another within each class, but it appears to work well in practice even when that independence assumption is not valid. It classifies data in two steps:

1. Training step: Using the training samples, the method estimates the parameters of a probability distribution, assuming features are conditionally independent given the class.

2. Prediction step: For any unseen test sample, the method computes the posterior probability of that sample belonging to each class. The method then classifies the test sample according the largest posterior probability.

The class-conditional independence assumption greatly simplifies the training step since you can estimate the one-dimensional class-conditional density for each feature individually. While the class-conditional independence between features is not true in general, research shows that this optimistic assumption works well in practice. This assumption of class independence allows the Naive Bayes classifier to better estimate the parameters required for accurate classification while using less training data than many other classifiers. This makes it particularly effective for datasets containing many predictors or features.

To learn how to prepare your data for Naive Bayes classification and create a classifier, see “Steps in Supervised Learning (Machine Learning)” on page 13-2.

Supported Distributions

Naive Bayes classification is based on estimating `P(X|Y)`, the probability or probability density of features `X` given class `Y`. The Naive Bayes classification object `NaiveBayes` provides support for normal (Gaussian), kernel, multinomial, and multivariate multinomial distributions. It is possible to use different distributions for different features.

Normal (Gaussian) Distribution

The `'normal'` distribution is appropriate for features that have normal distributions in each class. For each feature you model with a normal distribution, the Naive Bayes classifier estimates a separate normal distribution for each class by computing the mean and standard deviation of the training data in that class. For more information on normal distributions, see “Normal Distribution” on page B-83.

Kernel Distribution

The `'kernel'` distribution is appropriate for features that have a continuous distribution. It does not require a strong assumption such as a normal distribution and you can use it in cases where the distribution of a feature may be skewed or have multiple peaks or modes. It requires more computing time and more memory than the normal distribution. For each feature you model with a kernel distribution, the Naive Bayes classifier computes a separate kernel density estimate for each class based on the training data for that class. By default the kernel is the normal kernel, and the classifier selects a width automatically for each class and feature. It is possible to specify different kernels for each feature, and different widths for each feature or class.

Multinomial Distribution

The multinomial distribution (specify with the `'mn'` keyword) is appropriate when all features represent counts of a set of words or tokens. This is sometimes called the "bag of words" model. For example, an email spam classifier might be based on features that count the number of occurrences of various tokens in an email. One feature might count the number of exclamation points, another might count the number of times the word "money" appears, and another might count the number of times the recipient’s name appears. This is a Naive Bayes model under the further assumption that the total number of tokens (or the total document length) is independent of response class.

For the multinomial option, each feature represents the count of one token. The classifier counts the set of relative token probabilities separately for each class. The classifier defines the multinomial distribution for each row by the vector of probabilities for the corresponding class, and by `N`, the total token count for that row.

Classification is based on the relative frequencies of the tokens. For a row in which no token appears, `N` is 0 and no classification is possible. This classifier is not appropriate when the total number of tokens provides information about the response class.

Multivariate Multinomial Distribution

The multivariate multinomial distribution (specify with the `'mvmn'` keyword) is appropriate for categorical features. For example, you could fit a feature describing the weather in categories such as rain/sun/snow/clouds using the multivariate multinomial model. The feature categories are sometimes called the feature levels, and differ from the class levels for the response variable.

For each feature you model with a multivariate multinomial distribution, the Naive Bayes classifier computes a separate set of probabilities for the set of feature levels for each class.

Performance Curves

In this section...

Introduction to Performance Curves

After a classification algorithm such as `NaiveBayes` or `TreeBagger` has trained on data, you may want to examine the performance of the algorithm on a specific test dataset. One common way of doing this would be to compute a gross measure of performance such as quadratic loss or accuracy, averaged over the entire test dataset.

What are ROC Curves?

You may want to inspect the classifier performance more closely, for example, by plotting a Receiver Operating Characteristic (ROC) curve. By definition, a ROC curve [1,2] shows true positive rate versus false positive rate (equivalently, sensitivity versus 1–specificity) for different thresholds of the classifier output. You can use it, for example, to find the threshold that maximizes the classification accuracy or to assess, in more broad terms, how the classifier performs in the regions of high sensitivity and high specificity.

Evaluating Classifier Performance Using perfcurve

`perfcurve` computes measures for a plot of classifier performance. You can use this utility to evaluate classifier performance on test data after you train the classifier. Various measures such as mean squared error, classification error, or exponential loss can summarize the predictive power of a classifier in a single number. However, a performance curve offers more information as it lets you explore the classifier performance across a range of thresholds on its output.

You can use `perfcurve` with any classifier or, more broadly, with any method that returns a numeric score for an instance of input data. By convention adopted here,

- A high score returned by a classifier for any given instance signifies that the instance is likely from the positive class.
- A low score signifies that the instance is likely from the negative classes.

For some classifiers, you can interpret the score as the posterior probability of observing an instance of the positive class at point `X`. An example of such a score is the fraction of positive observations in a leaf of a decision tree. In this case, scores fall into the range from 0 to 1 and scores from positive and negative classes add up to unity. Other methods can return scores ranging between minus and plus infinity, without any obvious mapping from the score to the posterior class probability.

`perfcurve` does not impose any requirements on the input score range. Because of this lack of normalization, you can use `perfcurve` to process scores returned by any classification, regression, or fit method. `perfcurve` does not make any assumptions about the nature of input scores or relationships between the scores for different classes. As an example, consider a problem with three classes, `A`, `B`, and `C`, and assume that the scores returned by some classifier for two instances are as follows:

	`A`	`B`	`C`
instance 1	0.4	0.5	0.1
instance 2	0.4	0.1	0.5

If you want to compute a performance curve for separation of classes `A` and `B`, with `C` ignored, you need to address the ambiguity in selecting `A` over `B`. You could opt to use the score ratio, `s(A)/s(B)`, or score difference, `s(A)-s(B)`; this choice could depend on the nature of these scores and their normalization. `perfcurve` always takes one score per instance. If you only supply scores for class `A`, `perfcurve` does not distinguish between observations 1 and 2. The performance curve in this case may not be optimal.

`perfcurve` is intended for use with classifiers that return scores, not those that return only predicted classes. As a counter-example, consider a decision tree that returns only hard classification labels, 0 or 1, for data with two classes. In this case, the performance curve reduces to a single point because classified instances can be split into positive and negative categories in one way only.

For input, `perfcurve` takes true class labels for some data and scores assigned by a classifier to these data. By default, this utility computes a Receiver Operating Characteristic (ROC) curve and returns values of 1–specificity, or false positive rate, for `X` and sensitivity, or true positive rate, for `Y`. You can choose other criteria for `X` and `Y` by selecting one out of several provided criteria or specifying an arbitrary criterion through an anonymous function. You can display the computed performance curve using `plot(X,Y)`.

`perfcurve` can compute values for various criteria to plot either on the *x*- or the *y*-axis. All such criteria are described by a 2-by-2 confusion matrix, a 2-by-2 cost matrix, and a 2-by-1 vector of scales applied to class counts.

The `confusion` matrix, `C`, is defined as

$$\begin{pmatrix} TP & FN \\ FP & TN \end{pmatrix}$$

where

- P stands for "positive".
- N stands for "negative".
- T stands for "true".
- F stands for "false".

For example, the first row of the confusion matrix defines how the classifier identifies instances of the positive class: `C(1,1)` is the count of correctly identified positive instances and `C(1,2)` is the count of positive instances misidentified as negative.

The cost matrix defines the cost of misclassification for each category:

$$\begin{pmatrix} Cost(P \mid P) & Cost(N \mid P) \\ Cost(P \mid N) & Cost(N \mid N) \end{pmatrix}$$

where `Cost(I|J)` is the cost of assigning an instance of class `J` to class `I`. Usually `Cost(I|J)=0` for `I=J`. For flexibility, `perfcurve` allows you to specify nonzero costs for correct classification as well.

The two scales include prior information about class probabilities. `perfcurve` computes these scales by taking `scale(P)=prior(P)*N` and `scale(N)=prior(N)*P` and normalizing the sum `scale(P)+scale(N)` to 1. `P=TP+FN` and `N=TN+FP` are the total instance counts in the positive and negative class, respectively. The function then applies the scales as multiplicative factors to the counts from the corresponding class: `perfcurve` multiplies counts from the positive class by `scale(P)` and counts from the negative class by `scale(N)`. Consider, for example, computation of positive predictive value, `PPV = TP/(TP+FP)`. `TP` counts come from the positive class and `FP` counts come from the negative class. Therefore, you need to scale `TP` by `scale(P)` and `FP` by `scale(N)`, and the modified formula for `PPV` with prior probabilities taken into account is now:

$$PPV = \frac{scale(P) * TP}{scale(P) * TP + scale(N) * FP}$$

If all scores in the data are above a certain threshold, `perfcurve` classifies all instances as `'positive'`. This means that `TP` is the total number of instances in the positive class and `FP` is the total number of instances in the negative class. In this case, `PPV` is simply given by the prior:

$$PPV = \frac{prior(P)}{prior(P) + prior(N)}$$

The `perfcurve` function returns two vectors, `X` and `Y`, of performance measures. Each measure is some function of `confusion`, `cost`, and `scale` values. You can request specific measures by name or provide a function handle to compute a custom measure. The function you provide should take `confusion`, `cost`, and `scale` as its three inputs and return a vector of output values.

The criterion for `X` must be a monotone function of the positive classification count, or equivalently, threshold for the supplied scores. If `perfcurve` cannot perform a one-to-one mapping between values of the `X` criterion and score thresholds, it exits with an error message.

By default, `perfcurve` computes values of the `X` and `Y` criteria for all possible score thresholds. Alternatively, it can compute a reduced number of specific `X` values supplied as an input argument. In either case, for `M` requested values, `perfcurve` computes `M+1` values for `X` and `Y`. The first value out of these `M+1` values is special. `perfcurve` computes it by setting the `TP` instance count

to zero and setting TN to the total count in the negative class. This value corresponds to the 'reject all' threshold. On a standard ROC curve, this translates into an extra point placed at (0,0).

If there are NaN values among input scores, perfcurve can process them in either of two ways:

- It can discard rows with NaN scores.
- It can add them to false classification counts in the respective class.

That is, for any threshold, instances with NaN scores from the positive class are counted as false negative (FN), and instances with NaN scores from the negative class are counted as false positive (FP). In this case, the first value of X or Y is computed by setting TP to zero and setting TN to the total count minus the NaN count in the negative class. For illustration, consider an example with two rows in the positive and two rows in the negative class, each pair having a NaN score:

Class	Score
Negative	0.2
Negative	NaN
Positive	0.7
Positive	NaN

If you discard rows with NaN scores, then as the score cutoff varies, perfcurve computes performance measures as in the following table. For example, a cutoff of 0.5 corresponds to the middle row where rows 1 and 3 are classified correctly, and rows 2 and 4 are omitted.

TP	FN	FP	TN
0	1	0	1
1	0	0	1
1	0	1	0

If you add rows with NaN scores to the false category in their respective classes, perfcurve computes performance measures as in the following table. For example, a cutoff of 0.5 corresponds to the middle row where now rows

2 and 4 are counted as incorrectly classified. Notice that only the FN and FP columns differ between these two tables.

TP	FN	FP	TN
0	2	1	1
1	1	1	1
1	1	2	0

For data with three or more classes, perfcurve takes one positive class and a list of negative classes for input. The function computes the X and Y values using counts in the positive class to estimate TP and FN, and using counts in all negative classes to estimate TN and FP. perfcurve can optionally compute Y values for each negative class separately and, in addition to Y, return a matrix of size M-by-C, where M is the number of elements in X or Y and C is the number of negative classes. You can use this functionality to monitor components of the negative class contribution. For example, you can plot TP counts on the X-axis and FP counts on the Y-axis. In this case, the returned matrix shows how the FP component is split across negative classes.

You can also use perfcurve to estimate confidence intervals. perfcurve computes confidence bounds using either cross-validation or bootstrap. If you supply cell arrays for labels and scores, perfcurve uses cross-validation and treats elements in the cell arrays as cross-validation folds. If you set input parameter NBoot to a positive integer, perfcurve generates nboot bootstrap replicas to compute pointwise confidence bounds.

perfcurve estimates the confidence bounds using one of two methods:

- Vertical averaging (VA) — estimate confidence bounds on Y and T at fixed values of X. Use the XVals input parameter to use this method for computing confidence bounds.
- Threshold averaging (TA) — estimate confidence bounds for X and Y at fixed thresholds for the positive class score. Use the TVals input parameter to use this method for computing confidence bounds.

To use observation weights instead of observation counts, you can use the 'Weights' parameter in your call to perfcurve. When you use this parameter, to compute X, Y and T or to compute confidence bounds by cross-validation, perfcurve uses your supplied observation weights instead of

observation counts. To compute confidence bounds by bootstrap, `perfcurve` samples N out of N with replacement using your weights as multinomial sampling probabilities.

13

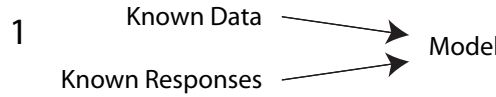
Nonparametric Supervised Learning

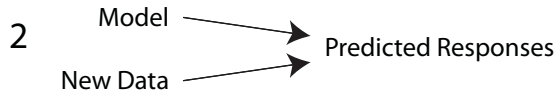
Supervised Learning (Machine Learning) Workflow and Algorithms

In this section...

Steps in Supervised Learning (Machine Learning)

Supervised learning (machine learning) takes a known set of input data and known responses to the data, and seeks to build a predictor model that generates reasonable predictions for the response to new data.





Suppose you want to predict if someone will have a heart attack within a year. You have a set of data on previous people, including age, weight, height, blood pressure, etc. You know if the previous people had heart attacks within a year of their data measurements. So the problem is combining all the existing data into a model that can predict whether a new person will have a heart attack within a year.

Supervised learning splits into two broad categories:

- Classification for responses that can have just a few known values, such as `'true'` or `'false'`. Classification algorithms apply to nominal, not ordinal response values.

- Regression for responses that are a real number, such as miles per gallon for a particular car.

You can have trouble deciding whether you have a classification problem or a regression problem. In that case, create a regression model first, because they are often more computationally efficient.

While there are many Statistics Toolbox algorithms for supervised learning, most use the same basic workflow for obtaining a predictor model. (Detailed instruction on the steps for ensemble learning is in "Framework for Ensemble Learning" on page 13-51.) The steps for supervised learning are:

1 "Prepare Data" on page 13-3

2 "Choose an Algorithm" on page 13-4

3 "Fit a Model" on page 13-4

4 "Choose a Validation Method" on page 13-5

5 "Examine Fit and Update Until Satisfied" on page 13-6

6 "Use Fitted Model for Predictions" on page 13-6

Prepare Data

All supervised learning methods start with an input data matrix, usually called `X` here. Each row of `X` represents one observation. Each column of `X` represents one variable, or predictor. Represent missing entries with `NaN` values in `X`. Statistics Toolbox supervised learning algorithms can handle `NaN` values, either by ignoring them or by ignoring any row with a `NaN` value.

You can use various data types for response data `Y`. Each element in `Y` represents the response to the corresponding row of `X`. Observations with missing `Y` data are ignored.

- For regression, `Y` must be a numeric vector with the same number of elements as the number of rows of `X`.
- For classification, `Y` can be any of these data types. This table also contains the method of including missing entries.

Data Type	Missing Entry
Numeric vector	`NaN`
Categorical vector	`<undefined>`
Character array	Row of spaces
Cell array of strings	`''`
Logical vector	(Cannot represent)

Choose an Algorithm

There are tradeoffs between several characteristics of algorithms, such as:

- Speed of training
- Memory usage
- Predictive accuracy on new data
- Transparency or interpretability, meaning how easily you can understand the reasons an algorithm makes its predictions

Details of the algorithms appear in "Characteristics of Algorithms" on page 13-7. More detail about ensemble algorithms is in "Choose an Applicable Ensemble Method" on page 13-54.

Fit a Model

The fitting function you use depends on the algorithm you choose.

Algorithm	Fitting Function
Classification Trees	`ClassificationTree.fit`
Regression Trees	`RegressionTree.fit`
Discriminant Analysis (classification)	`ClassificationDiscriminant.fit`
Naive Bayes (classification)	`NaiveBayes.fit`

Algorithm	Fitting Function
Classification or Regression Ensembles	`fitensemble`
Classification or Regression Ensembles in Parallel	`TreeBagger`

Choose a Validation Method

The three main methods to examine the accuracy of the resulting fitted model are:

- Examine the resubstitution error. For examples, see:
  - "Example: Resubstitution Error of a Classification Tree" on page 13-34
  - "Example: Cross Validating a Regression Tree" on page 13-35
  - "Example: Test Ensemble Quality" on page 13-60
  - "Example: Resubstitution Error of a Discriminant Analysis Classifier" on page 12-17
- Examine the cross-validation error. For examples, see:
  - "Example: Cross Validating a Regression Tree" on page 13-35
  - "Example: Test Ensemble Quality" on page 13-60
  - "Example: Classification with Many Categorical Levels" on page 13-72
  - "Example: Cross Validating a Discriminant Analysis Classifier" on page 12-18
- Examine the out-of-bag error for bagged decision trees. For examples, see:
  - "Example: Test Ensemble Quality" on page 13-60
  - "Workflow Example: Regression of Insurance Risk Rating for Car Imports with TreeBagger" on page 13-97
  - "Workflow Example: Classifying Radar Returns for Ionosphere Data with TreeBagger" on page 13-106

Examine Fit and Update Until Satisfied

After validating the model, you might want to change it for better accuracy, better speed, or to use less memory.

- Change fitting parameters to try to get a more accurate model. For examples, see:
  - "Example: Tuning RobustBoost" on page 13-92
  - "Example: Unequal Classification Costs" on page 13-67
  - "Improving a Discriminant Analysis Classifier" on page 12-14
- Change fitting parameters to try to get a smaller model. This sometimes gives a model with more accuracy. For examples, see:
  - "Example: Selecting Appropriate Tree Depth" on page 13-36
  - "Example: Pruning a Classification Tree" on page 13-39
  - "Example: Surrogate Splits" on page 13-77
  - "Example: Regularizing a Regression Ensemble" on page 13-82
  - "Workflow Example: Regression of Insurance Risk Rating for Car Imports with TreeBagger" on page 13-97
  - "Workflow Example: Classifying Radar Returns for Ionosphere Data with TreeBagger" on page 13-106
- Try a different algorithm. For applicable choices, see:
  - "Characteristics of Algorithms" on page 13-7
  - "Choose an Applicable Ensemble Method" on page 13-54

When satisfied with a model of some types, you can trim it using the appropriate `compact` method (`compact` for classification trees, `compact` for classification ensembles, `compact` for regression trees, `compact` for regression ensembles, `compact` for discriminant analysis). `compact` removes training data and pruning information, so the model uses less memory.

Use Fitted Model for Predictions

To predict classification or regression response for most fitted models, use the `predict` method:

```
Ypredicted = predict(obj,Xnew)
```

- `obj` is the fitted model object.
- `Xnew` is the new input data.
- `Ypredicted` is the predicted response, either classification or regression.

For `classregtree`, use the `eval` method instead of `predict`.

Characteristics of Algorithms

This table shows typical characteristics of the various supervised learning algorithms. The characteristics in any particular case can vary from the listed ones. Use the table as a guide for your initial choice of algorithms, but be aware that the table can be inaccurate for some problems.

Characteristics of Supervised Learning Algorithms

Algorithm	Predictive Accuracy	Fitting Speed	Prediction Speed	Memory Usage	Easy to Interpret	Handles Categorical Predictors
Trees	Low	Fast	Fast	Low	Yes	Yes
Boosted Trees	High	Medium	Medium	Medium	No	Yes
Bagged Trees	High	Slow	Slow	High	No	Yes
SVM in Bioinformatics Toolbox™	High	Medium	*	*	*	No
Naive Bayes	Low	**	**	**	Yes	Yes
Nearest Neighbor	***	Fast***	Medium	High	No	Yes***
Discriminant Analysis	****	Fast	Fast	Low	Yes	No

* — SVM prediction speed and memory usage are good if there are few support vectors, but can be poor if there are many support vectors. When you use a kernel function, it can be difficult to interpret how SVM classifies data,

though the default linear scheme is easy to interpret. SVM is available if you have a Bioinformatics Toolbox license.

** — Naive Bayes speed and memory usage are good for simple distributions, but can be poor for kernel distributions and large data sets.

*** — Nearest Neighbor usually has good predictions in low dimensions, but can have poor predictions in high dimensions. For linear search, Nearest Neighbor does not perform any fitting. For *k*d-trees, Nearest Neighbor does perform fitting. Nearest Neighbor can have either continuous or categorical predictors, but not both.

**** — Discriminant Analysis is accurate when the modeling assumptions are satisfied (multivariate normal by class). Otherwise, the predictive accuracy varies.

Classification Using Nearest Neighbors

In this section...

Pairwise Distance

Categorizing query points based on their distance to points in a training dataset can be a simple yet effective way of classifying new points. You can use various metrics to determine the distance, described next. Use `pdist2` to find the distance between a sets of data and query points.

Distance Metrics

Given an *mx*-by-*n* data matrix `X`, which is treated as *mx* (1-by-*n*) row vectors $\mathtt{x}_1$, $\mathtt{x}_2$, ..., $\mathtt{x}_{mx}$, and *my*-by-*n* data matrix `Y`, which is treated as *my* (1-by-*n*) row vectors $\mathtt{y}_1$, $\mathtt{y}_2$, ...,$\mathtt{y}_{my}$, the various distances between the vector $\mathtt{x}_s$ and $\mathtt{y}_t$ are defined as follows:

- Euclidean distance

  $$d_{st}^2 = (x_s - y_t)(x_s - y_t)'$$

  The Euclidean distance is a special case of the Minkowski metric, where `p` = 2.

- Standardized Euclidean distance

  $$d_{st}^2 = (x_s - y_t)V^{-1}(x_s - y_t)'$$

  where `V` is the *n*-by-*n* diagonal matrix whose *j*th diagonal element is $\mathtt{S}(j)^2$, where `S` is the vector containing the inverse weights.

- Mahalanobis distance

  $$d_{st}^2 = (x_s - y_t)C^{-1}(x_s - y_t)'$$

  where `C` is the covariance matrix.

- City block metric

$$d_{st} = \sum_{j=1}^{n} \left| x_{sj} - y_{tj} \right|$$

The city block distance is a special case of the Minkowski metric, where p = 1.

- Minkowski metric

$$d_{st} = \sqrt[p]{\sum_{j=1}^{n} \left| x_{sj} - y_{tj} \right|^{p}}$$

For the special case of p = 1, the Minkowski metric gives the city block metric, for the special case of p = 2, the Minkowski metric gives the Euclidean distance, and for the special case of p = ∞, the Minkowski metric gives the Chebychev distance.

- Chebychev distance

$$d_{st} = \max_j \left\{ \left| x_{sj} - y_{tj} \right| \right\}$$

The Chebychev distance is a special case of the Minkowski metric, where p = ∞.

- Cosine distance

$$d_{st} = \left(1 - \frac{x_s y_t'}{\sqrt{(x_s x_s')(y_t y_t')}} \right)$$

- Correlation distance

$$d_{st} = 1 - \frac{(x_s - \bar{x}_s)(y_t - \bar{y}_t)'}{\sqrt{(x_s - \bar{x}_s)(x_s - \bar{x}_s)'} \sqrt{(y_t - \bar{y}_t)(y_t - \bar{y}_t)'}}$$

where

$$\bar{x}_s = \frac{1}{n}\sum_j x_{sj}$$

and

$$\bar{y}_t = \frac{1}{n}\sum_j y_{tj}$$

- Hamming distance

$$d_{st} = (\#(x_{sj} \neq y_{tj}) / n)$$

- Jaccard distance

$$d_{st} = \frac{\#\left[\left(x_{sj} \neq y_{tj}\right) \cap \left(\left(x_{sj} \neq 0\right) \cup \left(y_{tj} \neq 0\right)\right)\right]}{\#\left[\left(x_{sj} \neq 0\right) \cup \left(y_{tj} \neq 0\right)\right]}$$

- Spearman distance

$$d_{st} = 1 - \frac{(r_s - \bar{r}_s)(r_t - \bar{r}_t)'}{\sqrt{(r_s - \bar{r}_s)(r_s - \bar{r}_s)'}\sqrt{(r_t - \bar{r}_t)(r_t - \bar{r}_t)'}}$$

  where

  - r_{sj} is the rank of x_{sj} taken over x_{1j}, x_{2j}, ...$x_{mx,j}$, as computed by `tiedrank`.
  - r_{tj} is the rank of y_{tj} taken over y_{1j}, y_{2j}, ...$y_{my,j}$, as computed by `tiedrank`.
  - r_s and r_t are the coordinate-wise rank vectors of x_s and y_t, i.e., $r_s = (r_{s1}, r_{s2}, \ldots r_{sn})$ and $r_t = (r_{t1}, r_{t2}, \ldots r_{tn})$.

  - $\bar{r}_s = \frac{1}{n}\sum_j r_{sj} = \frac{(n+1)}{2}$.

  - $\bar{r}_t = \frac{1}{n}\sum_j r_{tj} = \frac{(n+1)}{2}$.

k-Nearest Neighbor Search and Radius Search

Given a set X of n points and a distance function, k-nearest neighbor (kNN) search lets you find the k closest points in X to a query point or set of points `Y`. The kNN search technique and kNN-based algorithms are widely used as benchmark learning rules. The relative simplicity of the kNN search technique makes it easy to compare the results from other classification techniques to kNN results. The technique has been used in various areas such as:

- bioinformatics
- image processing and data compression
- document retrieval
- computer vision
- multimedia database
- marketing data analysis

You can use kNN search for other machine learning algorithms, such as:

- kNN classification
- local weighted regression
- missing data imputation and interpolation
- density estimation

You can also use kNN search with many distance-based learning functions, such as K-means clustering.

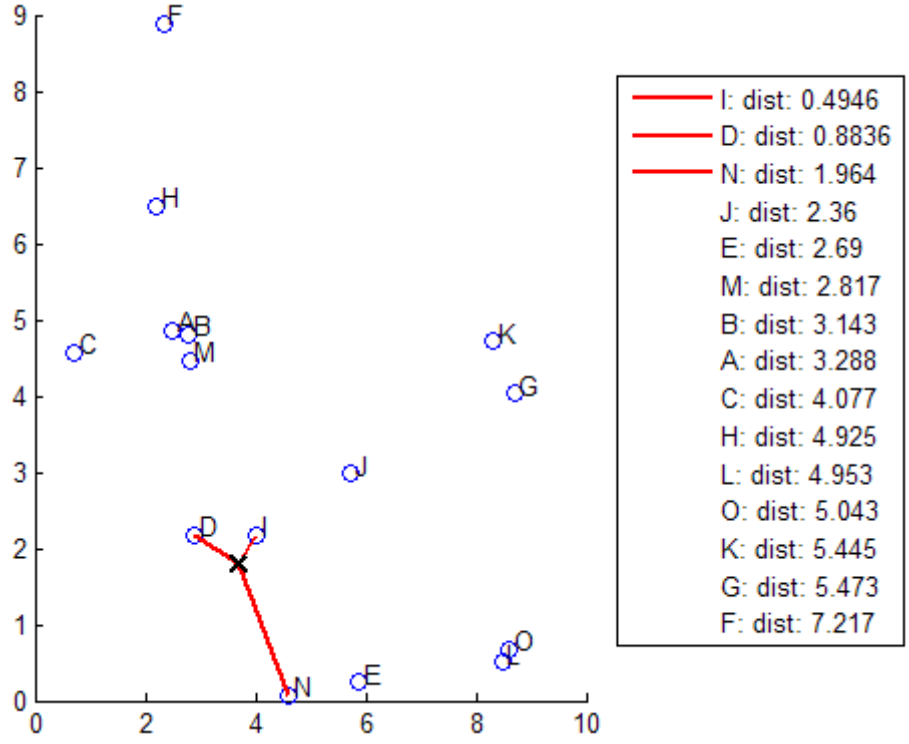
In contrast, for a positive real value `r`, `rangesearch` finds all points in `X` that are within a distance `r` of each point in `Y`. This fixed-radius search is closely related to kNN search, as it supports the same distance metrics and search classes, and uses the same search algorithms.

k-Nearest Neighbor Search Using Exhaustive Search

When your input data meets any of the following criteria, `knnsearch` uses the exhaustive search method by default to find the k-nearest neighbors:

- The number of columns of `X` is more than 10.
- `X` is sparse.
- The distance measure is either:
  - `'seuclidean'`
  - `'mahalanobis'`
  - `'cosine'`
  - `'correlation'`
  - `'spearman'`
  - `'hamming'`
  - `'jaccard'`
  - A custom distance function

`knnsearch` also uses the exhaustive search method if your search object is an `ExhaustiveSearcher` object. The exhaustive search method finds the distance from each query point to every point in `X`, ranks them in ascending order, and returns the k points with the smallest distances. For example, this diagram shows the $k = 3$ nearest neighbors.



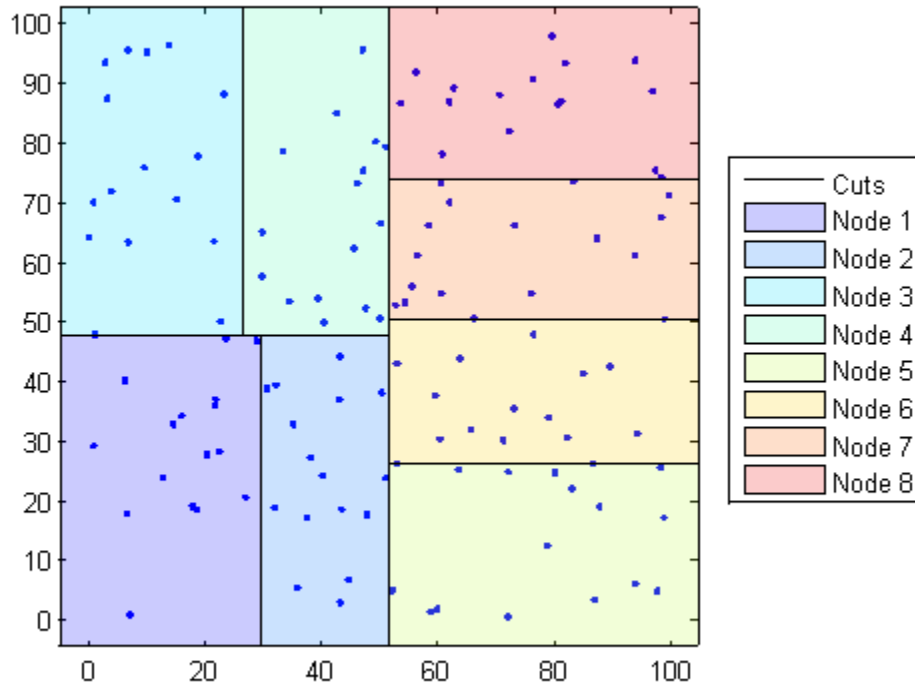
k-Nearest Neighbor Search Using a *k*d-Tree

When your input data meets all of the following criteria, `knnsearch` creates a *k*d-tree by default to find the *k*-nearest neighbors:

- The number of columns of `X` is less than 10.
- `X` is not sparse.
- The distance measure is either:
  - `'euclidean'` (default)
  - `'cityblock'`
  - `'minkowski'`
  - `'chebychev'`

`knnsearch` also uses a *k*d-tree if your search object is a `KDTreeSearcher` object.

*k*d-trees divide your data into nodes with at most `BucketSize` (default is 50) points per node, based on coordinates (as opposed to categories). The following diagrams illustrate this concept using `patch` objects to color code the different "buckets."



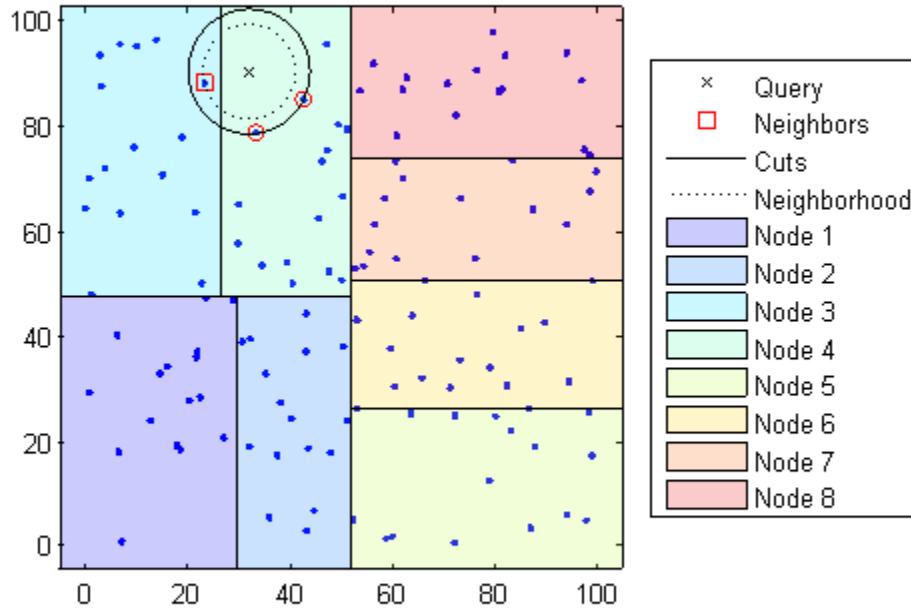
When you want to find the *k*-nearest neighbors to a given query point, `knnsearch` does the following:

1. Determines the node to which the query point belongs. In the following example, the query point (32,90) belongs to Node 4.

2. Finds the closest k points within that node and its distance to the query point. In the following example, the points in red circles are equidistant from the query point, and are the closest points to the query point within Node 4.

3. Chooses all other nodes having any area that is within the same distance, in any direction, from the query point to the kth closest point. In this example, only Node 3 overlaps the solid black circle centered at the query point with radius equal to the distance to the closest points within Node 4.

4. Searches nodes within that range for any points closer to the query point. In the following example, the point in a red square is slightly closer to the query point than those within Node 4.



Using a *k*d-tree for large datasets with fewer than 10 dimensions (columns) can be much more efficient than using the exhaustive search method, as `knnsearch` needs to calculate only a subset of the distances. To maximize the efficiency of *k*d-trees, use a `KDTreeSearcher` object.

What Are Search Objects?

Basically, objects are a convenient way of storing information. Classes of related objects (for example, all search objects) have the same properties with values and types relevant to a specified search method. In addition to storing information within objects, you can perform certain actions (called *methods*) on objects.

All search objects have a `knnsearch` method specific to that class. This lets you efficiently perform a *k*-nearest neighbors search on your object for that specific object type. In addition, there is a generic `knnsearch` function that searches without creating or using an object.

To determine which type of object and search method is best for your data, consider the following:

- Does your data have many columns, say more than 10? The `ExhaustiveSearcher` object may perform better.
- Is your data sparse? Use the `ExhaustiveSearcher` object.
- Do you want to use one of these distance measures to find the nearest neighbors? Use the `ExhaustiveSearcher` object.
  - `'seuclidean'`
  - `'mahalanobis'`
  - `'cosine'`
  - `'correlation'`
  - `'spearman'`
  - `'hamming'`
  - `'jaccard'`
  - A custom distance function

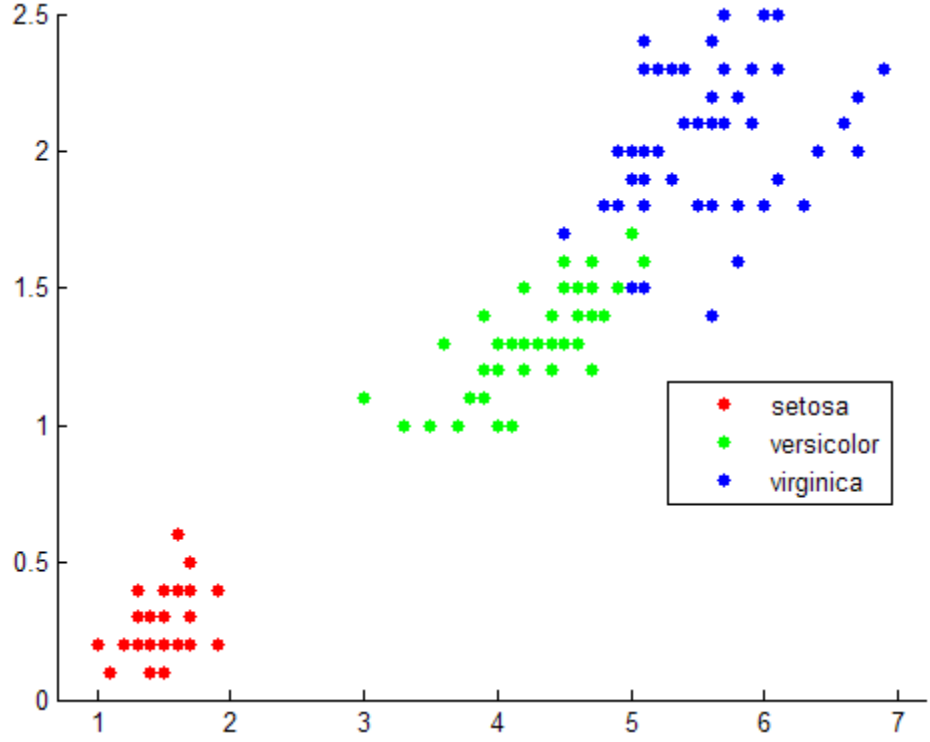
- Is your dataset huge (but with fewer than 10 columns)? Use the `KDTreeSearcher` object.
- Are you searching for the nearest neighbors for a large number of query points? Use the `KDTreeSearcher` object.

For more detailed information on object-oriented programming in MATLAB, see *Object-Oriented Programming*.

Example: Classifying Query Data Using knnsearch

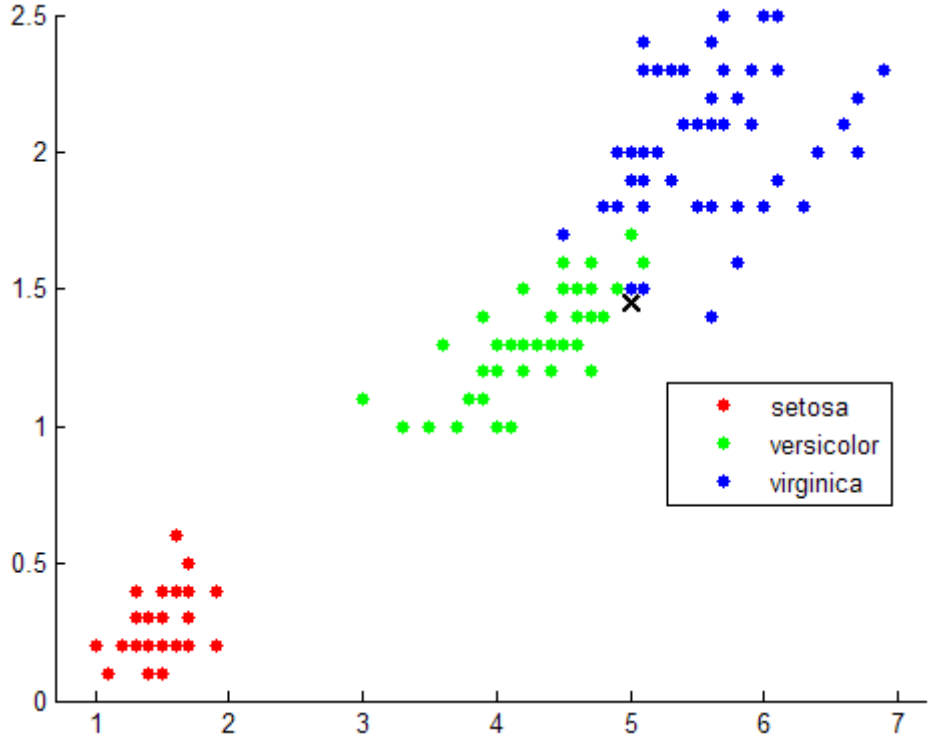
1 Classify a new point based on the last two columns of the Fisher iris data. Using only the last two columns makes it easier to plot:

```
load fisheriris
x = meas(:,3:4);
gscatter(x(:,1),x(:,2),species)
set(legend,'location','best')
```



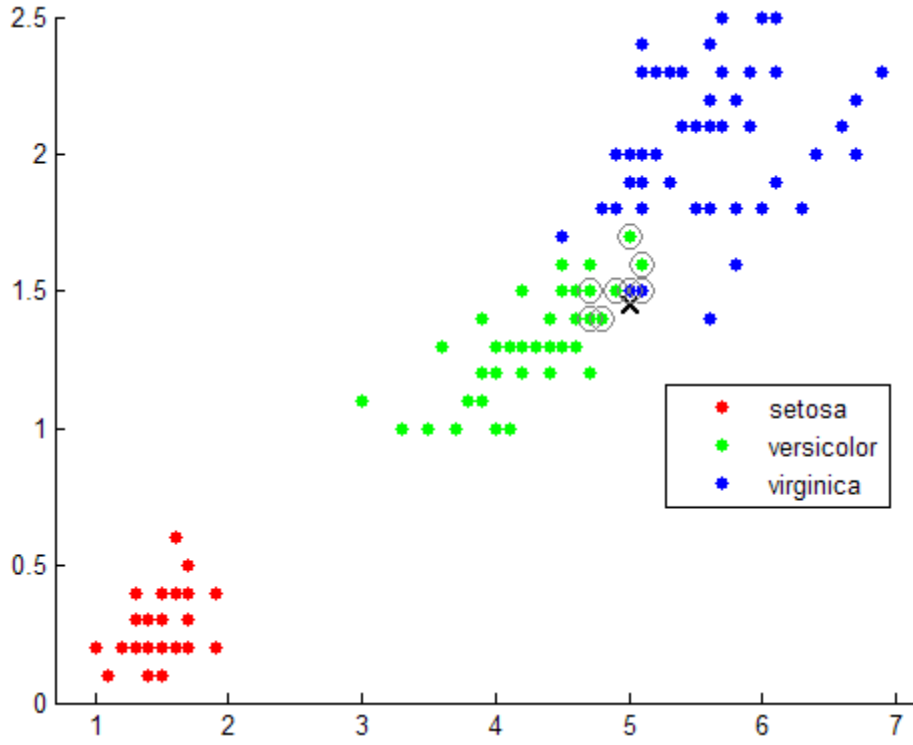
2 Plot the new point:

```
newpoint = [5 1.45];
line(newpoint(1),newpoint(2),'marker','x','color','k',...
   'markersize',10,'linewidth',2)
```



3 Find the 10 sample points closest to the new point:

```
[n,d] = knnsearch(x,newpoint,'k',10)
line(x(n,1),x(n,2),'color',[.5 .5 .5],'marker','o',...
    'linestyle','none','markersize',10)
```



4 It appears that `knnsearch` has found only the nearest eight neighbors. In fact, this particular dataset contains duplicate values:

```
x(n,:)

ans =

    5.0000    1.5000
    4.9000    1.5000
    4.9000    1.5000
    5.1000    1.5000
    5.1000    1.6000
    4.8000    1.4000
    5.0000    1.7000
    4.7000    1.4000
    4.7000    1.4000
```

```
    4.7000    1.5000
```

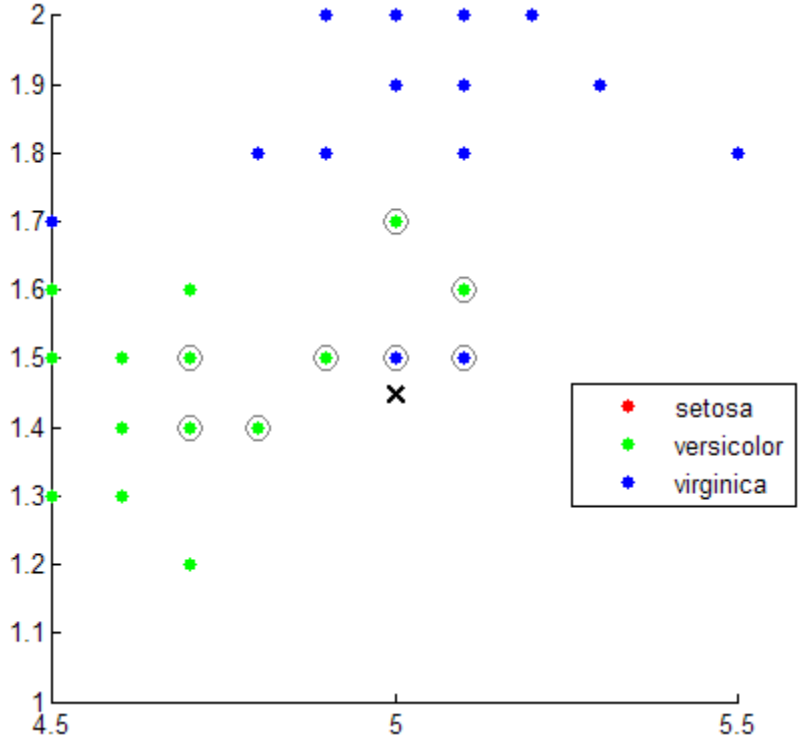
5 To make duplicate values visible on the plot, use the following code:

```
% jitter to make repeated points visible
xj = x + .05*(rand(150,2)-.5);
gscatter(xj(:,1),xj(:,2),species)
```

The jittered points do not affect any analysis of the data, only the visualization. This example does not jitter the points.

6 Make the axes equal so the calculated distances correspond to the apparent distances on the plot axis equal and zoom in to see the neighbors better:

```
set(gca,'xlim',[4.5 5.5],'ylim',[1 2]); axis square
```



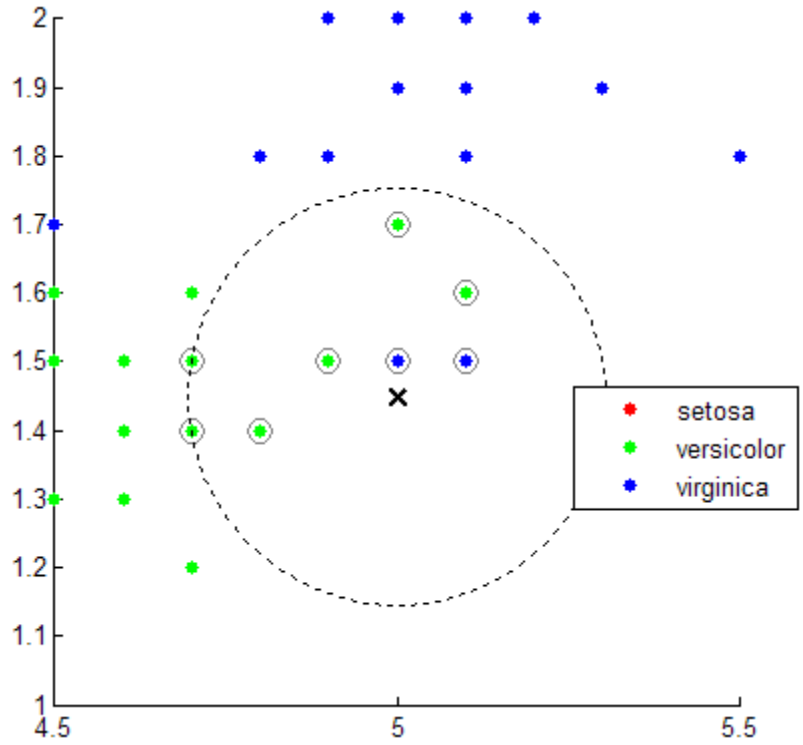
7 Find the species of the 10 neighbors:

```
tabulate(species(n))

       Value    Count   Percent
   virginica        2     20.00%
  versicolor        8     80.00%
```

Using a rule based on the majority vote of the 10 nearest neighbors, you can classify this new point as a versicolor.

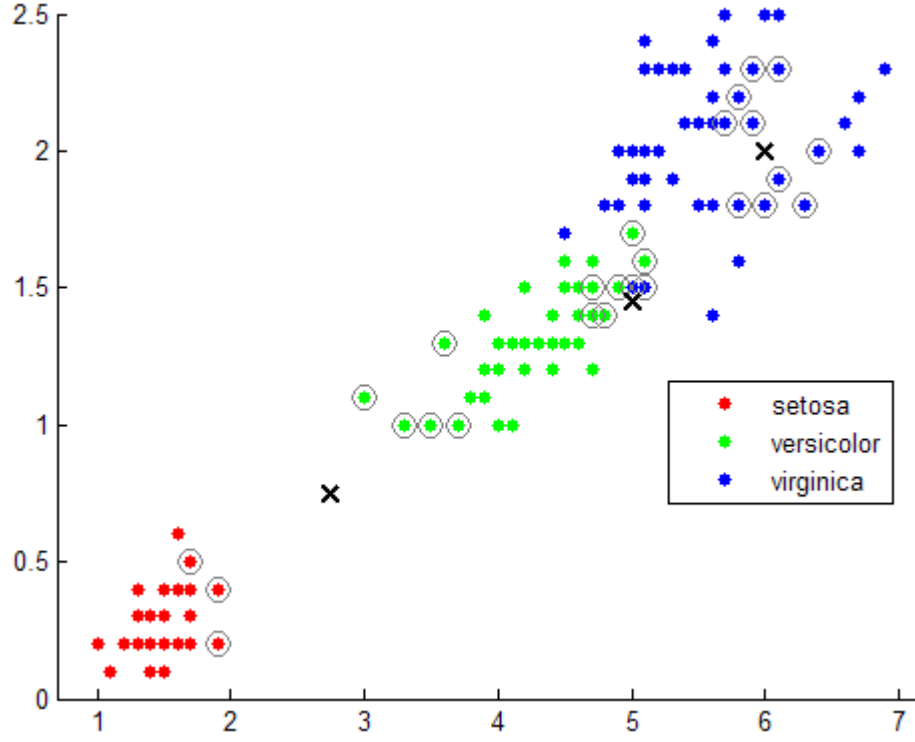
8 Visually identify the neighbors by drawing a circle around the group of them:

```
% Define the center and diameter of a circle, based on the
% location of the new point:
ctr = newpoint - d(end);
diameter = 2*d(end);
% Draw a circle around the 10 nearest neighbors:
h = rectangle('position',[ctr,diameter,diameter],...
   'curvature',[1 1]);
set(h,'linestyle',':')
```



9 Using the same dataset, find the 10 nearest neighbors to three new points:

```
figure
newpoint2 = [5 1.45;6 2;2.75 .75];
gscatter(x(:,1),x(:,2),species)
legend('location','best')
[n2,d2] = knnsearch(x,newpoint2,'k',10);
line(x(n2,1),x(n2,2),'color',[.5 .5 .5],'marker','o',...
   'linestyle','none','markersize',10)
line(newpoint2(:,1),newpoint2(:,2),'marker','x','color','k',...
   'markersize',10,'linewidth',2,'linestyle','none')
```



10 Find the species of the 10 nearest neighbors for each new point:

```
tabulate(species(n2(1,:)))
       Value    Count   Percent
   virginica        2     20.00%
  versicolor        8     80.00%

tabulate(species(n2(2,:)))
      Value    Count   Percent
  virginica       10    100.00%

tabulate(species(n2(3,:)))
       Value    Count   Percent
  versicolor        7     70.00%
      setosa        3     30.00%
```

For further examples using `knnsearch` methods and function, see the individual reference pages.

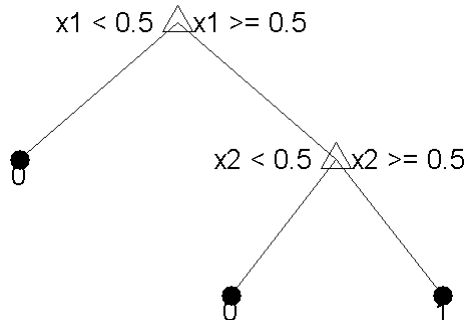
Classification Trees and Regression Trees

In this section...

What Are Classification Trees and Regression Trees?

Classification trees and regression trees predict responses to data. To predict a response, follow the decisions in the tree from the root (beginning) node down to a leaf node. The leaf node contains the response. Classification trees give responses that are nominal, such as `'true'` or `'false'`. Regression trees give numeric responses.

Statistics Toolbox trees are binary. Each step in a prediction involves checking the value of one predictor (variable). For example, here is a simple classification tree:



This tree predicts classifications based on two predictors, `x1` and `x2`. To predict, start at the top node, represented by a triangle (Δ). The first decision is whether `x1` is smaller than `0.5`. If so, follow the left branch, and see that the tree classifies the data as type `0`.

If, however, `x1` exceeds `0.5`, then follow the right branch to the lower-right triangle node. Here the tree asks if `x2` is smaller than `0.5`. If so, then follow the left branch to see that the tree classifies the data as type `0`. If not, then follow the right branch to see that the that the tree classifies the data as type `1`.

To learn how to prepare your data for classification or regression using decision trees, see "Steps in Supervised Learning (Machine Learning)" on page 13-2.

Example: Creating a Classification Tree

To create a classification tree for the `ionosphere` data:

```
load ionosphere % contains X and Y variables
ctree = ClassificationTree.fit(X,Y)

ctree =

ClassificationTree:
           PredictorNames: {1x34 cell}
    CategoricalPredictors: []
             ResponseName: 'Y'
               ClassNames: {'b'  'g'}
           ScoreTransform: 'none'
            NObservations: 351
```

Example: Creating a Regression Tree

To create a regression tree for the `carsmall` data based on the `Horsepower` and `Weight` vectors for data, and `MPG` vector for response:

```
load carsmall % contains Horsepower, Weight, MPG
X = [Horsepower Weight];
rtree = RegressionTree.fit(X,MPG)
```

```
rtree =

RegressionTree:
           PredictorNames: {'x1'  'x2'}
    CategoricalPredictors: []
             ResponseName: 'Y'
        ResponseTransform: 'none'
            NObservations: 94
```

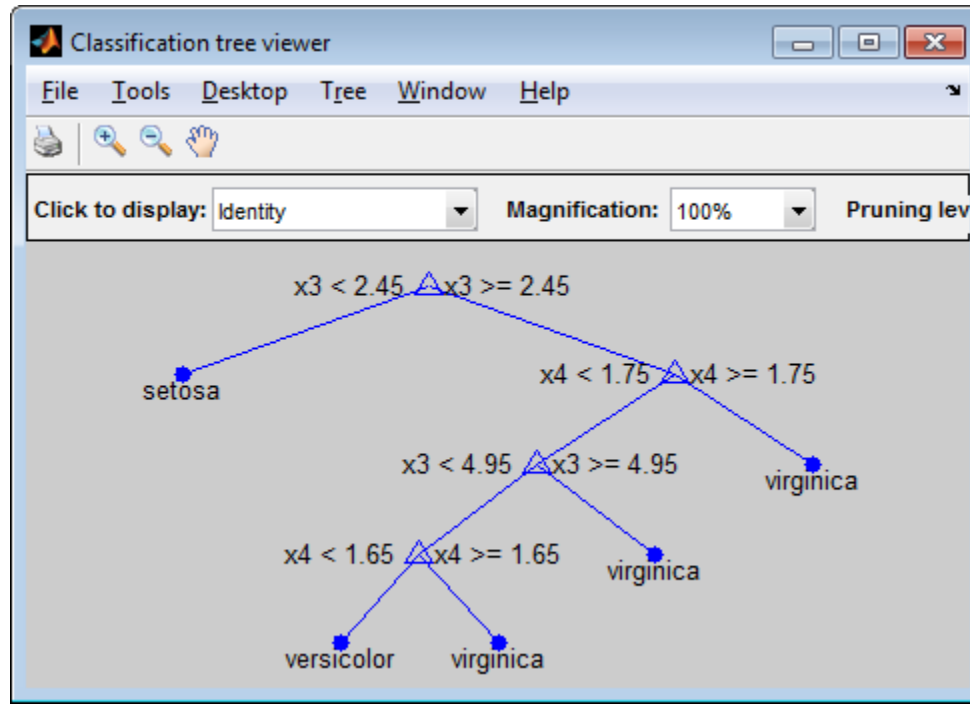
Viewing a Tree

There are two ways to view a tree:

- `view(tree)` returns a text description of the tree.
- `view(tree,'mode','graph')` returns a graphic description of the tree.

"Example: Creating a Classification Tree" on page 13-28 has the following two views:

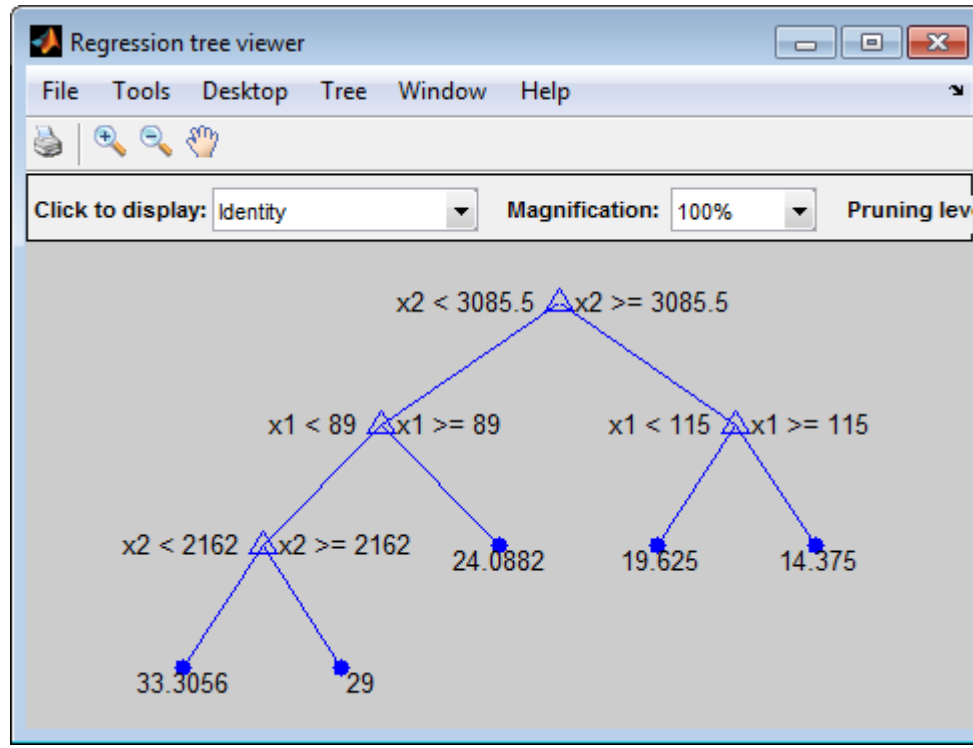
```
load fisheriris
ctree = ClassificationTree.fit(meas,species);
view(ctree)

Decision tree for classification
1  if x3<2.45 then node 2 elseif x3>=2.45 then node 3 else setosa
2  class = setosa
3  if x4<1.75 then node 4 elseif x4>=1.75 then node 5 else versicolor
4  if x3<4.95 then node 6 elseif x3>=4.95 then node 7 else versicolor
5  class = virginica
6  if x4<1.65 then node 8 elseif x4>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(ctree,'mode','graph')
```



Similarly, "Example: Creating a Regression Tree" on page 13-28 has the following two views:

```
load carsmall % contains Horsepower, Weight, MPG
X = [Horsepower Weight];
rtree = RegressionTree.fit(X,MPG,'MinParent',30);
view(rtree)

Decision tree for regression
1  if x2<3085.5 then node 2 elseif x2>=3085.5 then node 3 else 23.7181
2  if x1<89 then node 4 elseif x1>=89 then node 5 else 28.7931
3  if x1<115 then node 6 elseif x1>=115 then node 7 else 15.5417
4  if x2<2162 then node 8 elseif x2>=2162 then node 9 else 30.9375
5  fit = 24.0882
6  fit = 19.625
7  fit = 14.375
```

```
8   fit = 33.3056
9   fit = 29

view(rtree,'mode','graph')
```



How the Fit Methods Create Trees

The `ClassificationTree.fit` and `RegressionTree.fit` methods perform the following steps to create decision trees:

1. Start with all input data, and examine all possible binary splits on every predictor.
2. Select a split with best optimization criterion.

- If the split leads to a child node having too few observations (less than the `MinLeaf` parameter), select a split with the best optimization criterion subject to the `MinLeaf` constraint.

3. Impose the split.

4. Repeat recursively for the two child nodes.

The explanation requires two more items: description of the optimization criterion, and stopping rule.

Stopping rule: Stop splitting when any of the following hold:

- The node is *pure*.
  - For classification, a node is pure if it contains only observations of one class.
  - For regression, a node is pure if the mean squared error (MSE) for the observed response in this node drops below the MSE for the observed response in the entire data multiplied by the tolerance on quadratic error per node (`qetoler` parameter).
- There are fewer than `MinParent` observations in this node.
- Any split imposed on this node would produce children with fewer than `MinLeaf` observations.

Optimization criterion:

- Regression: mean-squared error (MSE). Choose a split to minimize the MSE of predictions compared to the training data.
- Classification: One of three measures, depending on the setting of the `SplitCriterion` name-value pair:
  - `'gdi'` (Gini's diversity index, the default)
  - `'twoing'`
  - `'deviance'`

  For details, see `ClassificationTree` "Definitions" on page 20-210.

For a continuous predictor, a tree can split halfway between any two adjacent unique values found for this predictor. For a categorical predictor with L levels, a classification tree needs to consider $2^{L-1}-1$ splits. To obtain this formula, observe that you can assign L distinct values to the left and right nodes in 2^L ways. Two out of these 2^L configurations would leave either left or right node empty, and therefore should be discarded. Now divide by 2 because left and right can be swapped. A classification tree can thus process only categorical predictors with a moderate number of levels. A regression tree employs a computational shortcut: it sorts the levels by the observed mean response, and considers only the $L-1$ splits between the sorted levels.

Predicting Responses With Classification Trees and Regression Trees

After creating a tree, you can easily predict responses for new data. Suppose `Xnew` is new data that has the same number of columns as the original data `X`. To predict the classification or regression based on the tree and the new data, enter

```
Ynew = predict(tree,Xnew);
```

For each row of data in `Xnew`, `predict` runs through the decisions in `tree` and gives the resulting prediction in the corresponding element of `Ynew`. For more information for classification, see the classification `predict` reference page; for regression, see the regression `predict` reference page.

For example, to find the predicted classification of a point at the mean of the `ionosphere` data:

```
load ionosphere % contains X and Y variables
ctree = ClassificationTree.fit(X,Y);
Ynew = predict(ctree,mean(X))

Ynew =
    'g'
```

To find the predicted `MPG` of a point at the mean of the `carsmall` data:

```
load carsmall % contains Horsepower, Weight, MPG
X = [Horsepower Weight];
rtree = RegressionTree.fit(X,MPG);
```

```
Ynew = predict(rtree,mean(X))

Ynew =
   28.7931
```

Improving Classification Trees and Regression Trees

You can tune trees by setting name-value pairs in `ClassificationTree.fit` and `RegressionTree.fit`. The remainder of this section describes how to determine the quality of a tree, how to decide which name-value pairs to set, and how to control the size of a tree:

Examining Resubstitution Error

Resubstitution error is the difference between the response training data and the predictions the tree makes of the response based on the input training data. If the resubstitution error is high, you cannot expect the predictions of the tree to be good. However, having low resubstitution error does not guarantee good predictions for new data. Resubstitution error is often an overly optimistic estimate of the predictive error on new data.

Example: Resubstitution Error of a Classification Tree. Examine the resubstitution error of a default classification tree for the Fisher iris data:

```
load fisheriris
ctree = ClassificationTree.fit(meas,species);
resuberror = resubLoss(ctree)

resuberror =
    0.0200
```

The tree classifies nearly all the Fisher iris data correctly.

Cross Validation

To get a better sense of the predictive accuracy of your tree for new data, cross validate the tree. By default, cross validation splits the training data into 10 parts at random. It trains 10 new trees, each one on nine parts of the data. It then examines the predictive accuracy of each new tree on the data not included in training that tree. This method gives a good estimate of the predictive accuracy of the resulting tree, since it tests the new trees on new data.

Example: Cross Validating a Regression Tree. Examine the resubstitution and cross-validation accuracy of a regression tree for predicting mileage based on the `carsmall` data:

```
load carsmall
X = [Acceleration Displacement Horsepower Weight];
rtree = RegressionTree.fit(X,MPG);
resuberror = resubLoss(rtree)

resuberror =
    4.7188
```

The resubstitution loss for a regression tree is the mean-squared error. The resulting value indicates that a typical predictive error for the tree is about the square root of 4.7, or a bit over 2.

Now calculate the error by cross validating the tree:

```
cvrtree = crossval(rtree);
cvloss = kfoldLoss(cvrtree)

cvloss =
   23.4808
```

The cross-validated loss is almost 25, meaning a typical predictive error for the tree on new data is about 5. This demonstrates that cross-validated loss is usually higher than simple resubstitution loss.

Control Depth or "Leafiness"

When you grow a decision tree, consider its simplicity and predictive power. A deep tree with many leaves is usually highly accurate on the training data.

However, the tree is not guaranteed to show a comparable accuracy on an independent test set. A leafy tree tends to overtrain, and its test accuracy is often far less than its training (resubstitution) accuracy. In contrast, a shallow tree does not attain high training accuracy. But a shallow tree can be more robust — its training accuracy could be close to that of a representative test set. Also, a shallow tree is easy to interpret.

If you do not have enough data for training and test, estimate tree accuracy by cross validation.

For an alternative method of controlling the tree depth, see "Pruning" on page 13-39.

Example: Selecting Appropriate Tree Depth. This example shows how to control the depth of a decision tree, and how to choose an appropriate depth.

1. Load the `ionosphere` data:

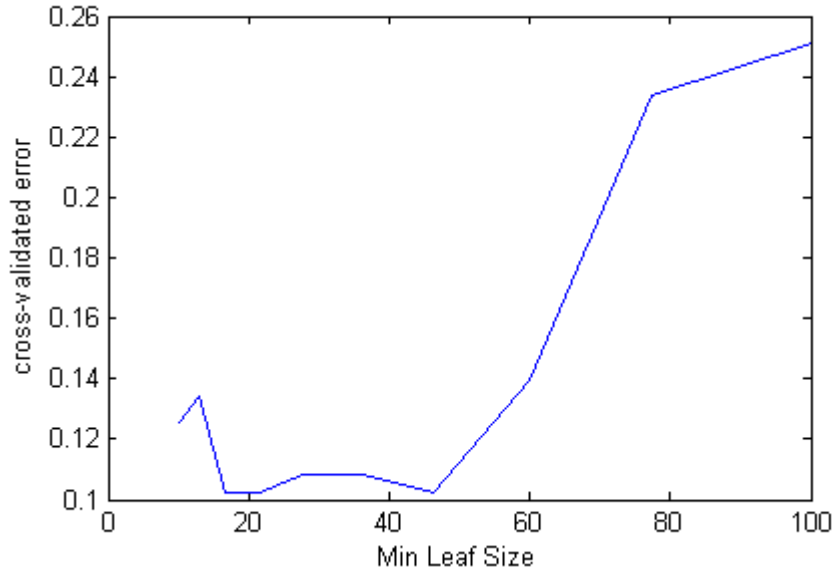
```
load ionosphere
```

2. Generate minimum leaf occupancies for classification trees from `10` to `100`, spaced exponentially apart:

```
leafs = logspace(1,2,10);
```

3. Create cross validated classification trees for the `ionosphere` data with minimum leaf occupancies from `leafs`:

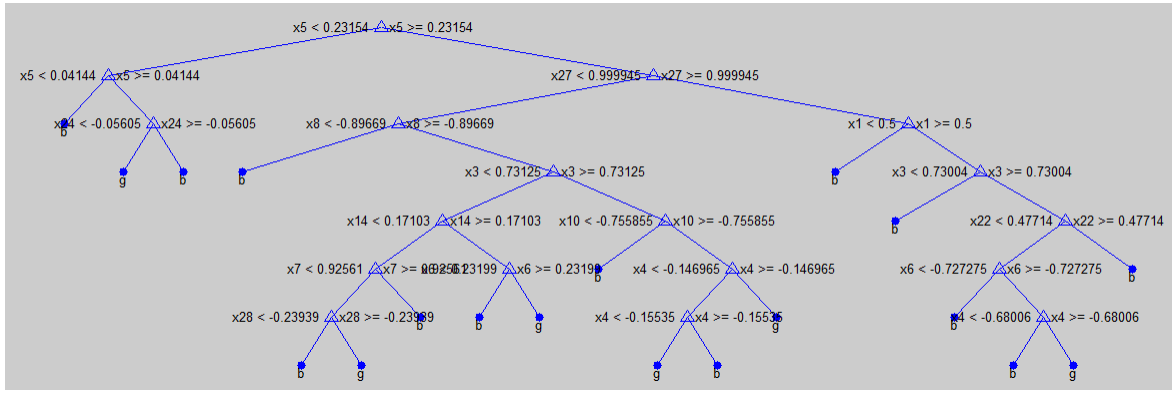
```
N = numel(leafs);
err = zeros(N,1);
for n=1:N
    t = ClassificationTree.fit(X,Y,'crossval','on',...
        'minleaf',leafs(n));
    err(n) = kfoldLoss(t);
end
plot(leafs,err);
xlabel('Min Leaf Size');
ylabel('cross-validated error');
```



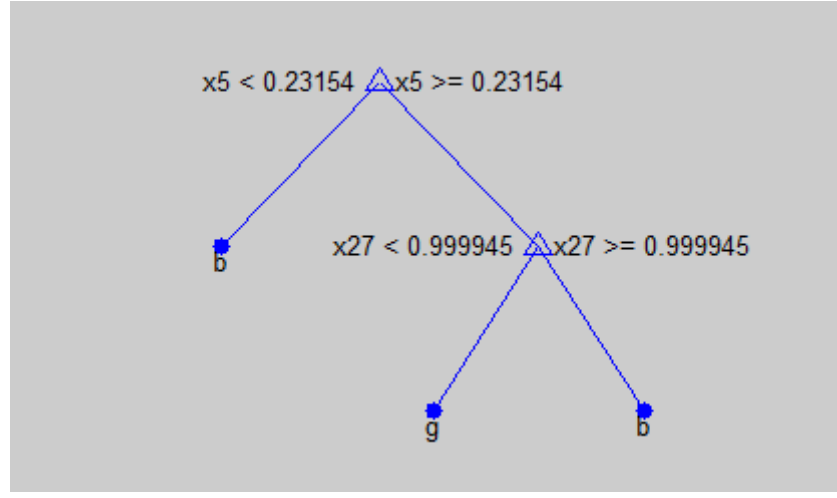
The best leaf size is between about 20 and 50 observations per leaf.

4 Compare the near-optimal tree with at least 40 observations per leaf with the default tree, which uses 10 observations per parent node and 1 observation per leaf.

```
DefaultTree = ClassificationTree.fit(X,Y);
view(DefaultTree,'mode','graph')
```




```
OptimalTree = ClassificationTree.fit(X,Y,'minleaf',40);
view(OptimalTree,'mode','graph')
```




```
resubOpt = resubLoss(OptimalTree);
lossOpt = kfoldLoss(crossval(OptimalTree));
resubDefault = resubLoss(DefaultTree);
lossDefault = kfoldLoss(crossval(DefaultTree));
resubOpt,resubDefault,lossOpt,lossDefault

resubOpt =
    0.0883
```

```
resubDefault =
    0.0114

lossOpt =
    0.1054

lossDefault =
    0.1026
```

The near-optimal tree is much smaller and gives a much higher resubstitution error. Yet it gives similar accuracy for cross-validated data.

Pruning

Pruning optimizes tree depth (leafiness) is by merging leaves on the same tree branch. “Control Depth or “Leafiness”” on page 13-35 describes one method for selecting the optimal depth for a tree. Unlike in that section, you do not need to grow a new tree for every node size. Instead, grow a deep tree, and prune it to the level you choose.

Prune a tree at the command line using the `prune` method (classification) or `prune` method (regression). Alternatively, prune a tree interactively with the tree viewer:

```
view(tree,'mode','graph')
```

To prune a tree, the tree must contain a pruning sequence. By default, both `ClassificationTree.fit` and `RegressionTree.fit` calculate a pruning sequence for a tree during construction. If you construct a tree with the `'Prune'` name-value pair set to `'off'`, or if you prune a tree to a smaller level, the tree does not contain the full pruning sequence. Generate the full pruning sequence with the `prune` method (classification) or `prune` method (regression).

Example: Pruning a Classification Tree. This example creates a classification tree for the `ionosphere` data, and prunes it to a good level.

1 Load the `ionosphere` data:

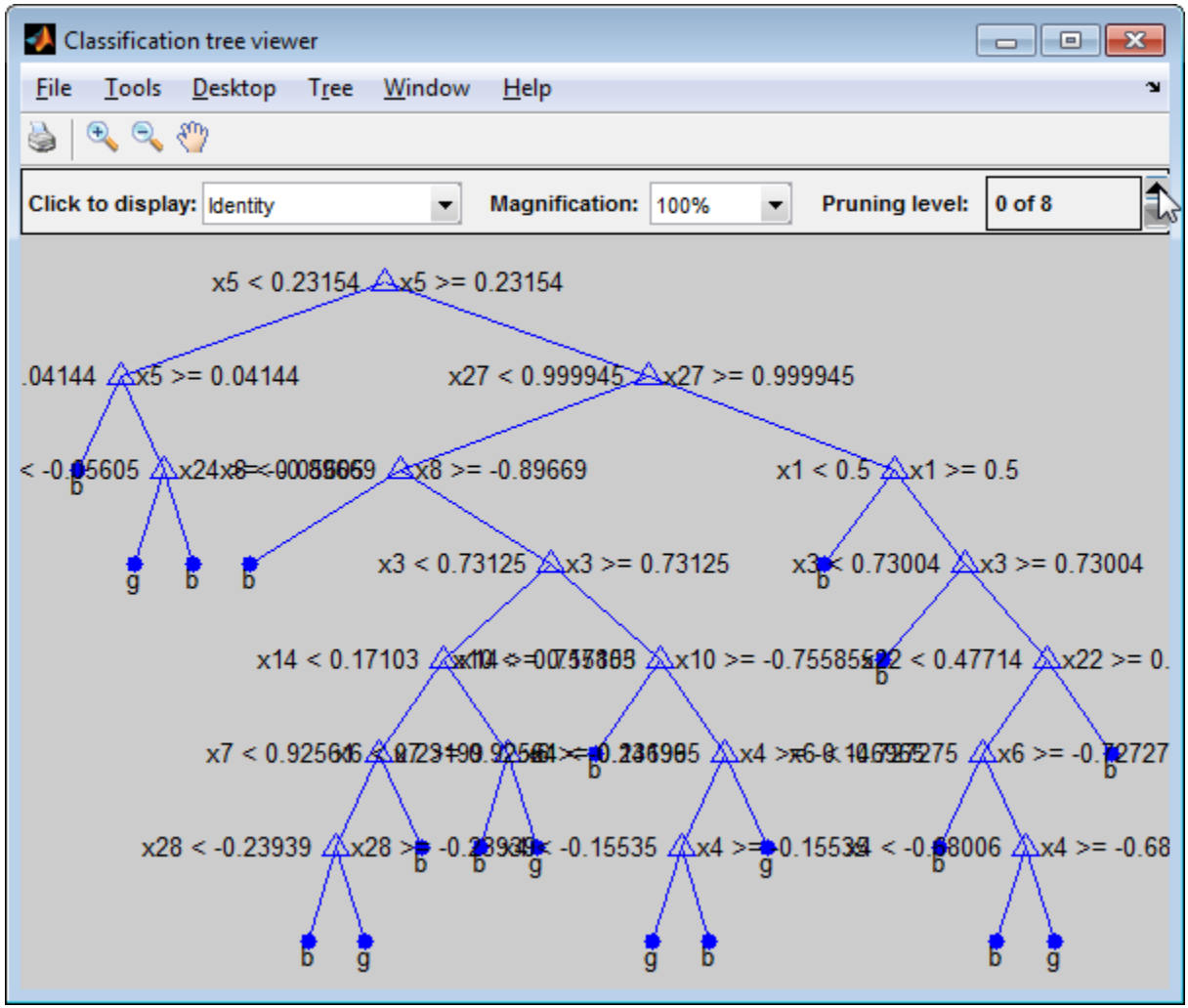
```
load ionosphere
```

2 Construct a default classification tree for the data:

```
tree = ClassificationTree.fit(X,Y);
```

3 View the tree in the interactive viewer:

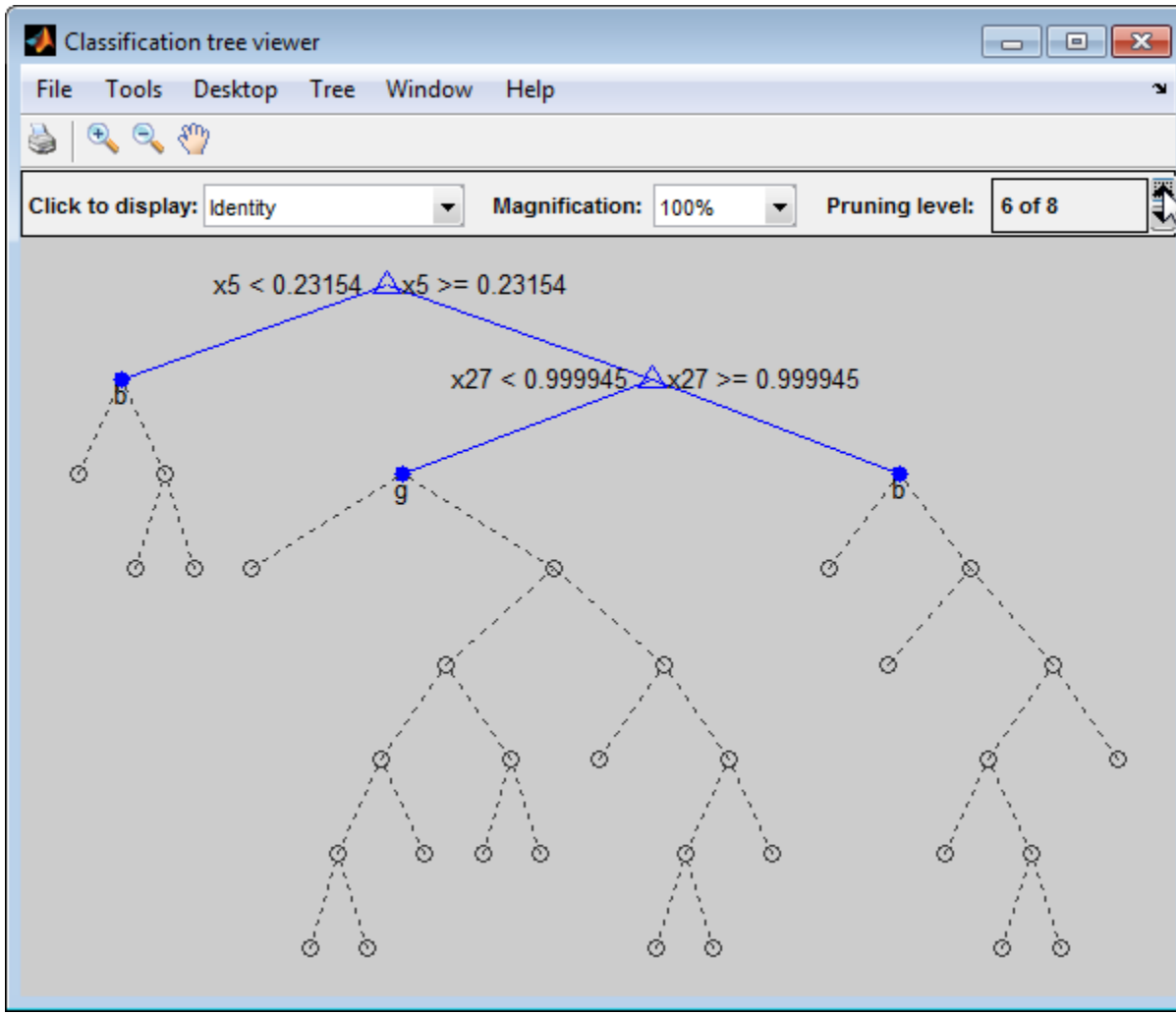
```
view(tree,'mode','graph')
```



4 Find the optimal pruning level by minimizing cross-validated loss:

```
[~,~,~,bestlevel] = cvLoss(tree,...
    'subtrees','all','treesize','min')

bestlevel =
     6
```

5 Prune the tree to level `6` in the interactive viewer:



The pruned tree is the same as the near-optimal tree in "Example: Selecting Appropriate Tree Depth" on page 13-36.

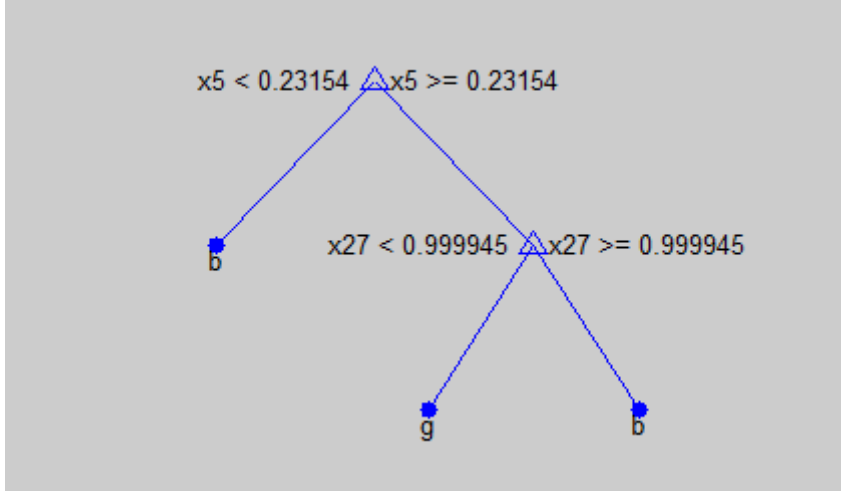
6 Set `'treesize'` to `'se'` (default) to find the maximal pruning level for which the tree error does not exceed the error from the best level plus one standard deviation:

```
[~,~,~,bestlevel] = cvLoss(tree,'subtrees','all')

bestlevel =
     6
```

In this case the level is the same for either setting of `'treesize'`.

7 Prune the tree to use it for other purposes:

```
tree = prune(tree,'Level',6);
view(tree,'mode','graph')
```



Alternative: classregtree

The `ClassificationTree` and `RegressionTree` classes are new in MATLAB R2011a. Previously, you represented both classification trees and regression trees with a `classregtree` object. The new classes provide all the functionality of the `classregtree` class, and are more convenient when used in conjunction with “Ensemble Methods” on page 13-51.

Before the `classregtree` class, there were `treefit`, `treedisp`, `treeval`, `treeprune`, and `treetest` functions. Statistics Toolbox software maintains these only for backward compatibility.

Example: Creating Classification Trees Using classregtree

This example uses Fisher's iris data in `fisheriris.mat` to create a classification tree for predicting species using measurements of sepal length, sepal width, petal length, and petal width as predictors. Here, the predictors are continuous and the response is categorical.

1. Load the data and use the `classregtree` constructor of the `classregtree` class to create the classification tree:

```
load fisheriris

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica
```

   `t` is a `classregtree` object and can be operated on with any class method.

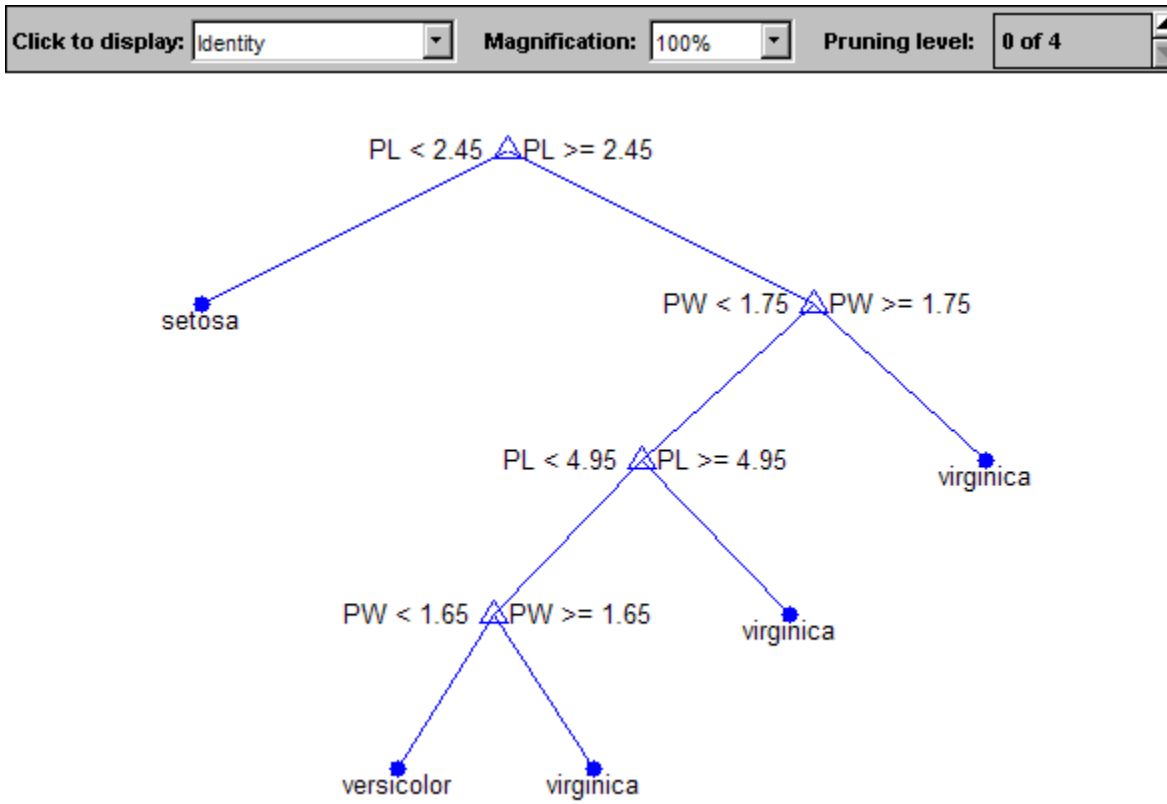
2. Use the `type` method of the `classregtree` class to show the type of the tree:

```
treetype = type(t)
treetype =
classification
```

   `classregtree` creates a classification tree because `species` is a cell array of strings, and the response is assumed to be categorical.

3. To view the tree, use the `view` method of the `classregtree` class:

```
view(t)
```



The tree predicts the response values at the circular leaf nodes based on a series of questions about the iris at the triangular branching nodes. A `true` answer to any question follows the branch to the left. A `false` follows the branch to the right.

4 The tree does not use sepal measurements for predicting species. These can go unmeasured in new data, and you can enter them as `NaN` values for predictions. For example, to use the tree to predict the species of an iris with petal length `4.8` and petal width `1.6`, type:

```
predicted = t([NaN NaN 4.8 1.6])
predicted =
    'versicolor'
```

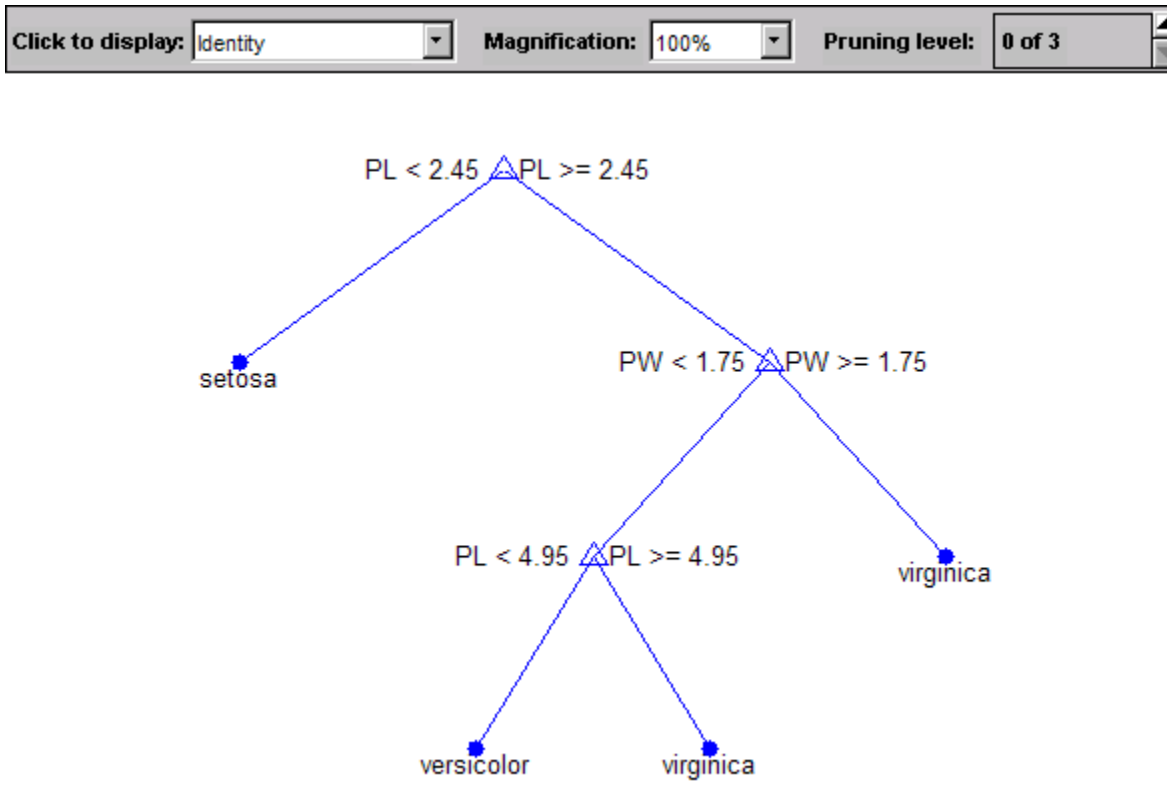
The object allows for functional evaluation, of the form `t(X)`. This is a shorthand way of calling the `eval` method of the `classregtree` class. The predicted species is the left leaf node at the bottom of the tree in the previous view.

5 You can use a variety of methods of the `classregtree` class, such as `cutvar` and `cuttype` to get more information about the split at node 6 that makes the final distinction between `versicolor` and `virginica`:

```
var6 = cutvar(t,6) % What variable determines the split?
var6 =
    'PW'

type6 = cuttype(t,6) % What type of split is it?
type6 =
    'continuous'
```

6 Classification trees fit the original (training) data well, but can do a poor job of classifying new values. Lower branches, especially, can be strongly affected by outliers. A simpler tree often avoids overfitting. You can use the `prune` method of the `classregtree` class to find the next largest tree from an optimal pruning sequence:

```
pruned = prune(t,'level',1)
pruned =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  class = versicolor
7  class = virginica

view(pruned)
```



To find the best classification tree, employing the techniques of resubstitution and cross validation, use the `test` method of the `classregtree` class.

Example: Creating Regression Trees Using classregtree

This example uses the data on cars in `carsmall.mat` to create a regression tree for predicting mileage using measurements of weight and the number of cylinders as predictors. Here, one predictor (weight) is continuous and the other (cylinders) is categorical. The response (mileage) is continuous.

1 Load the data and use the `classregtree` constructor of the `classregtree` class to create the regression tree:

```
load carsmall

t = classregtree([Weight, Cylinders],MPG,...
                 'cat',2,'splitmin',20,...
                 'names',{'W','C'})

t =

Decision tree for regression
 1  if W<3085.5 then node 2 elseif W>=3085.5 then node 3 else 23.7181
 2  if W<2371 then node 4 elseif W>=2371 then node 5 else 28.7931
 3  if C=8 then node 6 elseif C in {4 6} then node 7 else 15.5417
 4  if W<2162 then node 8 elseif W>=2162 then node 9 else 32.0741
 5  if C=6 then node 10 elseif C=4 then node 11 else 25.9355
 6  if W<4381 then node 12 elseif W>=4381 then node 13 else 14.2963
 7  fit = 19.2778
 8  fit = 33.3056
 9  fit = 29.6111
10  fit = 23.25
11  if W<2827.5 then node 14 elseif W>=2827.5 then node 15 else 27.2143
12  if W<3533.5 then node 16 elseif W>=3533.5 then node 17 else 14.8696
13  fit = 11
14  fit = 27.6389
15  fit = 24.6667
16  fit = 16.6
17  fit = 14.3889
```

`t` is a `classregtree` object and can be operated on with any of the methods of the class.

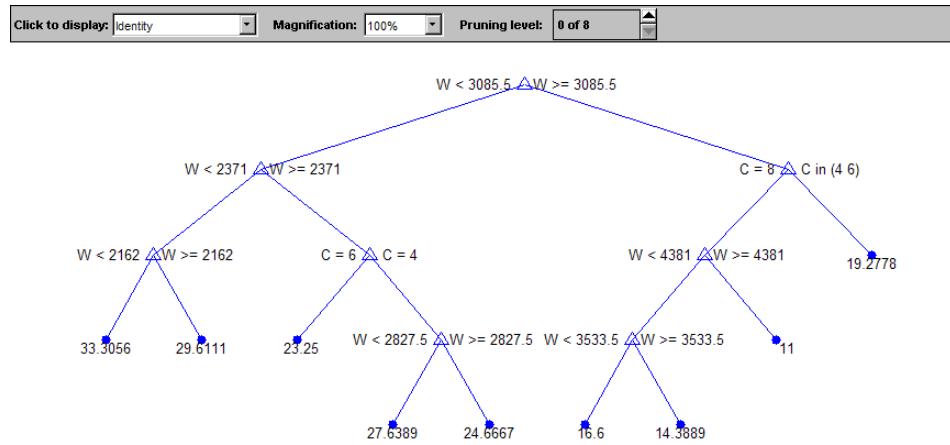
2 Use the `type` method of the `classregtree` class to show the type of the tree:

```
treetype = type(t)
treetype =
regression
```

`classregtree` creates a regression tree because `MPG` is a numerical vector, and the response is assumed to be continuous.

3 To view the tree, use the `view` method of the `classregtree` class:

```
view(t)
```



The tree predicts the response values at the circular leaf nodes based on a series of questions about the car at the triangular branching nodes. A `true` answer to any question follows the branch to the left; a `false` follows the branch to the right.

4 Use the tree to predict the mileage for a 2000-pound car with either 4, 6, or 8 cylinders:

```
mileage2K = t([2000 4; 2000 6; 2000 8])
mileage2K =
   33.3056
   33.3056
   33.3056
```

The object allows for functional evaluation, of the form `t(X)`. This is a shorthand way of calling the `eval` method of the `classregtree` class.

5 The predicted responses computed above are all the same. This is because they follow a series of splits in the tree that depend only on weight, terminating at the left-most leaf node in the view above. A 4000-pound car, following the right branch from the top of the tree, leads to different predicted responses:

```
mileage4K = t([4000 4; 4000 6; 4000 8])
```

```
mileage4K =
   19.2778
   19.2778
   14.3889
```

6 You can use a variety of other methods of the `classregtree` class, such as `cutvar`, `cuttype`, and `cutcategories`, to get more information about the split at node 3 that distinguishes the 8-cylinder car:

```
var3 = cutvar(t,3) % What variable determines the split?
var3 =
    'C'

type3 = cuttype(t,3) % What type of split is it?
type3 =
    'categorical'

c = cutcategories(t,3) % Which classes are sent to the left
                       % child node, and which to the right?
c =
    [8]    [1x2 double]
c{1}
ans =
     8
c{2}
ans =
     4     6
```

Regression trees fit the original (training) data well, but may do a poor job of predicting new values. Lower branches, especially, may be strongly affected by outliers. A simpler tree often avoids over-fitting. To find the best regression tree, employing the techniques of resubstitution and cross validation, use the `test` method of the `classregtree` class.

Ensemble Methods

In this section...

Framework for Ensemble Learning

You have several methods for melding results from many weak learners into one high-quality ensemble predictor. These methods follow, as closely as possible, the same syntax, so you can try different methods with only minor changes in your commands.

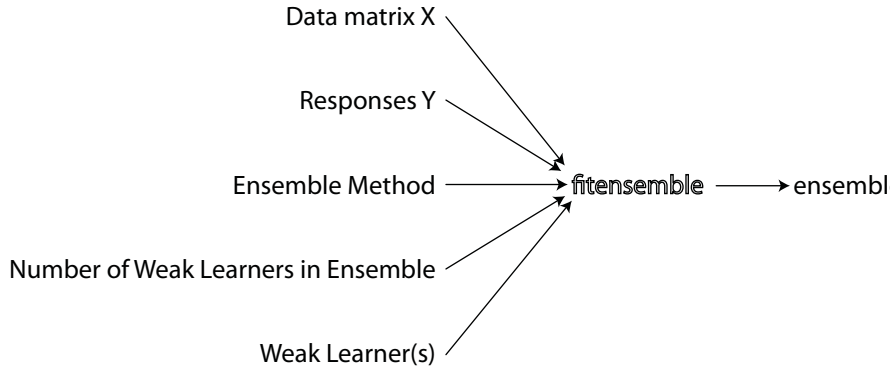
Create an ensemble with the `fitensemble` function. The syntax of `fitensemble` is

```
ens = fitensemble(X,Y,model,numberens,learners)
```

- `X` is the matrix of data, each row containing one observation, each column contains one predictor variable.
- `Y` is the responses, with the same number of observations as rows in `X`.
- `model` is a string naming the type of ensemble.
- `numberens` is the number of weak learners in `ens` from each element of `learners`. So the number of elements in `ens` is `numberens` times the number of elements in `learners`.

- `learners` is a string naming a weak learner, is a weak learner template, or is a cell array of such templates.

Pictorially, here is the information you need to create an ensemble:



For all classification or nonlinear regression problems, follow these steps to create an ensemble:

1 "Put Predictor Data in a Matrix" on page 13-52

2 "Prepare Response Data" on page 13-53

3 "Choose an Applicable Ensemble Method" on page 13-54

4 "Set the Number of Ensemble Members" on page 13-55

5 "Prepare the Weak Learners" on page 13-55

6 "Call fitensemble" on page 13-56

Put Predictor Data in a Matrix

All supervised learning methods start with a data matrix, usually called `X` in this documentation. Each row of `X` represents one observation. Each column of `X` represents one variable, or predictor.

Currently, you can use only decision trees as learners for ensembles. Decision trees can handle `NaN` values in `X`. Such values are called "missing." If you have

some missing values in a row of `X`, a decision tree finds optimal splits using nonmissing values only. If an entire row consists of `NaN`, `fitensemble` ignores that row. If you have data with a large fraction of missing values in `X`, use surrogate decision splits. For examples of surrogate splits, see "Example: Unequal Classification Costs" on page 13-67 and "Example: Surrogate Splits" on page 13-77.

Prepare Response Data

You can use a wide variety of data types for response data.

- For regression ensembles, `Y` must be a numeric vector with the same number of elements as the number of rows of `X`.
- For classification ensembles, `Y` can be any of the following data types. The table also contains the method of including missing entries.

Data Type	Missing Entry
Numeric vector	`NaN`
Categorical vector	`<undefined>`
Character array	Row of spaces
Cell array of strings	`''`
Logical vector	(not possible to represent)

`fitensemble` ignores missing values in `Y` when creating an ensemble.

For example, suppose your response data consists of three observations in the following order: `true`, `false`, `true`. You could express `Y` as:

- `[1;0;1]` (numeric vector)
- `nominal({'true','false','true'})` (categorical vector)
- `[true;false;true]` (logical vector)
- `['true ';'false';'true ']` (character array, padded with spaces so each row has the same length)
- `{'true','false','true'}` (cell array of strings)

Use whichever data type is most convenient. Since you cannot represent missing values with logical entries, do not use logical entries when you have missing values in `Y`.

Choose an Applicable Ensemble Method

`fitensemble` uses one of these algorithms to create an ensemble.

- For classification with two classes:
  - `'AdaBoostM1'`
  - `'LogitBoost'`
  - `'GentleBoost'`
  - `'RobustBoost'`
  - `'Bag'`
- For classification with three or more classes:
  - `'AdaBoostM2'`
  - `'Bag'`
- For regression:
  - `'LSBoost'`
  - `'Bag'`

Since `'Bag'` applies to all methods, indicate whether you want a classifier or regressor with the `type` name-value pair set to `'classification'` or `'regression'`.

For descriptions of the various algorithms, and aid in choosing which applies to your data, see "Ensemble Algorithms" on page 13-118. The following table gives characteristics of the various algorithms. In the table titles:

- `Regress.` — Regression
- `Classif.` — Classification
- `Preds.` — Predictors
- `Estim.` — Estimate

- `Gen.` — Generalization
- `Pred.` — Prediction
- `Mem.` — Memory usage

Algorithm	Regress.	Binary Classif.	Binary Classif. Multi-Level Preds.	Classif. 3+ Classes	Auto Estim. Gen. Error	Fast Train	Fast Pred.	Low Mem.
`Bag`	×	×		×	×			
`AdaBoostM1`		×				×	×	×
`AdaBoostM2`				×		×	×	×
`LogitBoost`		×	×			×	×	×
`GentleBoost`		×	×			×	×	×
`RobustBoost`		×					×	×
`LSBoost`	×					×	×	×

Set the Number of Ensemble Members

Choosing the size of an ensemble involves balancing speed and accuracy.

- Larger ensembles take longer to train and to generate predictions.
- Some ensemble algorithms can become overtrained (inaccurate) when too large.

To set an appropriate size, consider starting with several dozen to several hundred members in an ensemble, training the ensemble, and then checking the ensemble quality, as in "Example: Test Ensemble Quality" on page 13-60. If it appears that you need more members, add them using the `resume` method (classification) or the `resume` method (regression). Repeat until adding more members does not improve ensemble quality.

Prepare the Weak Learners

Currently there is one built-in weak learner type: `'Tree'`. To create an ensemble with the default tree options, pass in `'Tree'` as the weak learner.

To set a nondefault classification tree learner, create a classification tree template with the `ClassificationTree.template` method.

Similarly, to set a nondefault regression tree learner, create a regression tree template with the `RegressionTree.template` method.

While you can give `fitensemble` a cell array of learner templates, the most common usage is to give just one weak learner template.

For examples using a template, see "Example: Unequal Classification Costs" on page 13-67 and "Example: Surrogate Splits" on page 13-77.

Common Settings for Weak Learners.

- The depth of the weak learner tree makes a difference for training time, memory usage, and predictive accuracy. You control the depth with two parameters:
  - `MinLeaf` — Each leaf has at least `MinLeaf` observations. Set small values of `MinLeaf` to get a deep tree.
  - `MinParent` — Each branch node in the tree has at least `MinParent` observations. Set small values of `MinParent` to get a deep tree.

  If you supply both `MinParent` and `MinLeaf`, the learner uses the setting that gives larger leaves:

  ```
  MinParent = max(MinParent,2*MinLeaf)
  ```

- `Surrogate` — Grow decision trees with surrogate splits when `Surrogate` is `'on'`. Use surrogate splits when your data has missing values.

  Note Surrogate splits cause training to be slower and use more memory.

Call fitensemble

The syntax of `fitensemble` is

```
ens = fitensemble(X,Y,model,numberens,learners)
```

- `X` is the matrix of data. Each row contains one observation, and each column contains one predictor variable.
- `Y` is the responses, with the same number of observations as rows in `X`.
- `model` is a string naming the type of ensemble.
- `numberens` is the number of weak learners in `ens` from each element of `learners`. So the number of elements in `ens` is `numberens` times the number of elements in `learners`.
- `learners` is a string naming a weak learner, a weak learner template, or a cell array of such strings and templates.

The result of `fitensemble` is an ensemble object, suitable for making predictions on new data. For a basic example of creating a classification ensemble, see "Creating a Classification Ensemble" on page 13-58. For a basic example of creating a regression ensemble, see "Creating a Regression Ensemble" on page 13-59.

Where to Set Name-Value Pairs. There are several name-value pairs you can pass to `fitensemble`, and several that apply to the weak learners (`ClassificationTree.template` and `RegressionTree.template`). To determine which option (name-value pair) is appropriate, the ensemble or the weak learner:

- Use template name-value pairs to control the characteristics of the weak learners.
- Use `fitensemble` name-value pairs to control the ensemble as a whole, either for algorithms or for structure.

For example, to have an ensemble of boosted classification trees with each tree deeper than the default, set the `ClassificationTree.template` name-value pairs (`MinLeaf` and `MinParent`) to smaller values than the defaults. This causes the trees to be leafier (deeper).

To name the predictors in the ensemble (part of the structure of the ensemble), use the `PredictorNames` name-value pair in `fitensemble`.

Basic Ensemble Examples

Creating a Classification Ensemble

Create a classification ensemble for the Fisher iris data, and use it to predict the classification of a flower with average measurements.

1. Load the data:

```
load fisheriris
```

2. The predictor data `X` is the `meas` matrix.

3. The response data `Y` is the `species` cell array.

4. The only boosted classification ensemble for three or more classes is `'AdaBoostM2'`.

5. For this example, arbitrarily take an ensemble of `100` trees.

6. Use a default tree template.

7. Create the ensemble:

```
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree')

ens =
classreg.learning.classif.ClassificationEnsemble:
           PredictorNames: {'x1'  'x2'  'x3'  'x4'}
    CategoricalPredictors: []
             ResponseName: 'Y'
                ClassNames: {'setosa'  'versicolor'  'virginica'}
           ScoreTransform: 'none'
            NObservations: 150
                 NTrained: 100
                   Method: 'AdaBoostM2'
            LearnerNames: {'Tree'}
     ReasonForTermination: [1x77 char]
                  FitInfo: [100x1 double]
       FitInfoDescription: [2x83 char]
```

8. Predict the classification of a flower with average measurements:

```
flower = predict(ens,mean(meas))

flower =
    'versicolor'
```

Creating a Regression Ensemble

Create a regression ensemble to predict mileage of cars based on their horsepower and weight, trained on the `carsmall` data. Use the resulting ensemble to predict the mileage of a car with 150 horsepower weighing 2750 lbs.

1 Load the data:

```
load carsmall
```

2 Prepare the input data.

```
X = [Horsepower Weight];
```

3 The response data `Y` is `MPG`.

4 The only boosted regression ensemble type is `'LSBoost'`.

5 For this example, arbitrarily take an ensemble of `100` trees.

6 Use a default tree template.

7 Create the ensemble:

```
ens = fitensemble(X,MPG,'LSBoost',100,'Tree')

ens =
classreg.learning.regr.RegressionEnsemble:
           PredictorNames: {'x1'  'x2'}
    CategoricalPredictors: []
             ResponseName: 'Y'
        ResponseTransform: 'none'
            NObservations: 94
                 NTrained: 100
                   Method: 'LSBoost'
             LearnerNames: {'Tree'}
```

```
    ReasonForTermination: [1x77 char]
                 FitInfo: [100x1 double]
       FitInfoDescription: [2x83 char]
           Regularization: []
```

8 Predict the mileage of a car with 150 horsepower weighing 2750 lbs:

```
mileage = ens.predict([150 2750])

mileage =
   22.6735
```

Test Ensemble Quality

Usually you cannot evaluate the predictive quality of an ensemble based on its performance on training data. Ensembles tend to "overtrain," meaning they produce overly optimistic estimates of their predictive power. This means the result of `resubLoss` for classification (`resubLoss` for regression) usually indicates lower error than you get on new data.

To obtain a better idea of the quality of an ensemble, use one of these methods:

- Evaluate the ensemble on an independent test set (useful when you have a lot of training data).
- Evaluate the ensemble by cross validation (useful when you don't have a lot of training data).
- Evaluate the ensemble on out-of-bag data (useful when you create a bagged ensemble with `fitensemble`).

Example: Test Ensemble Quality

This example uses a bagged ensemble so it can use all three methods of evaluating ensemble quality.

1 Generate an artificial dataset with 20 predictors. Each entry is a random number from 0 to 1. The initial classification:

$Y = 1$ when $X(1) + X(2) + X(3) + X(4) + X(5) > 2.5$
$Y = 0$ otherwise.

```
rng(1,'twister') % for reproducibility
X = rand(2000,20);
Y = sum(X(:,1:5),2) > 2.5;
```

In addition, to add noise to the results, randomly switch 10% of the classifications:

```
idx = randsample(2000,200);
Y(idx) = ~Y(idx);
```

2 Independent Test Set

Create independent training and test sets of data. Use 70% of the data for a training set by calling `cvpartition` with the `holdout` option:

```
cvpart = cvpartition(Y,'holdout',0.3);
Xtrain = X(training(cvpart),:);
Ytrain = Y(training(cvpart),:);
Xtest = X(test(cvpart),:);
Ytest = Y(test(cvpart),:);
```

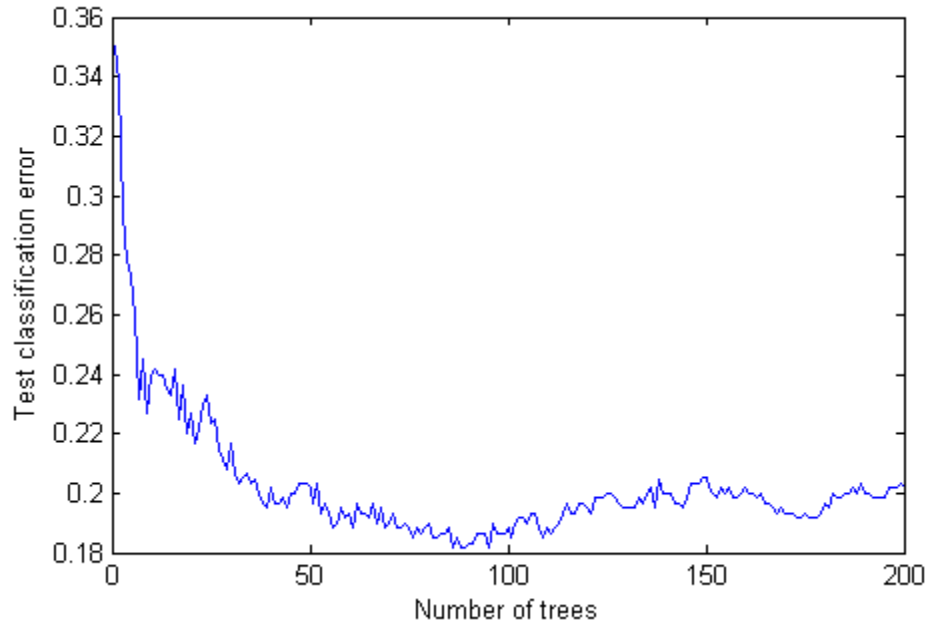
3 Create a bagged classification ensemble of 200 trees from the training data:

```
bag = fitensemble(Xtrain,Ytrain,'Bag',200,'Tree',...
    'type','classification')

bag =

classreg.learning.classif.ClassificationBaggedEnsemble:
           PredictorNames: {1x20 cell}
    CategoricalPredictors: []
             ResponseName: 'Y'
                ClassNames: [0 1]
           ScoreTransform: 'none'
            NObservations: 1400
                 NTrained: 200
                   Method: 'Bag'
             LearnerNames: {'Tree'}
     ReasonForTermination: [1x77 char]
                  FitInfo: []
       FitInfoDescription: 'None'
```

```
          FResample: 1
            Replace: 1
  UseObsForLearner: [1400x200 logical]
```

4 Plot the loss (misclassification) of the test data as a function of the number of trained trees in the ensemble:

```
figure;
plot(loss(bag,Xtest,Ytest,'mode','cumulative'));
xlabel('Number of trees');
ylabel('Test classification error');
```



5 Cross validation

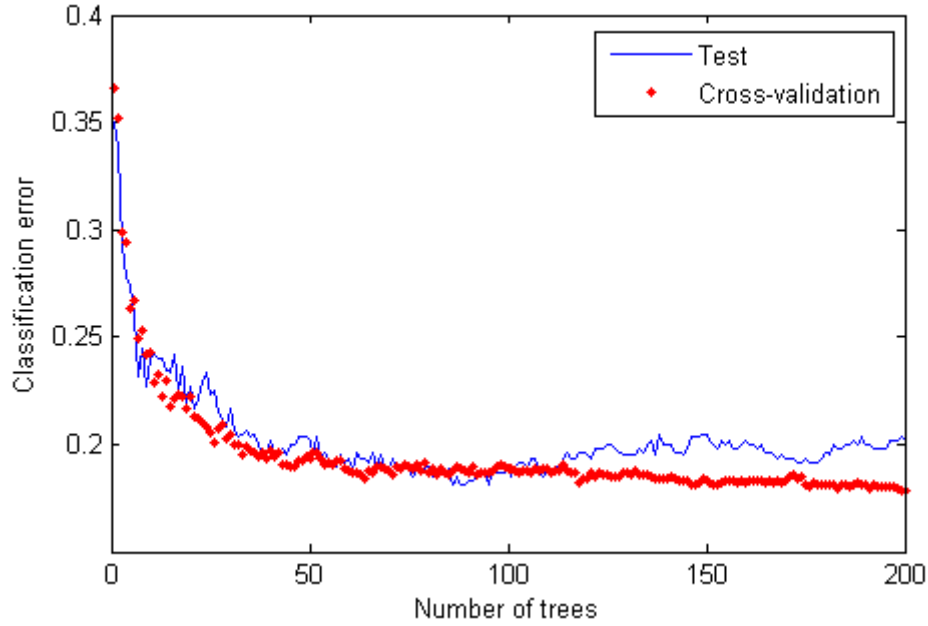
Generate a five-fold cross-validated bagged ensemble:

```
cv = fitensemble(X,Y,'Bag',200,'Tree',...
    'type','classification','kfold',5)
```

```
cv =

classreg.learning.partition.ClassificationPartitionedEnsemble:
      CrossValidatedModel: 'Bag'
           PredictorNames: {1x20 cell}
    CategoricalPredictors: []
             ResponseName: 'Y'
            NObservations: 2000
                    KFold: 5
                Partition: [1x1 cvpartition]
           NTrainedPerFold: [200 200 200 200 200]
               ClassNames: [0 1]
           ScoreTransform: 'none'
```

6 Examine the cross validation loss as a function of the number of trees in the ensemble:

```
figure;
plot(loss(bag,Xtest,Ytest,'mode','cumulative'));
hold
plot(kfoldLoss(cv,'mode','cumulative'),'r.');
hold off;
xlabel('Number of trees');
ylabel('Classification error');
legend('Test','Cross-validation','Location','NE');
```

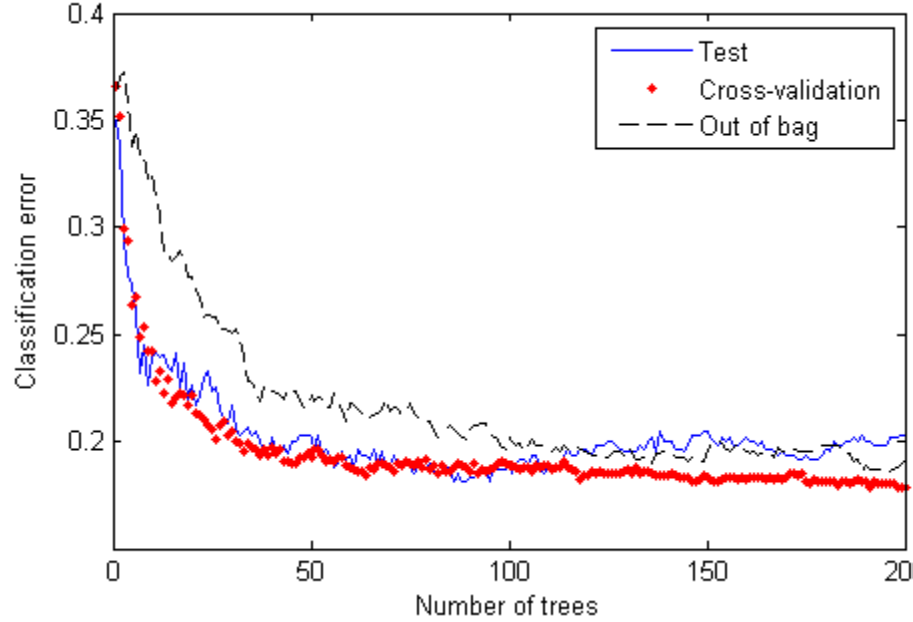


Cross validating gives comparable estimates to those of the independent set.

7 Out-of-Bag Estimates

Generate the loss curve for out-of-bag estimates, and plot it along with the other curves:

```
figure;
plot(loss(bag,Xtest,Ytest,'mode','cumulative'));
hold
plot(kfoldLoss(cv,'mode','cumulative'),'r.');
plot(oobLoss(bag,'mode','cumulative'),'k--');
hold off;
xlabel('Number of trees');
ylabel('Classification error');
legend('Test','Cross-validation','Out of bag','Location','NE');
```



The out-of-bag estimates are again comparable to those of the other methods.

Classification: Imbalanced Data or Unequal Misclassification Costs

In many real-world applications, you might prefer to treat classes in your data asymmetrically. For example, you might have data with many more observations of one class than of any other. Or you might work on a problem in which misclassifying observations of one class has more severe consequences than misclassifying observations of another class. In such situations, you can use two optional parameters for `fitensemble`: `prior` and `cost`.

By using `prior`, you set prior class probabilities (that is, class probabilities used for training). Use this option if some classes are under- or overrepresented in your training set. For example, you might obtain your training data by simulation. Because simulating class `A` is more expensive than class `B`, you opt to generate fewer observations of class `A` and more

observations of class `B`. You expect, however, that class `A` and class `B` are mixed in a different proportion in the real world. In this case, set prior probabilities for class `A` and `B` approximately to the values you expect to observe in the real world. `fitensemble` normalizes prior probabilities to make them add up to `1`; multiplying all prior probabilities by the same positive factor does not affect the result of classification.

If classes are adequately represented in the training data but you want to treat them asymmetrically, use the `cost` parameter. Suppose you want to classify benign and malignant tumors in cancer patients. Failure to identify a malignant tumor (false negative) has far more severe consequences than misidentifying benign as malignant (false positive). You should assign high cost to misidentifying malignant as benign and low cost to misidentifying benign as malignant.

You must pass misclassification costs as a square matrix with nonnegative elements. Element `C(i,j)` of this matrix is the cost of classifying an observation into class `j` if the true class is `i`. The diagonal elements `C(i,i)` of the cost matrix must be `0`. For the example above, you can choose malignant tumor to be class 1 and benign tumor to be class 2. Then you can set the cost matrix to

$$\begin{bmatrix} 0 & c \\ 1 & 0 \end{bmatrix}$$

where $c > 1$ is the cost of misidentifying a malignant tumor as benign. Costs are relative—multiplying all costs by the same positive factor does not affect the result of classification.

If you have only two classes, `fitensemble` adjusts their prior probabilities using $\tilde{P}_i = C_{ij} P_i$ for class $i = 1,2$ and $j \neq i$. P_i are prior probabilities either passed into `fitensemble` or computed from class frequencies in the training data, and $\tilde{P}_i$ are adjusted prior probabilities. Then `fitensemble` uses the default cost matrix

$$\begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix}$$

and these adjusted probabilities for training its weak learners. Manipulating the cost matrix is thus equivalent to manipulating the prior probabilities.

If you have three or more classes, `fitensemble` also converts input costs into adjusted prior probabilities. This conversion is more complex. First, `fitensemble` attempts to solve a matrix equation described in Zhou and Liu [12]. If it fails to find a solution, `fitensemble` applies the "average cost" adjustment described in Breiman et al. [4]. For more information, see .Zadrozny, Langford, and Abe [11]

Example: Unequal Classification Costs

This example uses data on patients with hepatitis to see if they live or die as a result of the disease. The data is described at `http://archive.ics.uci.edu/ml/datasets/Hepatitis`.

1. Load the data into a file named `hepatitis.txt`:

```
s = urlread(['http://archive.ics.uci.edu/ml/' ...
  'machine-learning-databases/hepatitis/hepatitis.data']);
fid = fopen('hepatitis.txt','w');
fwrite(fid,s);
fclose(fid);
```

2. Load the data `hepatitis.txt` into a dataset, with variable names describing the fields in the data:

```
VarNames = {'die_or_live' 'age' 'sex' 'steroid' 'antivirals' 'fatigue' ...
    'malaise' 'anorexia' 'liver_big' 'liver_firm' 'spleen_palpable' ...
    'spiders' 'ascites' 'varices' 'bilirubin' 'alk_phosphate' 'sgot' ...
    'albumin' 'protime' 'histology'};
ds = dataset('file','hepatitis.txt','VarNames',VarNames,...
    'Delimiter',',','ReadVarNames',false,'TreatAsEmpty','?',...
    'Format','%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f');
```

`ds` is a dataset with 155 observations and 20 variables:

```
size(ds)

ans =
```

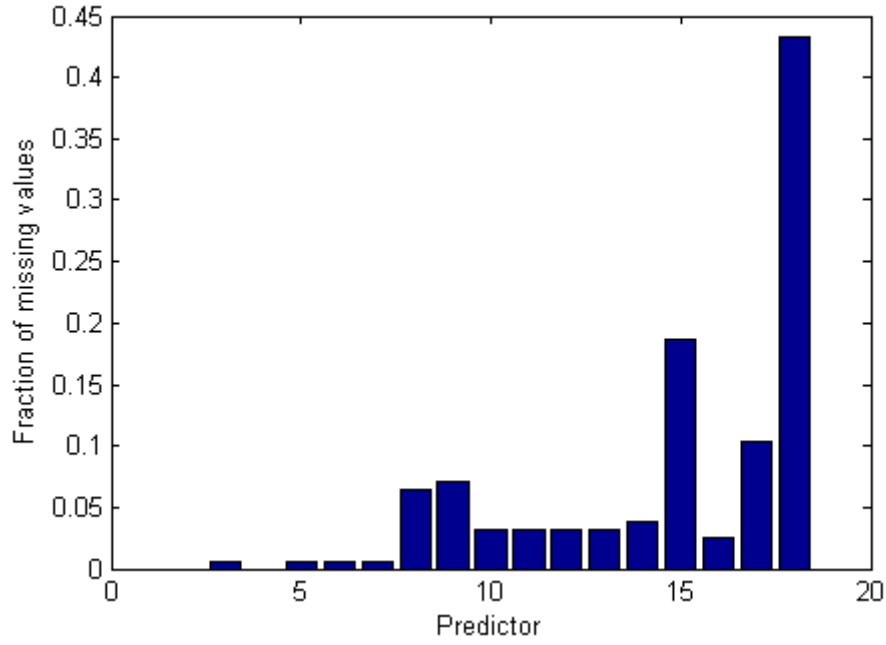
```
    155     20
```

3 Convert the data in the dataset to the format for ensembles: a numeric matrix of predictors, and a cell array with outcome names: `'Die'` or `'Live'`. The first field in the dataset has the outcomes.

```
X = double(ds(:,2:end));
ClassNames = {'Die' 'Live'};
Y = ClassNames(ds.die_or_live);
```

4 Inspect the data for missing values:

```
figure;
bar(sum(isnan(X),1)/size(X,1));
xlabel('Predictor');
ylabel('Fraction of missing values');
```



Most predictors have missing values, and one has nearly 45% of missing values. Therefore, use decision trees with surrogate splits for better accuracy. Because the dataset is small, training time with surrogate splits should be tolerable.

5 Create a classification tree template that uses surrogate splits:

```
rng(0,'twister') % for reproducibility
t = ClassificationTree.template('surrogate','on');
```

6 Examine the data or the description of the data to see which predictors are categorical:

```
X(1:5,:)

ans =

  Columns 1 through 6

   30.0000    2.0000    1.0000    2.0000    2.0000    2.0000
   50.0000    1.0000    1.0000    2.0000    1.0000    2.0000
   78.0000    1.0000    2.0000    2.0000    1.0000    2.0000
   31.0000    1.0000       NaN    1.0000    2.0000    2.0000
   34.0000    1.0000    2.0000    2.0000    2.0000    2.0000

  Columns 7 through 12

    2.0000    1.0000    2.0000    2.0000    2.0000    2.0000
    2.0000    1.0000    2.0000    2.0000    2.0000    2.0000
    2.0000    2.0000    2.0000    2.0000    2.0000    2.0000
    2.0000    2.0000    2.0000    2.0000    2.0000    2.0000
    2.0000    2.0000    2.0000    2.0000    2.0000    2.0000

  Columns 13 through 18

    2.0000    1.0000   85.0000   18.0000    4.0000       NaN
    2.0000    0.9000  135.0000   42.0000    3.5000       NaN
    2.0000    0.7000   96.0000   32.0000    4.0000       NaN
    2.0000    0.7000   46.0000   52.0000    4.0000   80.0000
    2.0000    1.0000       NaN  200.0000    4.0000       NaN
```

```
Column 19

    1.0000
    1.0000
    1.0000
    1.0000
    1.0000
```

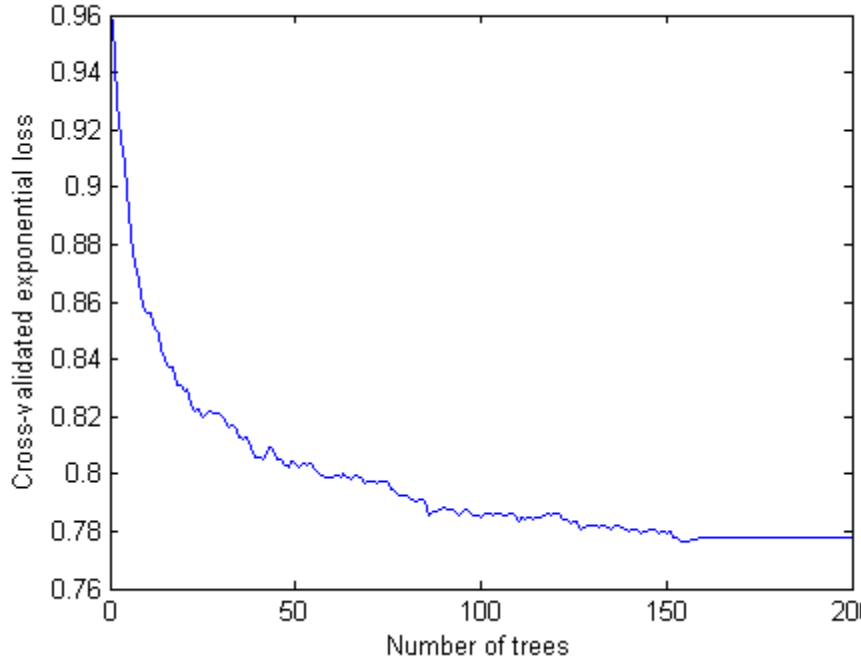
It appears that predictors 2 through 13 are categorical, as well as predictor 19. You can confirm this inference with the dataset description at http://archive.ics.uci.edu/ml/datasets/Hepatitis.

7 List the categorical variables:

```
ncat = [2:13,19];
```

8 Create a cross-validated ensemble using 200 learners and the GentleBoost algorithm:

```
a = fitensemble(X,Y,'GentleBoost',200,t,...
  'PredictorNames',VarNames(2:end),'LearnRate',0.1,...
  'CategoricalPredictors',ncat,'kfold',5);
figure;
plot(kfoldLoss(a,'mode','cumulative','lossfun','exponential'));
xlabel('Number of trees');
ylabel('Cross-validated exponential loss');
```



9 Inspect the confusion matrix to see which people the ensemble predicts correctly:

```
[Yfit,Sfit] = kfoldPredict(a); %
confusionmat(Y,Yfit,'order',ClassNames)

ans =
    16    16
    10   113
```

Of the 123 people who live, the ensemble predicts correctly that 113 will live. But for the 32 people who die of hepatitis, the ensemble only predicts correctly that half will die of hepatitis.

10 There are two types of error in the predictions of the ensemble:

- Predicting that the patient lives, but the patient dies

- Predicting that the patient dies, but the patient lives

Suppose you believe that the first error is five times worse than the second. Make a new classification cost matrix that reflects this belief:

```
cost.ClassNames = ClassNames;
cost.ClassificationCosts = [0 5; 1 0];
```

11 Create a new cross-validated ensemble using `cost` as misclassification cost, and inspect the resulting confusion matrix:

```
aC = fitensemble(X,Y,'GentleBoost',200,t,...
  'PredictorNames',VarNames(2:end),'LearnRate',0.1,...
  'CategoricalPredictors',ncat,'kfold',5,...
  'cost',cost);
[YfitC,SfitC] = kfoldPredict(aC);
confusionmat(Y,YfitC,'order',ClassNames)

ans =
    19    13
     9   114
```

As expected, the new ensemble does a better job classifying the people who die. Somewhat surprisingly, the new ensemble also does a better job classifying the people who live, though the result is not statistically significantly better. The results of the cross validation are random, so this result is simply a statistical fluctuation. The result seems to indicate that the classification of people who live is not very sensitive to the cost.

Example: Classification with Many Categorical Levels

Generally, you cannot use classification with more than 31 levels in any categorical predictor. However, two boosting algorithms can classify data with many categorical levels: `LogitBoost` and `GentleBoost`. For details, see "LogitBoost" on page 13-125 and "GentleBoost" on page 13-126.

This example uses demographic data from the U.S. Census, available at `http://archive.ics.uci.edu/ml/machine-learning-databases/adult/`. The objective of the researchers who posted the data is predicting whether an individual makes more than $50,000/year, based on a set of characteristics.

You can see details of the data, including predictor names, in the `adult.names` file at the site.

1. Load the `'adult.data'` file from the UCI Machine Learning Repository:

```
s = urlread(['http://archive.ics.uci.edu/ml/' ...
   'machine-learning-databases/adult/adult.data']);
```

2. `'adult.data'` represents missing data as `'?'`. Replace instances of missing data with the blank string `''`:

```
s = strrep(s,'?','');
```

3. Put the data into a MATLAB dataset array:

```
fid = fopen('adult.txt','w');
fwrite(fid,s);
fclose(fid);
clear s;
VarNames = {'age' 'workclass' 'fnlwgt' 'education' 'education_num' ...
    'marital_status' 'occupation' 'relationship' 'race' ...
    'sex' 'capital_gain' 'capital_loss' ...
    'hours_per_week' 'native_country' 'income'};
ds = dataset('file','adult.txt','VarNames',VarNames,...
    'Delimiter',',','ReadVarNames',false,'Format',...
   '%u%s%u%s%u%s%s%s%s%s%u%u%u%s%s');
cat = ~datasetfun(@isnumeric,ds(:,1:end-1)); % Logical indices
%                                             of categorical variables
catcol = find(cat); % indices of categorical variables
```

4. Many predictors in the data are categorical. Convert those fields in the dataset array to `nominal`:

```
ds.workclass = nominal(ds.workclass);
ds.education = nominal(ds.education);
ds.marital_status = nominal(ds.marital_status);
ds.occupation = nominal(ds.occupation);
ds.relationship = nominal(ds.relationship);
ds.race = nominal(ds.race);
ds.sex = nominal(ds.sex);
```

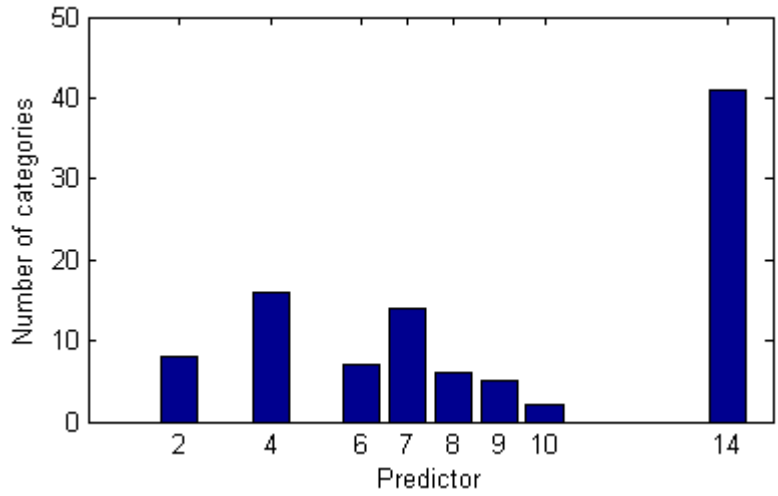
```
ds.native_country = nominal(ds.native_country);
ds.income = nominal(ds.income);
```

5 Convert the dataset array into numerical variables for `fitensemble`:

```
X = double(ds(:,1:end-1));
Y = ds.income;
```

6 Some variables have many levels. Plot the number of levels of each predictor:

```
ncat = zeros(1,numel(catcol));
for c=1:numel(catcol)
    [~,gn] = grp2idx(X(:,catcol(c)));
    ncat(c) = numel(gn);
end
figure;
bar(catcol,ncat);
xlabel('Predictor');
ylabel('Number of categories');
```



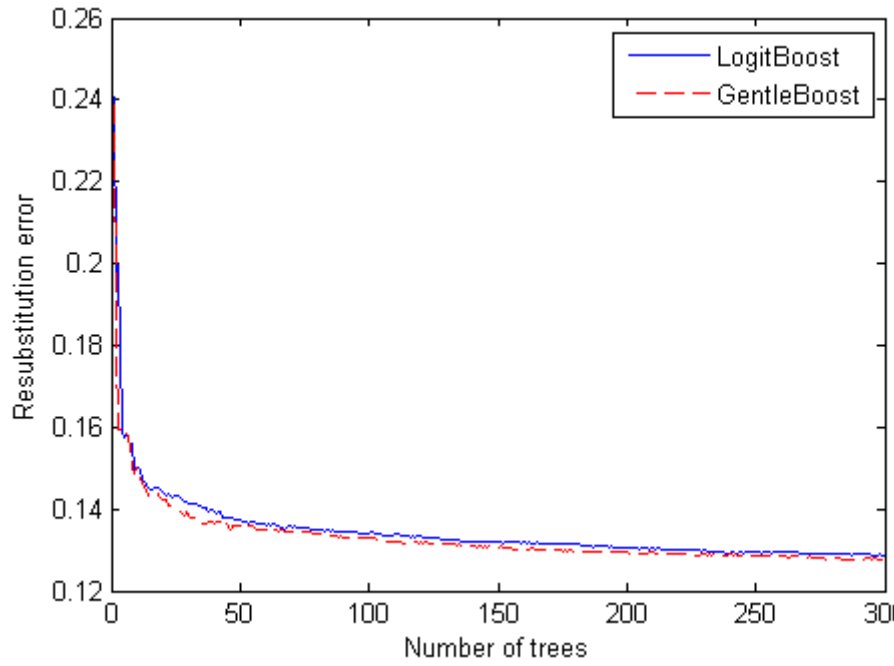
Predictor 14 (`'native_country'`) has more than 40 categorical levels. This is too many levels for any method except `LogitBoost` and `GentleBoost`.

7 Create classification ensembles using both `LogitBoost` and `GentleBoost`:

```
lb = fitensemble(X,Y,'LogitBoost',300,'Tree','CategoricalPredictors',cat,...
    'PredictorNames',VarNames(1:end-1),'ResponseName','income');
gb = fitensemble(X,Y,'GentleBoost',300,'Tree','CategoricalPredictors',cat,...
    'PredictorNames',VarNames(1:end-1),'ResponseName','income');
```

8 Examine the resubstitution error for the two ensembles:

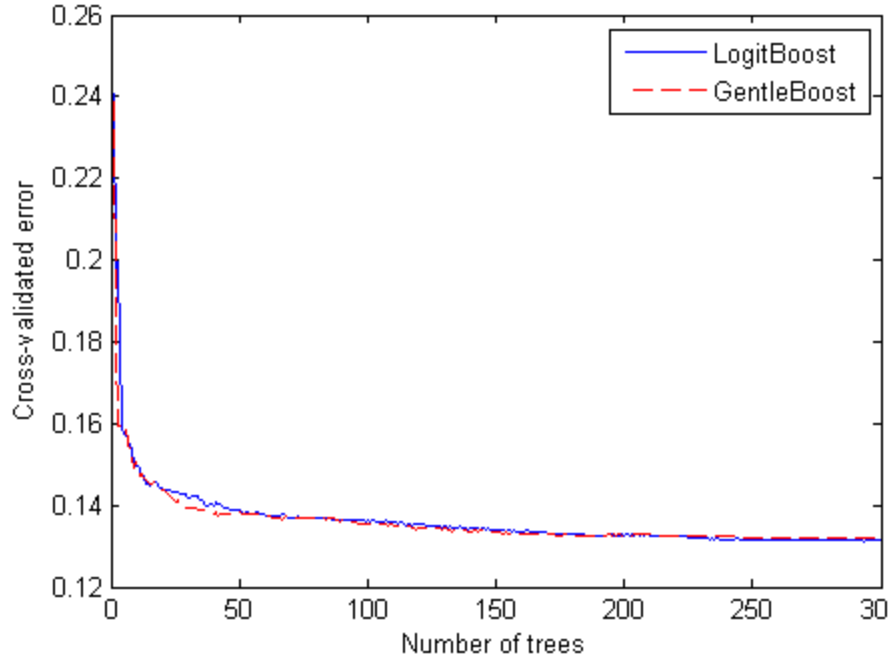
```
figure;
plot(resubLoss(lb,'mode','cumulative'));
hold on
plot(resubLoss(gb,'mode','cumulative'),'r--');
hold off
xlabel('Number of trees');
ylabel('Resubstitution error');
legend('LogitBoost','GentleBoost','Location','NE');
```



The algorithms have similar resubstitution error.

9 Estimate the generalization error for the two algorithms by cross validation.

```
lbcv = crossval(lb,'kfold',5);
gbcv = crossval(gb,'kfold',5);
figure;
plot(kfoldLoss(lbcv,'mode','cumulative'));
hold on
plot(kfoldLoss(gbcv,'mode','cumulative'),'r--');
hold off
xlabel('Number of trees');
ylabel('Cross-validated error');
legend('LogitBoost','GentleBoost','Location','NE');
```



The cross-validated loss is nearly the same as the resubstitution error.

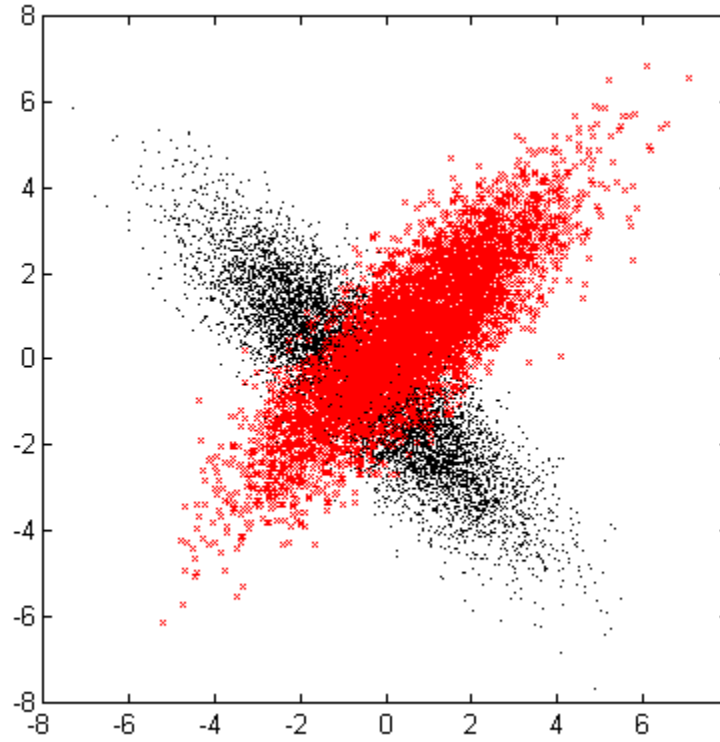
Example: Surrogate Splits

When you have missing data, trees and ensembles of trees give better predictions when they include surrogate splits. Furthermore, estimates of predictor importance are often different with surrogate splits. Eliminating unimportant predictors can save time and memory for predictions, and can make predictions easier to understand.

This example shows the effects of surrogate splits for predictions for data containing missing entries in both training and test sets. There is a redundant predictor in the data, which the surrogate split uses to infer missing values. While the example is artificial, it shows the value of surrogate splits with missing data.

1 Generate and plot two different normally-distributed populations, one with 5000 members, one with 10,000 members:

```
rng(1,'twister') % for reproducibility
N = 5000;
N1 = 2*N; % number in population 1
N2 = N; % number in population 2
mu1 = [-1 -1]/2; % mean of population 1
mu2 = [1 1]/2; % mean of population 2
S1 = [3   -2.5;...
   -2.5    3]; % variance of population 1
S2 = [3   2.5;...
   2.5    3]; % variance of population 2
X1 = mvnrnd(mu1,S1,N1); % population 1
X2 = mvnrnd(mu2,S2,N2); % population 2
X = [X1; X2]; % total population
Y = ones(N1+N2,1); % label population 1
Y(N1+1:end) = 2; % label population 2

figure
plot(X1(:,1),X1(:,2),'k.','MarkerSize',2)
hold on
plot(X2(:,1),X2(:,2),'rx','MarkerSize',3);
hold off
axis square
```



There is a good deal of overlap between the data points. You cannot expect perfect classification of this data.

2 Make a third predictor that is the same as the first component of `X`:

```
X = [X X(:,1)];
```

3 Remove half the values of predictor `1` at random:

```
X(rand(size(X(:,1))) < 0.5,1) = NaN;
```

4 Partition the data into a training set and a test set:

```
cv = cvpartition(Y,'holdout',0.3); % 30% test data
```

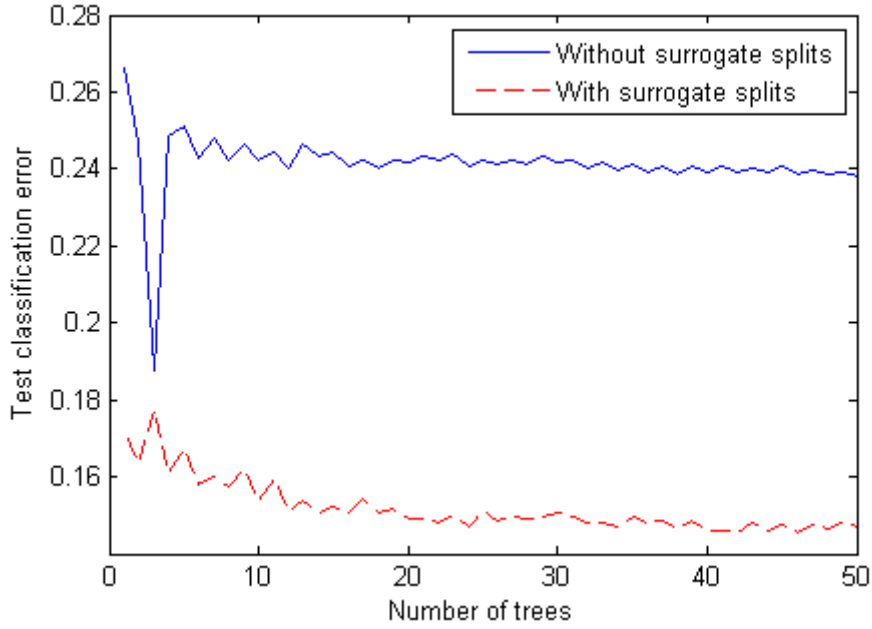
```
Xtrain = X(training(cv),:);
Ytrain = Y(training(cv));
Xtest = X(test(cv),:);
Ytest = Y(test(cv));
```

5 Create two `Bag` ensembles: one with surrogate splits, one without. First create the template for surrogate splits, then train both ensembles:

```
templS = ClassificationTree.template('surrogate','on');
bag = fitensemble(Xtrain,Ytrain,'Bag',50,'Tree',...
    'type','class','nprint',10);

Training Bag...
Grown weak learners: 10
Grown weak learners: 20
Grown weak learners: 30
Grown weak learners: 40
Grown weak learners: 50

bagS = fitensemble(Xtrain,Ytrain,'Bag',50,templS,...
    'type','class','nprint',10);

Training Bag...
Grown weak learners: 10
Grown weak learners: 20
Grown weak learners: 30
Grown weak learners: 40
Grown weak learners: 50
```

6 Examine the accuracy of the two ensembles for predicting the test data:

```
figure
plot(loss(bag,Xtest,Ytest,'mode','cumulative'));
hold on
plot(loss(bagS,Xtest,Ytest,'mode','cumulative'),'r--');
hold off;
legend('Without surrogate splits','With surrogate splits');
xlabel('Number of trees');
ylabel('Test classification error');
```



The ensemble with surrogate splits is obviously more accurate than the ensemble without surrogate splits.

7 Check the statistical significance of the difference in results with the McNemar test:

```
Yfit = predict(bag,Xtest);
YfitS = predict(bagS,Xtest);
N10 = sum(Yfit==Ytest & YfitS~=Ytest);
N01 = sum(Yfit~=Ytest & YfitS==Ytest);
mcnemar = (abs(N10-N01) - 1)^2/(N10+N01);
pval = 1 - chi2cdf(mcnemar,1)

pval =
     0
```

The extremely low p-value indicates that the ensemble with surrogate splits is better in a statistically significant manner.

Ensemble Regularization

Regularization is a process of choosing fewer weak learners for an ensemble in a way that does not diminish predictive performance. Currently you can regularize regression ensembles.

The `regularize` method finds an optimal set of learner weights α_t that minimize

$$\sum_{n=1}^{N} w_n g\left(\left(\sum_{t=1}^{T}\alpha_t h_t\left(x_n\right)\right), y_n\right) + \lambda\sum_{t=1}^{T}|\alpha_t|.$$

Here

- $\lambda \geq 0$ is a parameter you provide, called the lasso parameter.
- h_t is a weak learner in the ensemble trained on N observations with predictors x_n, responses y_n, and weights w_n.
- $g(f,y) = (f - y)^2$ is the squared error.

The ensemble is regularized on the same (x_n,y_n,w_n) data used for training, so

$$\sum_{n=1}^{N} w_n g\left(\left(\sum_{t=1}^{T}\alpha_t h_t\left(x_n\right)\right), y_n\right)$$

is the ensemble resubstitution error (MSE).

If you use $\lambda = 0$, `regularize` finds the weak learner weights by minimizing the resubstitution MSE. Ensembles tend to overtrain. In other words, the resubstitution error is typically smaller than the true generalization error. By making the resubstitution error even smaller, you are likely to make the ensemble accuracy worse instead of improving it. On the other hand, positive values of λ push the magnitude of the α_t coefficients to 0. This often improves the generalization error. Of course, if you choose λ too large, all the optimal coefficients are 0, and the ensemble does not have any accuracy. Usually you can find an optimal range for λ in which the accuracy of the regularized ensemble is better or comparable to that of the full ensemble without regularization.

A nice feature of lasso regularization is its ability to drive the optimized coefficients precisely to zero. If a learner's weight a_t is 0, this learner can be excluded from the regularized ensemble. In the end, you get an ensemble with improved accuracy and fewer learners.

Example: Regularizing a Regression Ensemble

This example uses data for predicting the insurance risk of a car based on its many attributes.

1 Load the `imports-85` data into the MATLAB workspace:

```
load imports-85;
```

2 Look at a description of the data to find the categorical variables and predictor names:

```
Description

Description =
1985 Auto Imports Database from the UCI repository
http://archive.ics.uci.edu/ml/machine-learning-databases/autos/imports-85.names
Variables have been reordered to place variables with numeric values (referred
to as "continuous" on the UCI site) to the left and categorical values to the
right. Specifically, variables 1:16 are: symboling, normalized-losses,
wheel-base, length, width, height, curb-weight, engine-size, bore, stroke,
compression-ratio, horsepower, peak-rpm, city-mpg, highway-mpg, and price.
Variables 17:26 are: make, fuel-type, aspiration, num-of-doors, body-style,
drive-wheels, engine-location, engine-type, num-of-cylinders, and fuel-system.
```

The objective of this process is to predict the "symboling," the first variable in the data, from the other predictors. "symboling" is an integer from `-3` (good insurance risk) to `3` (poor insurance risk). You could use a classification ensemble to predict this risk instead of a regression ensemble. As stated in "Steps in Supervised Learning (Machine Learning)" on page 13-2, when you have a choice between regression and classification, you should try regression first. Furthermore, this example is to show regularization, which currently works only for regression.

3 Prepare the data for ensemble fitting:

```
Y = X(:,1);
X(:,1) = [];
VarNames = {'normalized-losses' 'wheel-base' 'length' 'width' 'height' ...
  'curb-weight' 'engine-size' 'bore' 'stroke' 'compression-ratio' ...
  'horsepower' 'peak-rpm' 'city-mpg' 'highway-mpg' 'price' 'make' ...
  'fuel-type' 'aspiration' 'num-of-doors' 'body-style' 'drive-wheels' ...
  'engine-location' 'engine-type' 'num-of-cylinders' 'fuel-system'};
catidx = 16:25; % indices of categorical predictors
```

4 Create a regression ensemble from the data using 300 default trees:

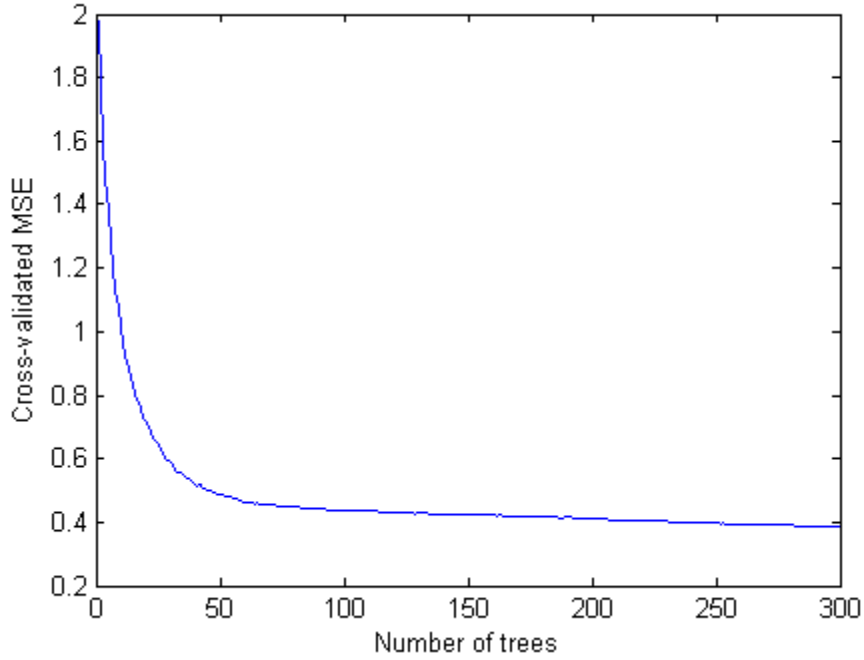
```
ls = fitensemble(X,Y,'LSBoost',300,'Tree','LearnRate',0.1,...
    'PredictorNames',VarNames,'ResponseName','symboling',...
    'CategoricalPredictors',catidx)

ls =

classreg.learning.regr.RegressionEnsemble:
           PredictorNames: {1x25 cell}
    CategoricalPredictors: [16 17 18 19 20 21 22 23 24 25]
             ResponseName: 'symboling'
        ResponseTransform: 'none'
            NObservations: 205
                 NTrained: 300
                   Method: 'LSBoost'
             LearnerNames: {'Tree'}
     ReasonForTermination: [1x77 char]
                  FitInfo: [300x1 double]
       FitInfoDescription: [2x83 char]
           Regularization: []
```

The final line, `Regularization`, is empty (`[]`). To regularize the ensemble, you have to use the `regularize` method.

5 Cross validate the ensemble, and inspect its loss curve.

```
cv = crossval(ls,'kfold',5);
figure;
plot(kfoldLoss(cv,'mode','cumulative'));
```

```
xlabel('Number of trees');
ylabel('Cross-validated MSE');
```



It appears you might obtain satisfactory performance from a smaller ensemble, perhaps one containing from 50 to 100 trees.

6 Call the `regularize` method to try to find trees that you can remove from the ensemble. By default, `regularize` examines 10 values of the lasso (`Lambda`) parameter spaced exponentially.

```
ls = regularize(ls)

ls =

classreg.learning.regr.RegressionEnsemble:
           PredictorNames: {1x25 cell}
    CategoricalPredictors: [16 17 18 19 20 21 22 23 24 25]
```

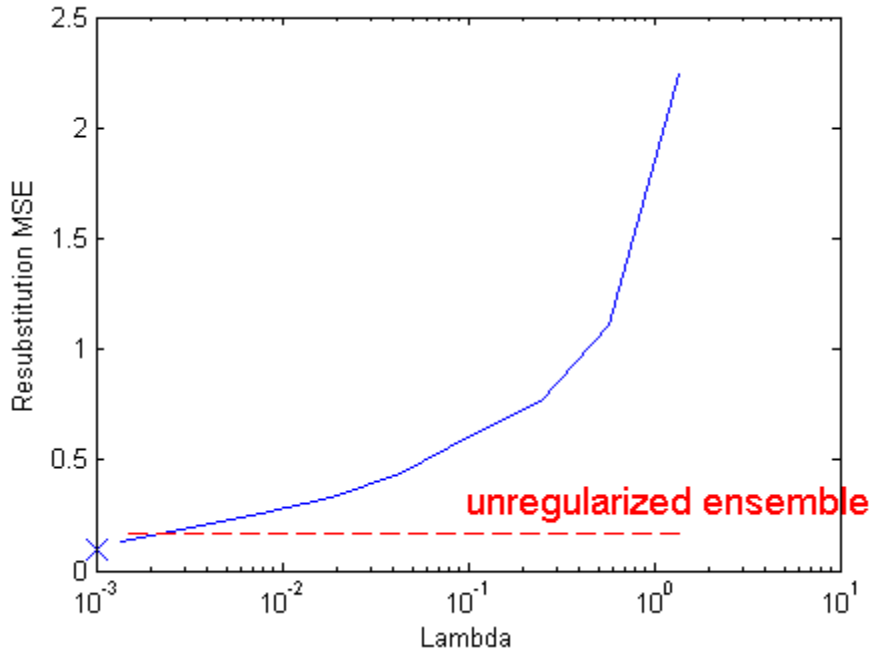
```
                ResponseName: 'symboling'
       ResponseTransform: 'none'
           NObservations: 205
                NTrained: 300
                  Method: 'LSBoost'
             LearnerNames: {'Tree'}
    ReasonForTermination: [1x77 char]
                 FitInfo: [300x1 double]
      FitInfoDescription: [2x83 char]
          Regularization: [1x1 struct]
```

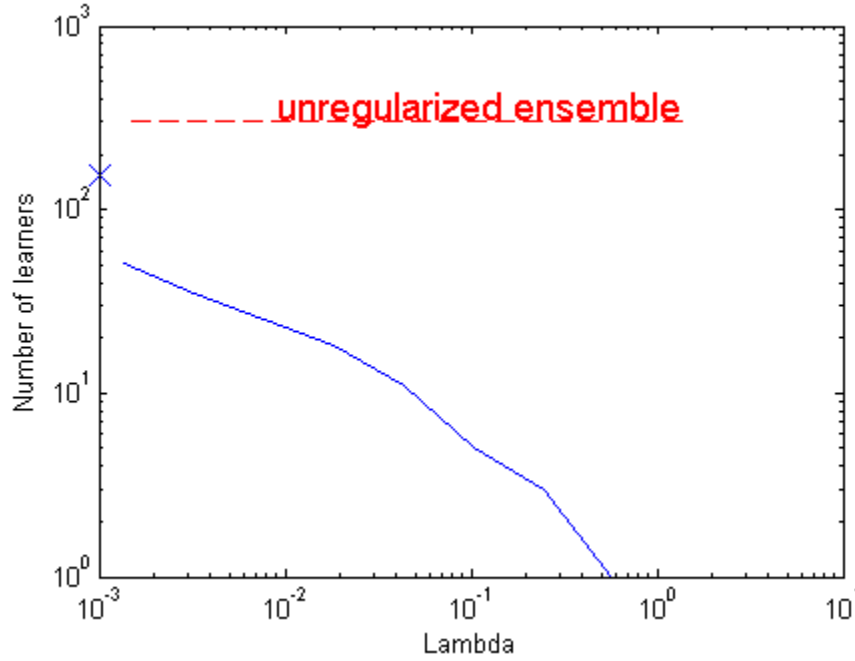
The `Regularization` property is no longer empty.

7 Plot the resubstitution mean-squared error (MSE) and number of learners with nonzero weights against the lasso parameter. Separately plot the value at `Lambda=0`. Use a logarithmic scale since the values of `Lambda` are exponentially spaced.

```
figure;
semilogx(ls.Regularization.Lambda,ls.Regularization.ResubstitutionMSE);
line([1e-3 1e-3],[ls.Regularization.ResubstitutionMSE(1) ...
     ls.Regularization.ResubstitutionMSE(1)],...
    'marker','x','markersize',12,'color','b');
r0 = resubLoss(ls);
line([ls.Regularization.Lambda(2) ls.Regularization.Lambda(end)],...
     [r0 r0],'color','r','LineStyle','--');
xlabel('Lambda');
ylabel('Resubstitution MSE');
annotation('textbox',[0.5 0.22 0.5 0.05],'String','unregularized ensemble',...
    'color','r','FontSize',14,'LineStyle','none');

figure;
loglog(ls.Regularization.Lambda,sum(ls.Regularization.TrainedWeights>0,1));
line([1e-3 1e-3],...
    [sum(ls.Regularization.TrainedWeights(:,1)>0) ...
    sum(ls.Regularization.TrainedWeights(:,1)>0)],...
    'marker','x','markersize',12,'color','b');
line([ls.Regularization.Lambda(2) ls.Regularization.Lambda(end)],...
    [ls.NTrained ls.NTrained],...
```

```
    'color','r','LineStyle','--');
xlabel('Lambda');
ylabel('Number of learners');
annotation('textbox',[0.3 0.8 0.5 0.05],'String','unregularized ensemble',...
    'color','r','FontSize',14,'LineStyle','none');
```



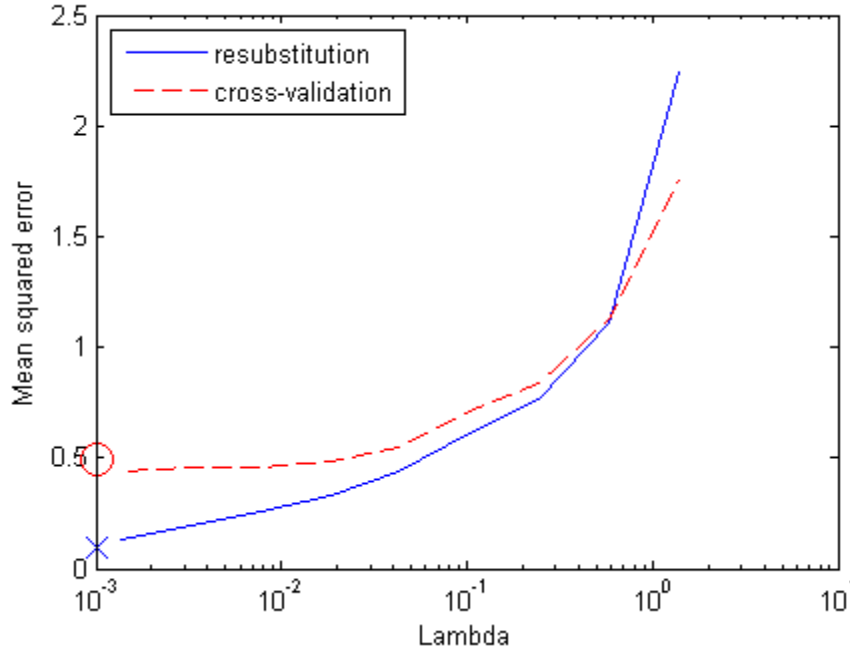


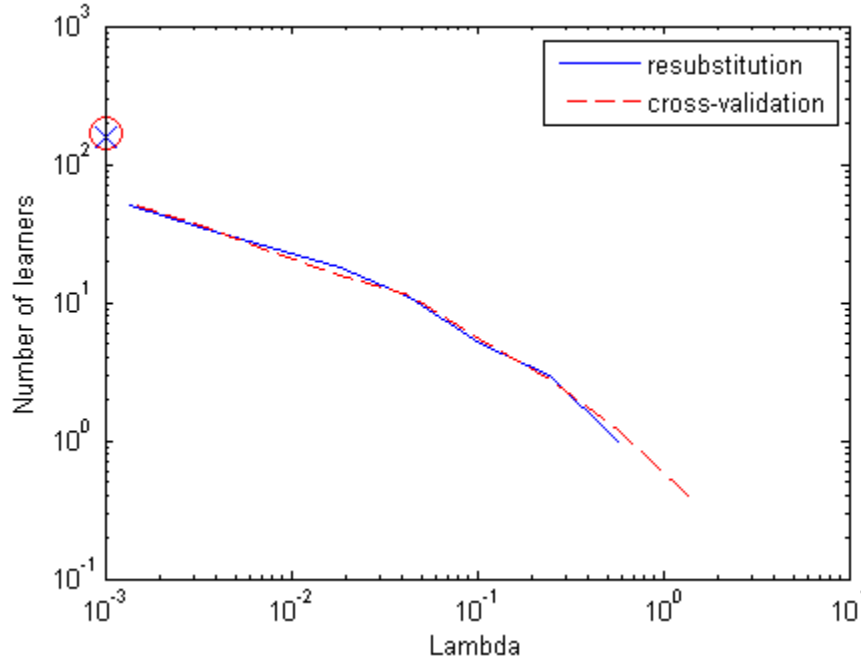
8 The resubstitution MSE values are likely to be overly optimistic. To obtain more reliable estimates of the error associated with various values of `Lambda`, cross validate the ensemble using `cvshrink`. Plot the resulting cross validation loss (MSE) and number of learners against `Lambda`.

```
rng(0,'Twister') % for reproducibility
[mse,nlearn] = cvshrink(ls,'lambda',ls.Regularization.Lambda,'kfold',5);

figure;
semilogx(ls.Regularization.Lambda,ls.Regularization.ResubstitutionMSE);
hold;
semilogx(ls.Regularization.Lambda,mse,'r--');
hold off;
xlabel('Lambda');
ylabel('Mean squared error');
legend('resubstitution','cross-validation','Location','NW');
```

```
line([1e-3 1e-3],[ls.Regularization.ResubstitutionMSE(1) ...
     ls.Regularization.ResubstitutionMSE(1)],...
    'marker','x','markersize',12,'color','b');
line([1e-3 1e-3],[mse(1) mse(1)],'marker','o',...
    'markersize',12,'color','r','LineStyle','--');

figure;
loglog(ls.Regularization.Lambda,sum(ls.Regularization.TrainedWeights>0,1));
hold;
loglog(ls.Regularization.Lambda,nlearn,'r--');
hold off;
xlabel('Lambda');
ylabel('Number of learners');
legend('resubstitution','cross-validation','Location','NE');
line([1e-3 1e-3],...
    [sum(ls.Regularization.TrainedWeights(:,1)>0) ...
    sum(ls.Regularization.TrainedWeights(:,1)>0)],...
    'marker','x','markersize',12,'color','b');
line([1e-3 1e-3],[nlearn(1) nlearn(1)],'marker','o',...
```

```
'markersize',12,'color','r','LineStyle','--');
```





Examining the cross-validated error shows that the cross-validation MSE is almost flat for `Lambda` up to a bit over `1e-2`.

9 Examine `ls.Regularization.Lambda` to find the highest value that gives MSE in the flat region (up to a bit over `1e-2`):

```
jj = 1:length(ls.Regularization.Lambda);
[jj;ls.Regularization.Lambda]

ans =

  Columns 1 through 6

    1.0000    2.0000    3.0000    4.0000    5.0000    6.0000
         0    0.0014    0.0033    0.0077    0.0183    0.0435

  Columns 7 through 10
```

```
    7.0000    8.0000    9.0000   10.0000
    0.1031    0.2446    0.5800    1.3754
```

Element `5` of `ls.Regularization.Lambda` has value `0.0183`, the largest in the flat range.

10 Reduce the ensemble size using the `shrink` method. `shrink` returns a compact ensemble with no training data. The generalization error for the new compact ensemble was already estimated by cross validation in `mse(5)`.

```
cmp = shrink(ls,'weightcolumn',5)

cmp =

classreg.learning.regr.CompactRegressionEnsemble:
           PredictorNames: {1x25 cell}
    CategoricalPredictors: [16 17 18 19 20 21 22 23 24 25]
             ResponseName: 'symboling'
        ResponseTransform: 'none'
                 NTrained: 18
```

There are only 18 trees in the new ensemble, notably reduced from the 300 in `ls`.

11 Compare the sizes of the ensembles:

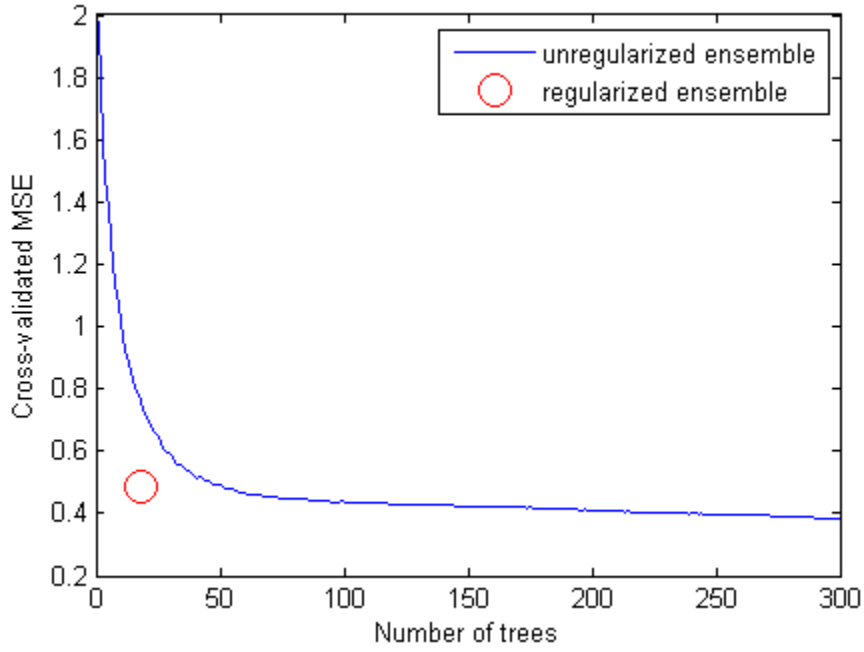
```
sz(1) = whos('cmp'); sz(2) = whos('ls');
[sz(1).bytes sz(2).bytes]

ans =
      162270     2791024
```

The reduced ensemble is about 6% the size of the original.

12 Compare the MSE of the reduced ensemble to that of the original ensemble:

```
figure;
plot(kfoldLoss(cv,'mode','cumulative'));
hold on
plot(cmp.NTrained,mse(5),'ro','MarkerSize',12);
xlabel('Number of trees');
```

```
ylabel('Cross-validated MSE');
legend('unregularized ensemble','regularized ensemble',...
    'Location','NE');
hold off
```



The reduced ensemble gives low loss while using many fewer trees.

Example: Tuning RobustBoost

The `RobustBoost` algorithm can make good classification predictions even when the training data has noise. However, the default `RobustBoost` parameters can produce an ensemble that does not predict well. This example shows one way of tuning the parameters for better predictive accuracy.

1 Generate data with label noise. This example has twenty uniform random numbers per observation, and classifies the observation as `1` if the sum of the first five numbers exceeds 2.5 (so is larger than average), and `0` otherwise:

```
rng(0,'twister') % for reproducibility
Xtrain = rand(2000,20);
Ytrain = sum(Xtrain(:,1:5),2) > 2.5;
```

2 To add noise, randomly switch 10% of the classifications:

```
idx = randsample(2000,200);
Ytrain(idx) = ~Ytrain(idx);
```

3 Create an ensemble with `AdaBoostM1` for comparison purposes:

```
ada = fitensemble(Xtrain,Ytrain,'AdaBoostM1',...
    300,'Tree','LearnRate',0.1);
```

4 Create an ensemble with `RobustBoost`. Since the data has 10% incorrect classification, perhaps an error goal of 15% is reasonable.

```
rb1 = fitensemble(Xtrain,Ytrain,'RobustBoost',300,...
   'Tree','RobustErrorGoal',0.15,'RobustMaxMargin',1);
```

5 Try setting a high value of the error goal, `0.6`. You get an error:

```
rb2 = fitensemble(Xtrain,Ytrain,'RobustBoost',300,'Tree','RobustErrorGoal',0.6)

Error using RobustBoost>RobustBoost.RobustBoost
For the chosen values of 'RobustMaxMargin' and 'RobustMarginSigma', you must set
'RobustErrorGoal' to a value between 0 and 0.5.
```

6 Create an ensemble with an error goal in the allowed range, `0.4`:

```
rb2 = fitensemble(Xtrain,Ytrain,'RobustBoost',300,...
   'Tree','RobustErrorGoal',0.4);
```

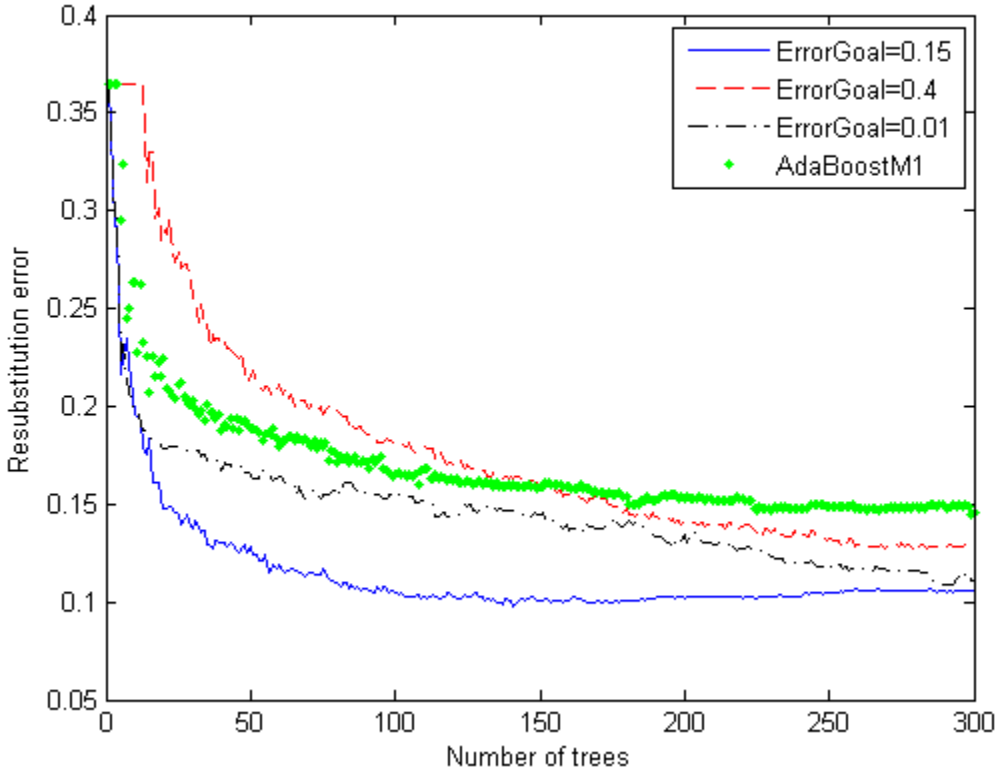
7 Create an ensemble with very optimistic error goal, `0.01`:

```
rb3 = fitensemble(Xtrain,Ytrain,'RobustBoost',300,...
   'Tree','RobustErrorGoal',0.01);
```

8 Compare the resubstitution error of the four ensembles:

```
figure
```

```
plot(resubLoss(rb1,'mode','cumulative'));
hold on
plot(resubLoss(rb2,'mode','cumulative'),'r--');
plot(resubLoss(rb3,'mode','cumulative'),'k-.');
plot(resubLoss(ada,'mode','cumulative'),'g.');
hold off;
xlabel('Number of trees');
ylabel('Resubstitution error');
legend('ErrorGoal=0.15','ErrorGoal=0.4','ErrorGoal=0.01',...
    'AdaBoostM1','Location','NE');
```

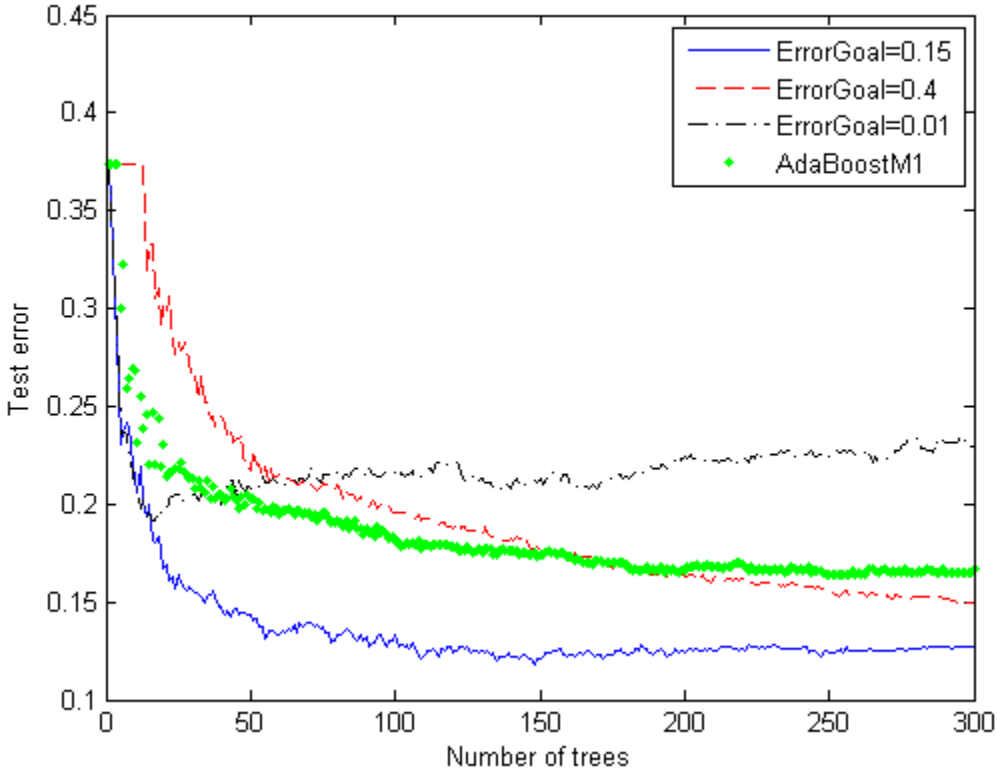


All the `RobustBoost` curves show lower resubstitution error than the `AdaBoostM1` curve. The error goal of `0.15` curve shows the lowest

resubstitution error over most of the range. However, its error is rising in the latter half of the plot, while the other curves are still descending.

9 Generate test data to see the predictive power of the ensembles. Test the four ensembles:

```
Xtest = rand(2000,20);
Ytest = sum(Xtest(:,1:5),2) > 2.5;
idx = randsample(2000,200);
Ytest(idx) = ~Ytest(idx);
figure;
plot(loss(rb1,Xtest,Ytest,'mode','cumulative'));
hold on
plot(loss(rb2,Xtest,Ytest,'mode','cumulative'),'r--');
plot(loss(rb3,Xtest,Ytest,'mode','cumulative'),'k-.');
plot(loss(ada,Xtest,Ytest,'mode','cumulative'),'g.');
hold off;
xlabel('Number of trees');
ylabel('Test error');
legend('ErrorGoal=0.15','ErrorGoal=0.4','ErrorGoal=0.01',...
    'AdaBoostM1','Location','NE');
```



The error curve for error goal 0.15 is lowest (best) in the plotted range. The curve for error goal 0.4 seems to be converging to a similar value for a large number of trees, but more slowly. `AdaBoostM1` has higher error than the curve for error goal 0.15. The curve for the too-optimistic error goal 0.01 remains substantially higher (worse) than the other algorithms for most of the plotted range.

TreeBagger Examples

`TreeBagger` ensembles have more functionality than those constructed with `fitensemble`; see TreeBagger Features Not in fitensemble on page 13-120. Also, some property and method names differ from their `fitensemble`

counterparts. This section contains examples of workflow for regression and classification that use this extra `TreeBagger` functionality.

Workflow Example: Regression of Insurance Risk Rating for Car Imports with TreeBagger

In this example, use a database of 1985 car imports with 205 observations, 25 input variables, and one response variable, insurance risk rating, or "symboling." The first 15 variables are numeric and the last 10 are categorical. The symboling index takes integer values from –3 to 3.

1 Load the dataset and split it into predictor and response arrays:

```
load imports-85;
Y = X(:,1);
X = X(:,2:end);
```

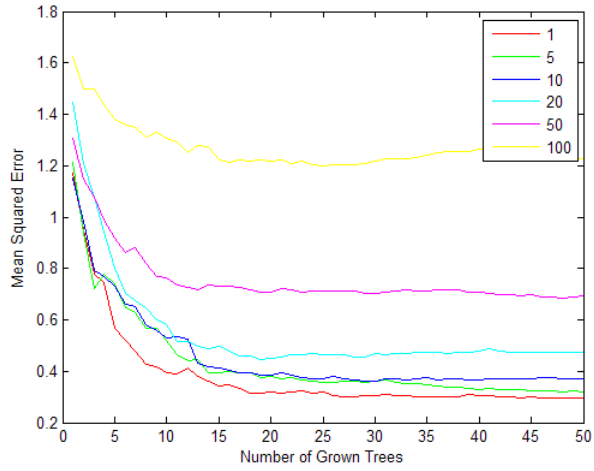
2 Because bagging uses randomized data drawings, its exact outcome depends on the initial random seed. To reproduce the exact results in this example, use the random stream settings:

```
rng(1945,'twister')
```

Finding the Optimal Leaf Size. For regression, the general rule is to set leaf size to 5 and select one third of input features for decision splits at random. In the following step, verify the optimal leaf size by comparing mean-squared errors obtained by regression for various leaf sizes. `oobError` computes MSE versus the number of grown trees. You must set `oobpred` to `'on'` to obtain out-of-bag predictions later.

```
leaf = [1 5 10 20 50 100];
col = 'rgbcmy';
figure(1);
for i=1:length(leaf)
    b = TreeBagger(50,X,Y,'method','r','oobpred','on',...
   'cat',16:25,'minleaf',leaf(i));
    plot(oobError(b),col(i));
    hold on;
end
xlabel('Number of Grown Trees');
ylabel('Mean Squared Error');
```

```
legend({'1' '5' '10' '20' '50' '100'},'Location','NorthEast');
hold off;
```



The red (leaf size 1) curve gives the lowest MSE values.

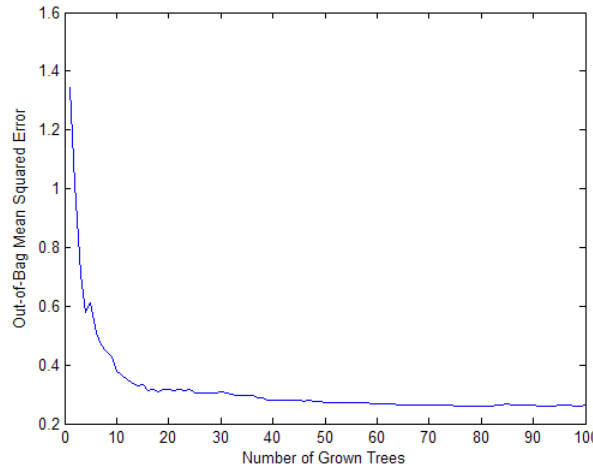
Estimating Feature Importance.

1 In practical applications, you typically grow ensembles with hundreds of trees. Only 50 trees were used in "Finding the Optimal Leaf Size" on page 13-97 for faster processing. Now that you have estimated the optimal leaf size, grow a larger ensemble with 100 trees and use it for estimation of feature importance:

```
b = TreeBagger(100,X,Y,'method','r','oobvarimp','on',...
'cat',16:25,'minleaf',1);
```

2 Inspect the error curve again to make sure nothing went wrong during training:

```
figure(2);
plot(oobError(b));
xlabel('Number of Grown Trees');
ylabel('Out-of-Bag Mean Squared Error');
```



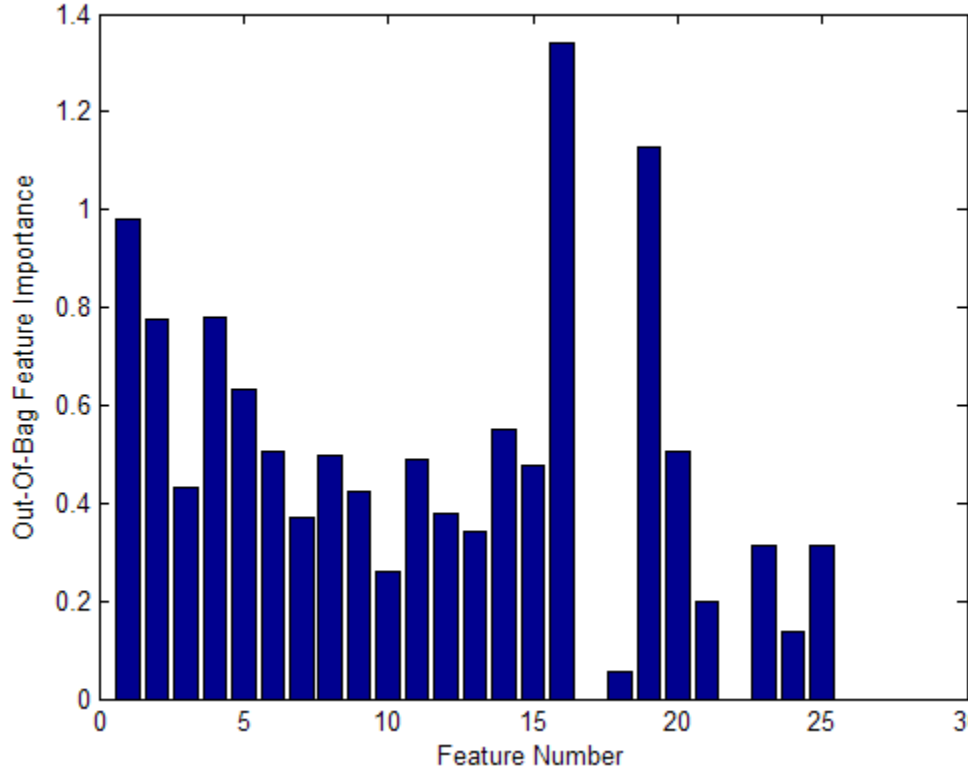
Prediction ability should depend more on important features and less on unimportant features. You can use this idea to measure feature importance.

For each feature, you can permute the values of this feature across all of the observations in the data set and measure how much worse the mean-squared error (MSE) becomes after the permutation. You can repeat this for each feature.

1 Using the following code, plot the increase in MSE due to permuting out-of-bag observations across each input variable. The `OOBPermutedVarDeltaError` array stores the increase in MSE averaged over all trees in the ensemble and divided by the standard deviation taken over the trees, for each variable. The larger this value, the more important the variable. Imposing an arbitrary cutoff at 0.65, you can select the five most important features.

```
figure(3);
bar(b.OOBPermutedVarDeltaError);
xlabel('Feature Number');
ylabel('Out-Of-Bag Feature Importance');
idxvar = find(b.OOBPermutedVarDeltaError>0.65)

idxvar =
```

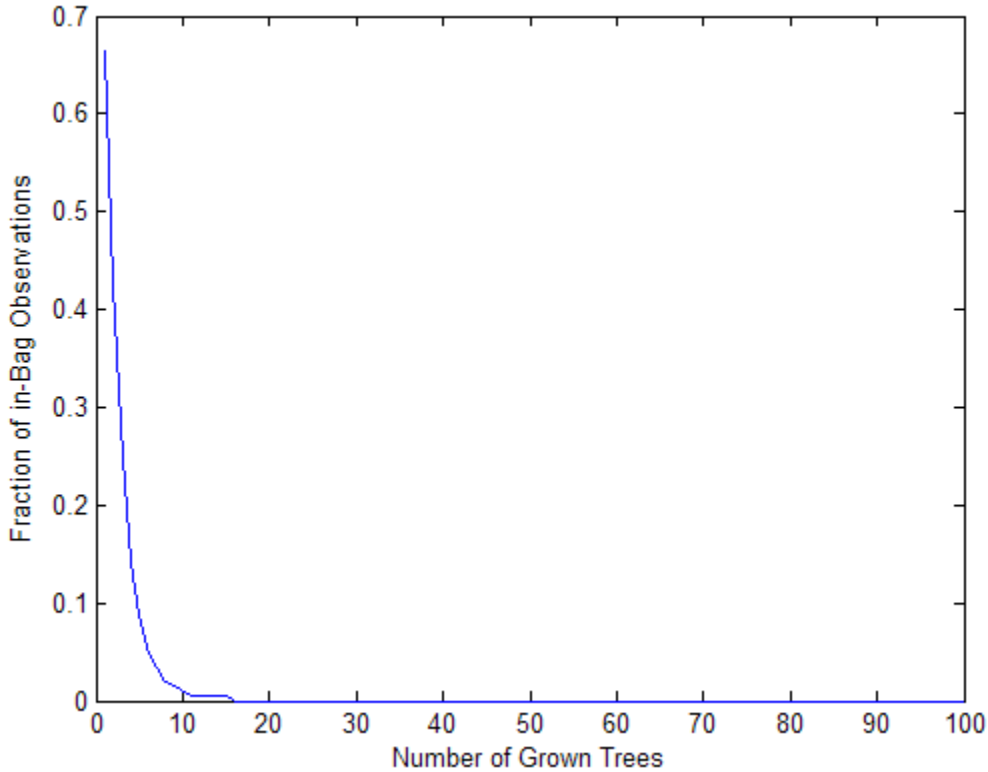
```
    1     2     4    16    19
```



2 The `OOBIndices` property of `TreeBagger` tracks which observations are out of bag for what trees. Using this property, you can monitor the fraction of observations in the training data that are in bag for all trees. The curve starts at approximately 2/3, the fraction of unique observations selected by one bootstrap replica, and goes down to 0 at approximately 10 trees.

```
finbag = zeros(1,b.NTrees);
for t=1:b.NTrees
    finbag(t) = sum(all(~b.OOBIndices(:,1:t),2));
end
finbag = finbag / size(X,1);
```

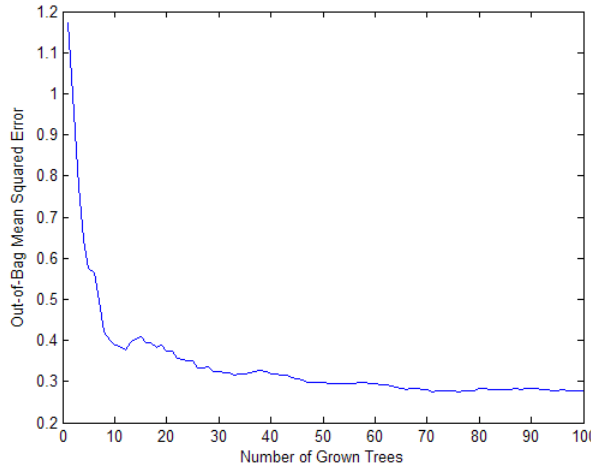
```
figure(4);
plot(finbag);
xlabel('Number of Grown Trees');
ylabel('Fraction of in-Bag Observations');
```

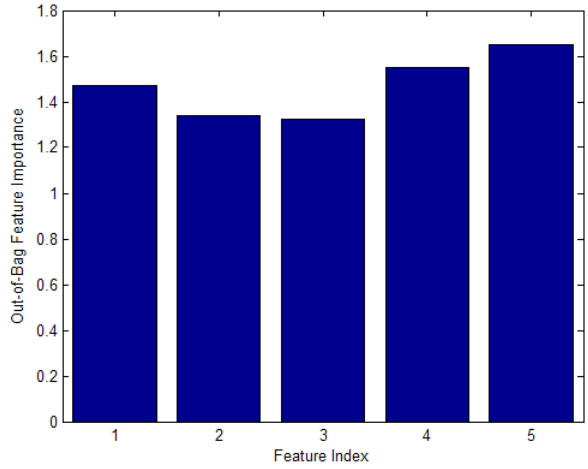


Growing Trees on a Reduced Set of Features. Using just the five most powerful features selected in "Estimating Feature Importance" on page 13-98, determine if it is possible to obtain a similar predictive power. To begin, grow 100 trees on these features only. The first three of the five selected features are numeric and the last two are categorical.

```
b5v = TreeBagger(100,X(:,idxvar),Y,'method','r',...
'oobvarimp','on','cat',4:5,'minleaf',1);
```

```
figure(5);
plot(oobError(b5v));
xlabel('Number of Grown Trees');
ylabel('Out-of-Bag Mean Squared Error');
figure(6);
bar(b5v.OOBPermutedVarDeltaError);
xlabel('Feature Index');
ylabel('Out-of-Bag Feature Importance');
```





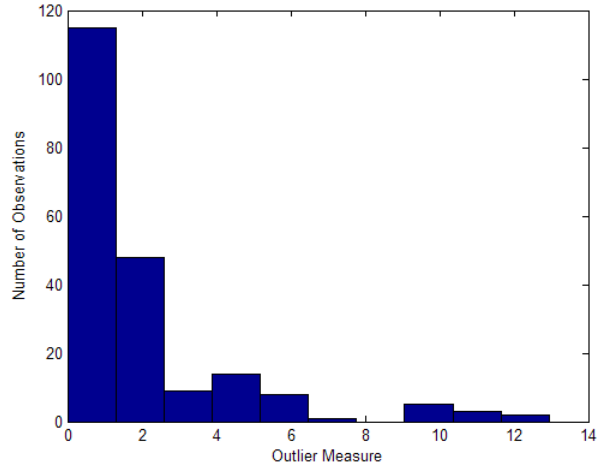
These five most powerful features give the same MSE as the full set, and the ensemble trained on the reduced set ranks these features similarly to each other. Features 1 and 2 from the reduced set perhaps could be removed without a significant loss in the predictive power.

Finding Outliers. To find outliers in the training data, compute the proximity matrix using `fillProximities`:

```
b5v = fillProximities(b5v);
```

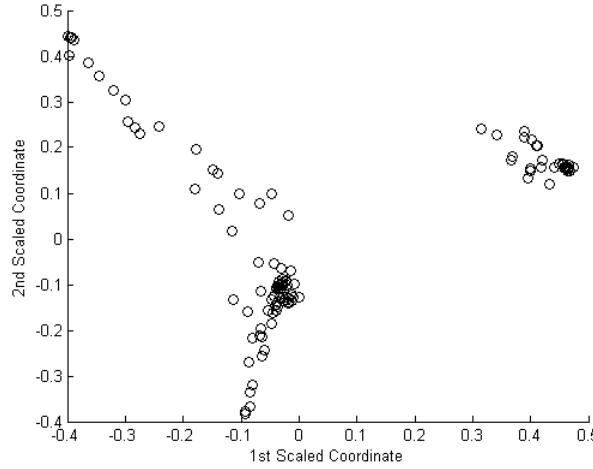
The method normalizes this measure by subtracting the mean outlier measure for the entire sample, taking the magnitude of this difference and dividing the result by the median absolute deviation for the entire sample:

```
figure(7);
hist(b5v.OutlierMeasure);
xlabel('Outlier Measure');
ylabel('Number of Observations');
```



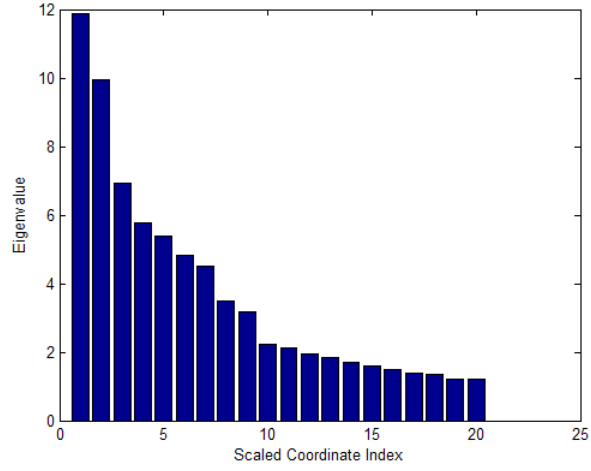
Discovering Clusters in the Data. By applying multidimensional scaling to the computed matrix of proximities, you can inspect the structure of the input data and look for possible clusters of observations. The `mdsProx` method returns scaled coordinates and eigenvalues for the computed proximity matrix. If run with the `colors` option, this method makes a scatter plot of two scaled coordinates, first and second by default.

```
figure(8);
[~,e] = mdsProx(b5v,'colors','k');
xlabel('1st Scaled Coordinate');
ylabel('2nd Scaled Coordinate');
```



Assess the relative importance of the scaled axes by plotting the first 20 eigenvalues:

```
figure(9);
bar(e(1:20));
xlabel('Scaled Coordinate Index');
ylabel('Eigenvalue');
```



Saving the Ensemble Configuration for Future Use. To use the trained ensemble for predicting the response on unseen data, store the ensemble to disk and retrieve it later. If you do not want to compute predictions for out-of-bag data or reuse training data in any other way, there is no need to store the ensemble object itself. Saving the compact version of the ensemble would be enough in this case. Extract the compact object from the ensemble:

```
c = compact(b5v)

c =

Ensemble with 100 decision trees:
Method:           regression
Nvars:                     5
```

This object can be now saved in a `*.mat` file as usual.

Workflow Example: Classifying Radar Returns for Ionosphere Data with TreeBagger

You can also use ensembles of decision trees for classification. For this example, use ionosphere data with 351 observations and 34 real-valued predictors. The response variable is categorical with two levels:

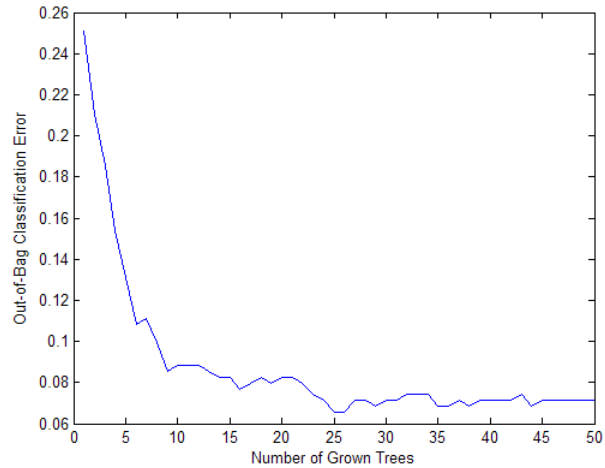
- `'g'` for good radar returns
- `'b'` for bad radar returns

The goal is to predict good or bad returns using a set of 34 measurements. The workflow resembles that for "Workflow Example: Regression of Insurance Risk Rating for Car Imports with TreeBagger" on page 13-97.

1 Fix the initial random seed, grow 50 trees, inspect how the ensemble error changes with accumulation of trees, and estimate feature importance. For classification, it is best to set the minimal leaf size to 1 and select the square root of the total number of features for each decision split at random. These are the default settings for a `TreeBagger` used for classification.

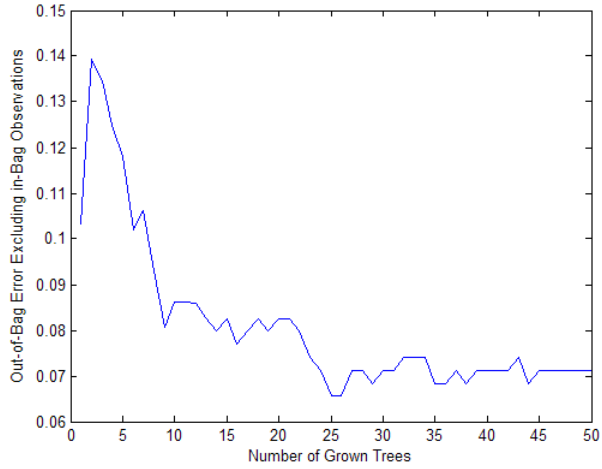
```
load ionosphere;
rng(1945,'twister')
b = TreeBagger(50,X,Y,'oobvarimp','on');
```

```
figure(10);
plot(oobError(b));
xlabel('Number of Grown Trees');
ylabel('Out-of-Bag Classification Error');
```



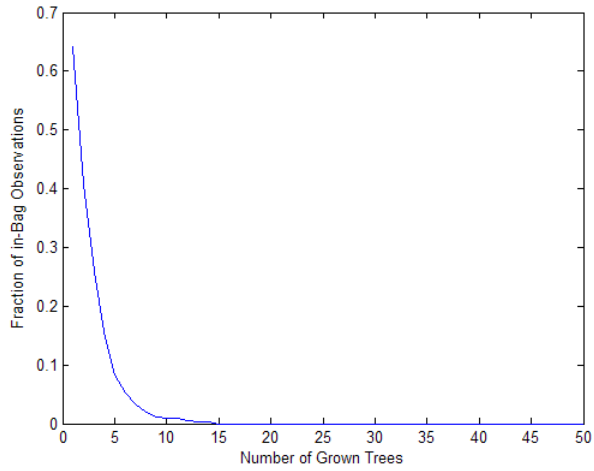
2 The method trains ensembles with few trees on observations that are in bag for all trees. For such observations, it is impossible to compute the true out-of-bag prediction, and `TreeBagger` returns the most probable class for classification and the sample mean for regression. You can change the default value returned for in-bag observations using the `DefaultYfit` property. If you set the default value to an empty string for classification, the method excludes in-bag observations from computation of the out-of-bag error. In this case, the curve is more variable when the number of trees is small, either because some observations are never out of bag (and are therefore excluded) or because their predictions are based on few trees.

```
b.DefaultYfit = '';
figure(11);
plot(oobError(b));
xlabel('Number of Grown Trees');
ylabel('Out-of-Bag Error Excluding in-Bag Observations');
```



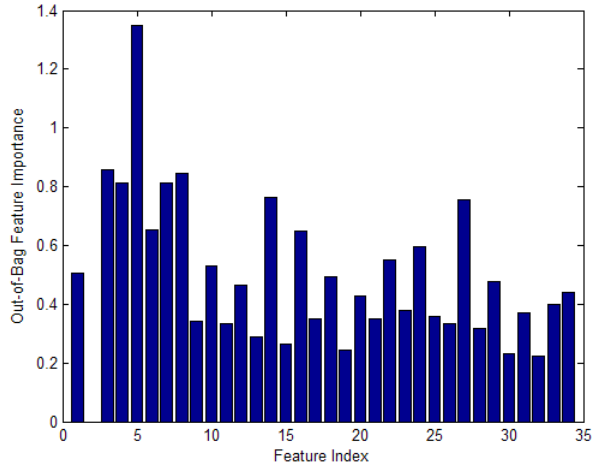
3 The `OOBIndices` property of `TreeBagger` tracks which observations are out of bag for what trees. Using this property, you can monitor the fraction of observations in the training data that are in bag for all trees. The curve starts at approximately 2/3, the fraction of unique observations selected by one bootstrap replica, and goes down to 0 at approximately 10 trees.

```
finbag = zeros(1,b.NTrees);
for t=1:b.NTrees
    finbag(t) = sum(all(~b.OOBIndices(:,1:t),2));
end
finbag = finbag / size(X,1);
figure(12);
plot(finbag);
xlabel('Number of Grown Trees');
ylabel('Fraction of in-Bag Observations');
```



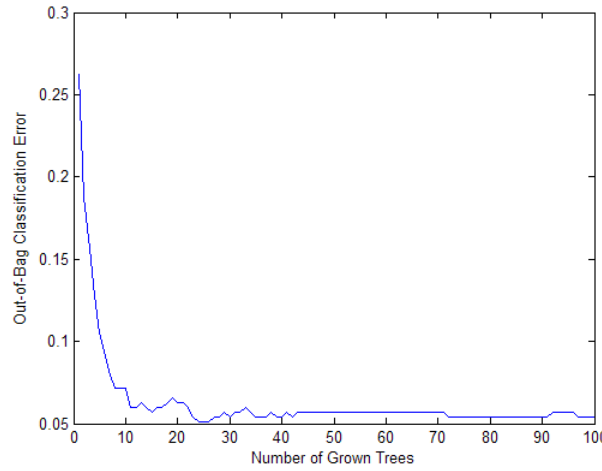
4 Estimate feature importance:

```
figure(13);
bar(b.OOBPermutedVarDeltaError);
xlabel('Feature Index');
ylabel('Out-of-Bag Feature Importance');
idxvar = find(b.OOBPermutedVarDeltaError>0.8)

idxvar =

     3     4     5     7     8
```



5 Having selected the five most important features, grow a larger ensemble on the reduced feature set. Save time by not permuting out-of-bag observations to obtain new estimates of feature importance for the reduced feature set (set `oobvarimp` to `'off'`). You would still be interested in obtaining out-of-bag estimates of classification error (set `oobpred` to `'on'`).

```
b5v = TreeBagger(100,X(:,idxvar),Y,'oobpred','on');
figure(14);
plot(oobError(b5v));
xlabel('Number of Grown Trees');
ylabel('Out-of-Bag Classification Error');
```

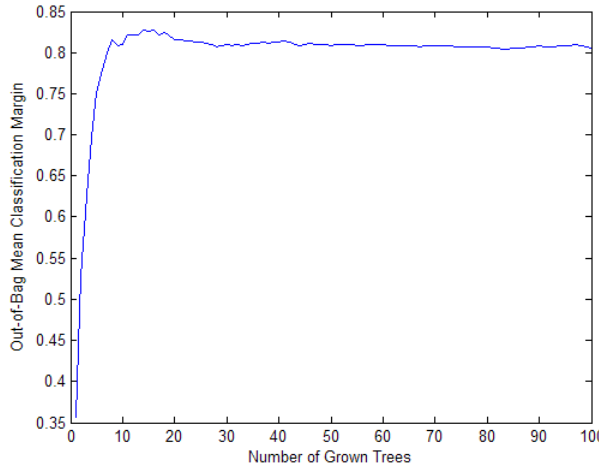


6 For classification ensembles, in addition to classification error (fraction of misclassified observations), you can also monitor the average classification margin. For each observation, the *margin* is defined as the difference between the score for the true class and the maximal score for other classes predicted by this tree. The cumulative classification margin uses the scores averaged over all trees and the mean cumulative classification margin is the cumulative margin averaged over all observations. The `oobMeanMargin` method with the `'mode'` argument set to `'cumulative'` (default) shows how the mean cumulative margin changes as the ensemble grows: every new element in the returned array represents the cumulative margin obtained by including a new tree in the ensemble. If training is successful, you would expect to see a gradual increase in the mean classification margin.

For decision trees, a classification score is the probability of observing an instance of this class in this tree leaf. For example, if the leaf of a grown decision tree has five `'good'` and three `'bad'` training observations in it, the scores returned by this decision tree for any observation fallen on this leaf are 5/8 for the `'good'` class and 3/8 for the `'bad'` class. These probabilities are called `'scores'` for consistency with other classifiers that might not have an obvious interpretation for numeric values of returned predictions.

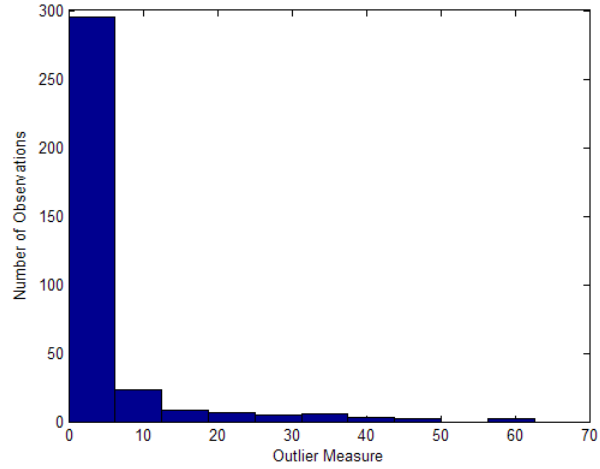
```
figure(15);
plot(oobMeanMargin(b5v));
```

```
xlabel('Number of Grown Trees');
ylabel('Out-of-Bag Mean Classification Margin');
```



7 Compute the matrix of proximities and look at the distribution of outlier measures. Unlike regression, outlier measures for classification ensembles are computed within each class separately.

```
b5v = fillProximities(b5v);
figure(16);
hist(b5v.OutlierMeasure);
xlabel('Outlier Measure');
ylabel('Number of Observations');
```



8 All extreme outliers for this dataset come from the `'good'` class:

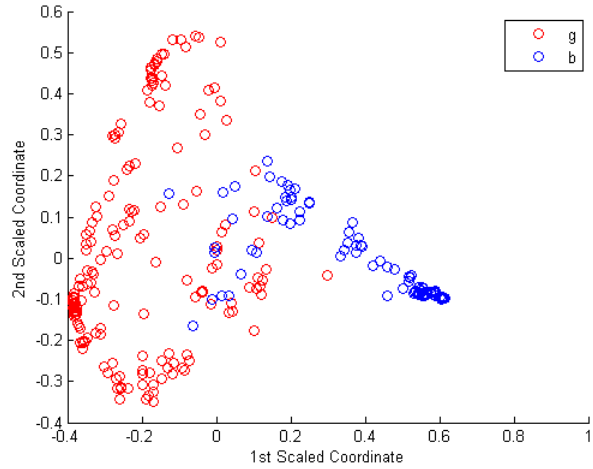
```
b5v.Y(b5v.OutlierMeasure>40)

ans =

    'g'
    'g'
    'g'
    'g'
    'g''
```

9 As for regression, you can plot scaled coordinates, displaying the two classes in different colors using the `colors` argument of `mdsProx`. This argument takes a string in which every character represents a color. To find the order of classes used by the ensemble, look at the `ClassNames` property:

```
b5v.ClassNames

ans =

    'g'
    'b'
```

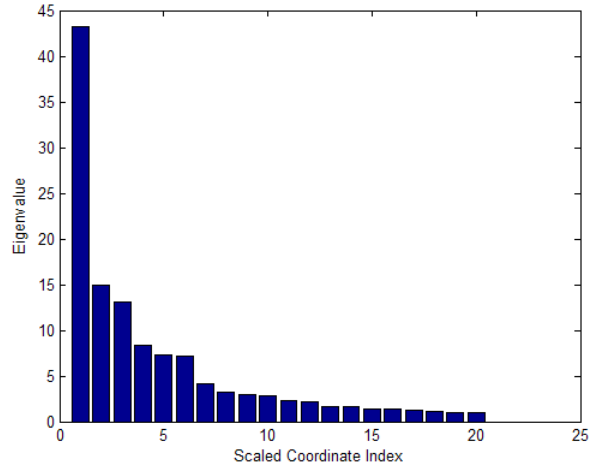
The 'good' class is first and the 'bad' class is second. Display scaled coordinates using red for 'good' and blue for 'bad' observations:

```
figure(17);
[s,e] = mdsProx(b5v,'colors','rb');
xlabel('1st Scaled Coordinate');
ylabel('2nd Scaled Coordinate');
```



10 Plot the first 20 eigenvalues obtained by scaling. The first eigenvalue in this case clearly dominates and the first scaled coordinate is most important.

```
figure(18);
bar(e(1:20));
xlabel('Scaled Coordinate Index');
ylabel('Eigenvalue');
```



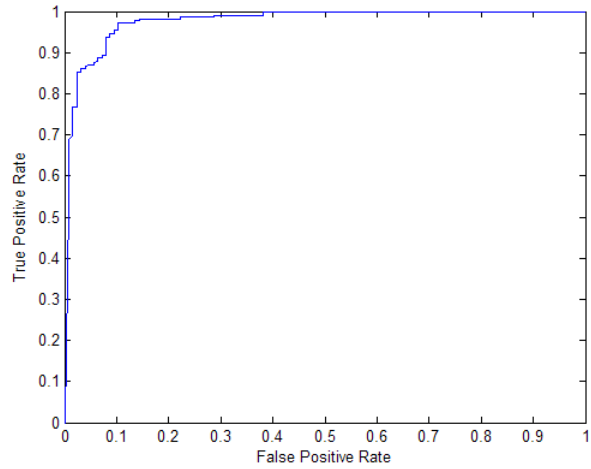
Plotting a Classification Performance Curve. Another way of exploring the performance of a classification ensemble is to plot its Receiver Operating Characteristic (ROC) curve or another performance curve suitable for the current problem. First, obtain predictions for out-of-bag observations. For a classification ensemble, the `oobPredict` method returns a cell array of classification labels (`'g'` or `'b'` for ionosphere data) as the first output argument and a numeric array of scores as the second output argument. The returned array of scores has two columns, one for each class. In this case, the first column is for the `'good'` class and the second column is for the `'bad'` class. One column in the score matrix is redundant because the scores represent class probabilities in tree leaves and by definition add up to 1.

```
[Yfit,Sfit] = oobPredict(b5v);
```

Use the `perfcurve` utility (see "Performance Curves" on page 12-32) to compute a performance curve. By default, `perfcurve` returns the standard ROC curve, which is the true positive rate versus the false positive rate. `perfcurve` requires true class labels, scores, and the positive class label for input. In this case, choose the `'good'` class as positive. The scores for this class are in the first column of `Sfit`.

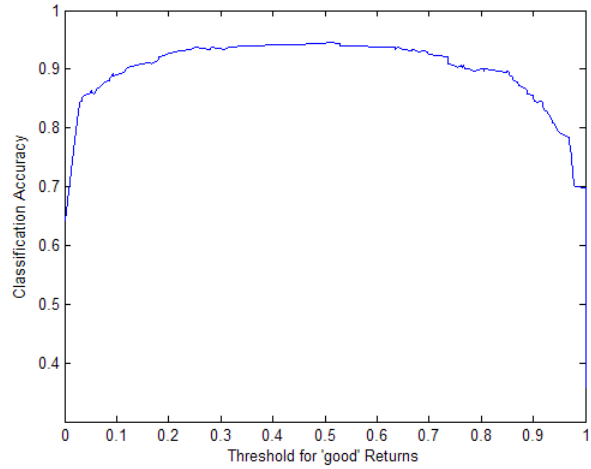
```
[fpr,tpr] = perfcurve(b5v.Y,Sfit(:,1),'g');
figure(19);
plot(fpr,tpr);
```

```
xlabel('False Positive Rate');
ylabel('True Positive Rate');
```



Instead of the standard ROC curve, you might want to plot, for example, ensemble accuracy versus threshold on the score for the `'good'` class. The `ycrit` input argument of `perfcurve` lets you specify the criterion for the *y*-axis, and the third output argument of `perfcurve` returns an array of thresholds for the positive class score. Accuracy is the fraction of correctly classified observations, or equivalently, 1 minus the classification error.

```
[fpr,accu,thre] = perfcurve(b5v.Y,Sfit(:,1),'g','ycrit','accu');
figure(20);
plot(thre,accu);
xlabel('Threshold for ''good'' Returns');
ylabel('Classification Accuracy');
```



The curve shows a flat region indicating that any threshold from 0.2 to 0.6 is a reasonable choice. By default, the function assigns classification labels using 0.5 as the boundary between the two classes. You can find exactly what accuracy this corresponds to:

```
i50 = find(accu>=0.50,1,'first')
accu(abs(thre-0.5)<eps)
```

returns

```
i50 =
    2

ans =
    0.9430
```

The maximal accuracy is a little higher than the default one:

```
[maxaccu,iaccu] = max(accu)
```

returns

```
maxaccu =
    0.9459
```

```
iaccu =
    91
```

The optimal threshold is therefore:

```
thre(iaccu)

ans =
    0.5056
```

Ensemble Algorithms

Bagging

Bagging, which stands for "bootstrap aggregation", is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, generate many bootstrap replicas of this dataset and grow decision trees on these replicas. Obtain each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, take an average over predictions from individual trees.

Bagged decision trees were introduced in MATLAB R2009a as `TreeBagger`. The `fitensemble` function lets you bag in a manner consistent with boosting. An ensemble of bagged trees, either `ClassificationBaggedEnsemble` or `RegressionBaggedEnsemble`, returned by `fitensemble` offers almost the same functionally as `TreeBagger`. Discrepancies between `TreeBagger` and

the new framework are described in detail in TreeBagger Features Not in fitensemble on page 13-120.

Bagging works by training learners on resampled versions of the data. This resampling is usually done by bootstrapping observations, that is, selecting *N* out of *N* observations with replacement for every new learner. In addition, every tree in the ensemble can randomly select predictors for decision splits—a technique known to improve the accuracy of bagged trees.

By default, the minimal leaf sizes for bagged trees are set to `1` for classification and `5` for regression. Trees grown with the default leaf size are usually very deep. These settings are close to optimal for the predictive power of an ensemble. Often you can grow trees with larger leaves without losing predictive power. Doing so reduces training and prediction time, as well as memory usage for the trained ensemble.

Another important parameter is the number of predictors selected at random for every decision split. This random selection is made for every split, and every deep tree involves many splits. By default, this parameter is set to a square root of the number of predictors for classification, and one third of predictors for regression.

Several features of bagged decision trees make them a unique algorithm. Drawing `N` out of `N` observations with replacement omits on average 37% of observations for each decision tree. These are "out-of-bag" observations. You can use them to estimate the predictive power and feature importance. For each observation, you can estimate the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. You can then compare the computed prediction against the observed response for this observation. By comparing the out-of-bag predicted responses against the observed responses for all observations used for training, you can estimate the average out-of-bag error. This out-of-bag average is an unbiased estimator of the true ensemble error. You can also obtain out-of-bag estimates of feature importance by randomly permuting out-of-bag data across one variable or column at a time and estimating the increase in the out-of-bag error due to this permutation. The larger the increase, the more important the feature. Thus, you need not supply test data for bagged ensembles because you obtain reliable estimates of the predictive power and feature importance in the process of training, which is an attractive feature of bagging.

Another attractive feature of bagged decision trees is the proximity matrix. Every time two observations land on the same leaf of a tree, their proximity increases by 1. For normalization, sum these proximities over all trees in the ensemble and divide by the number of trees. The resulting matrix is symmetric with diagonal elements equal to 1 and off-diagonal elements ranging from 0 to 1. You can use this matrix for finding outlier observations and discovering clusters in the data through multidimensional scaling.

For examples using bagging, see:

- "Example: Test Ensemble Quality" on page 13-60
- "Example: Surrogate Splits" on page 13-77
- "Workflow Example: Regression of Insurance Risk Rating for Car Imports with TreeBagger" on page 13-97
- "Workflow Example: Classifying Radar Returns for Ionosphere Data with TreeBagger" on page 13-106

For references related to bagging, see Breiman [1], [2], and [3].

Comparison of TreeBagger and Bagged Ensembles. `fitensemble` produces bagged ensembles that have most, but not all, of the functionality of `TreeBagger` objects. Additionally, some functionality has different names in the new bagged ensembles.

TreeBagger Features Not in fitensemble

Feature	TreeBagger Property	TreeBagger Method
Computation of proximity matrix	`Proximity`	`fillProximities`, `mdsProx`
Computation of outliers	`OutlierMeasure`	
Out-of-bag estimates of predictor importance	`OOBPermutedVarDeltaError`, `OOBPermutedVarDeltaMeanMargin`, `OOBPermutedVarCountRaiseMargin`	

TreeBagger Features Not in fitensemble (Continued)

Feature	TreeBagger Property	TreeBagger Method
Merging two ensembles trained separately		`append`
Parallel computation for creating ensemble	Set the `UseParallel` name-value pair to `'always'`; see Chapter 17, "Parallel Statistics"	

Differing Names Between TreeBagger and Bagged Ensembles

Feature	TreeBagger	Bagged Ensembles
Split criterion contributions for each predictor	`DeltaCritDecisionSplit` property	First output of `predictorImportance` (classification) or `predictorImportance` (regression)
Predictor associations	`VarAssoc` property	Second output of `predictorImportance` (classification) or `predictorImportance` (regression)
Error (misclassification probability or mean-squared error)	`error` and `oobError` methods	`loss` and `oobLoss` methods (classification); `loss` and `oobLoss` methods (regression)
Train additional trees and add to ensemble	`growTrees` method	`resume` method (classification); `resume` method (regression)
Mean classification margin per tree	`meanMargin` and `oobMeanMargin` methods	`edge` and `oobEdge` methods (classification);

In addition, two important changes were made to training and prediction for bagged classification ensembles:

- If you pass a misclassification cost matrix to `TreeBagger`, it passes this matrix along to the trees. If you pass a misclassification cost matrix to `fitensemble`, it uses this matrix to adjust the class prior probabilities.

`fitensemble` then passes the adjusted prior probabilities and the default cost matrix to the trees. The default cost matrix is `ones(K)-eye(K)` for `K` classes.

- Unlike the `loss` and `edge` methods in the new framework, the `TreeBagger` `error` and `meanMargin` methods do not normalize input observation weights of the prior probabilities in the respective class.

AdaBoostM1

`AdaBoostM1` is a very popular boosting algorithm for binary classification. The algorithm trains learners sequentially. For every learner with index t, `AdaBoostM1` computes the weighted classification error

$$\varepsilon_t = \sum_{n=1}^{N} d_n^{(t)} \mathrm{I}\left(y_n = h_t\left(x_n\right)\right)$$

- x_n is a vector of predictor values for observation n.
- y_n is the true class label.
- h_t is the prediction of learner (hypothesis) with index t.
- `I` is the indicator function.
- $d_n^{(t)}$ is the weight of observation n at step t.

`AdaBoostM1` then increases weights for observations misclassified by learner t and reduces weights for observations correctly classified by learner t. The next learner $t + 1$ is then trained on the data with updated weights $d_n^{(t+1)}$.

After training finishes, `AdaBoostM1` computes prediction for new data using

$$f\left(x\right) = \sum_{t=1}^{T} \alpha_t h_t\left(x\right),$$

where

$$\alpha_t = \frac{1}{2}\log\frac{1-\varepsilon_t}{\varepsilon_t}$$

are weights of the weak hypotheses in the ensemble.

Training by `AdaBoostM1` can be viewed as stagewise minimization of the exponential loss:

$$\sum_{n=1}^{N} w_n \exp\left(-y_n f\left(x_n\right)\right)$$

where

- $y_n \in \{-1,+1\}$ is the true class label.
- w_n are observation weights normalized to add up to 1.
- $f(x_n) \in (-\infty,+\infty)$ is the predicted classification score.

The observation weights w_n are the original observation weights you passed to `fitensemble`.

The second output from the `predict` method of an `AdaBoostM1` classification ensemble is an N-by-2 matrix of classification scores for the two classes and N observations. The second column in this matrix is always equal to minus the first column. `predict` returns two scores to be consistent with multiclass models, though this is redundant since the second column is always the negative of the first.

Most often `AdaBoostM1` is used with decision stumps (default) or shallow trees. If boosted stumps give poor performance, try setting the minimal parent node size to one quarter of the training data.

By default, the learning rate for boosting algorithms is `1`. If you set the learning rate to a lower number, the ensemble learns at a slower rate, but can converge to a better solution. `0.1` is a popular choice for the learning rate. Learning at a rate less than `1` is often called “shrinkage”.

For examples using `AdaBoostM1`, see "Example: Tuning RobustBoost" on page 13-92.

For references related to `AdaBoostM1`, see Freund and Schapire [6], Schapire et al. [10], Friedman, Hastie, and Tibshirani [8], and Friedman [7].

AdaBoostM2

`AdaBoostM2` is an extension of `AdaBoostM1` for multiple classes. Instead of weighted classification error, `AdaBoostM2` uses weighted pseudo-loss for N observations and K classes:

$$\varepsilon_t = \frac{1}{2}\sum_{n=1}^{N}\sum_{k\neq y_n} d_{n,k}^{(t)}\left(1 - h_t\left(x_n, y_n\right) + h_t\left(x_n, k\right)\right)$$

where

- $h_t(x_n,k)$ is the confidence of prediction by learner at step t into class k ranging from 0 (not at all confident) to 1 (highly confident).
- $d_{n,k}^{(t)}$ are observation weights at step t for class k.
- y_n is the true class label taking one of the K values.
- The second sum is over all classes other than the true class y_n.

Interpreting the pseudo-loss is harder than classification error, but the idea is the same. Pseudo-loss can be used as a measure of the classification accuracy from any learner in an ensemble. Pseudo-loss typically exhibits the same behavior as a weighted classification error for `AdaBoostM1`: the first few learners in a boosted ensemble give low pseudo-loss values. After the first few training steps, the ensemble begins to learn at a slower pace, and the pseudo-loss value approaches 0.5 from below.

For examples using `AdaBoostM2`, see "Creating a Classification Ensemble" on page 13-58.

For references related to `AdaBoostM2`, see Freund and Schapire [6].

LogitBoost

`LogitBoost` is another popular algorithm for binary classification. `LogitBoost` works similarly to `AdaBoostM1`, except it minimizes binomial deviance

$$\sum_{n=1}^{N} w_n \log\left(1+\exp\left(-2y_n f\left(x_n\right)\right)\right),$$

where

- $y_n \in \{-1,+1\}$ is the true class label.
- w_n are observation weights normalized to add up to 1.
- $f(x_n) \in (-\infty,+\infty)$ is the predicted classification score.

Binomial deviance assigns less weight to badly misclassified observations (observations with large negative values of $y_n f(x_n)$). `LogitBoost` can give better average accuracy than `AdaBoostM1` for data with poorly separable classes.

Learner t in a `LogitBoost` ensemble fits a regression model to response values

$$\tilde{y}_n = \frac{y_n^* - p_t\left(x_n\right)}{p_t\left(x_n\right)\left(1-p_t\left(x_n\right)\right)}$$

where

- $y^*_n \in \{0,+1\}$ are relabeled classes (0 instead of –1).
- $p_t(x_n)$ is the current ensemble estimate of the probability for observation x_n to be of class 1.

Fitting a regression model at each boosting step turns into a great computational advantage for data with multilevel categorical predictors. Take a categorical predictor with L levels. To find the optimal decision split on such a predictor, classification tree needs to consider $2^{L-1} - 1$ splits. A regression tree needs to consider only $L - 1$ splits, so the processing time

can be much shorter. `LogitBoost` is recommended for categorical predictors with many levels.

`fitensemble` computes and stores the mean-squared error

$$\sum_{n=1}^{N} d_n^{(t)} \left(\tilde{y}_n - h_t(x_n) \right)^2$$

in the `FitInfo` property of the ensemble object. Here

- $d_n^{(t)}$ are observation weights at step t (the weights add up to 1).
- $h_t(x_n)$ are predictions of the regression model h_t fitted to response values $\tilde{y}_n$.

Values y_n can range from $-\infty$ to $+\infty$, so the mean-squared error does not have well-defined bounds.

For examples using `LogitBoost`, see "Example: Classification with Many Categorical Levels" on page 13-72.

For references related to `LogitBoost`, see Friedman, Hastie, and Tibshirani [8].

GentleBoost

`GentleBoost` (also known as Gentle AdaBoost) combines features of `AdaBoostM1` and `LogitBoost`. Like `AdaBoostM1`, `GentleBoost` minimizes the exponential loss. But its numeric optimization is set up differently. Like `LogitBoost`, every weak learner fits a regression model to response values $y_n \in \{-1,+1\}$. This makes `GentleBoost` another good candidate for binary classification of data with multilevel categorical predictors.

`fitensemble` computes and stores the mean-squared error

$$\sum_{n=1}^{N} d_n^{(t)} \left(\tilde{y}_n - h_t(x_n) \right)^2$$

in the `FitInfo` property of the ensemble object, where

- $d_n^{(t)}$ are observation weights at step t (the weights add up to 1).
- $h_t(x_n)$ are predictions of the regression model h_t fitted to response values y_n.

As the strength of individual learners weakens, the weighted mean-squared error approaches 1.

For examples using `GentleBoost`, see "Example: Unequal Classification Costs" on page 13-67, "Example: Classification with Many Categorical Levels" on page 13-72.

For references related to `GentleBoost`, see Friedman, Hastie, and Tibshirani [8].

RobustBoost

Boosting algorithms such as `AdaBoostM1` and `LogitBoost` increase weights for misclassified observations at every boosting step. These weights can become very large. If this happens, the boosting algorithm sometimes concentrates on a few misclassified observations and neglects the majority of training data. Consequently the average classification accuracy suffers.

In this situation, you can try using `RobustBoost`. This algorithm does not assign almost the entire data weight to badly misclassified observations. It can produce better average classification accuracy.

Unlike `AdaBoostM1` and `LogitBoost`, `RobustBoost` does not minimize a specific loss function. Instead, it maximizes the number of observations with the classification margin above a certain threshold.

`RobustBoost` trains based on time evolution. The algorithm starts at $t = 0$. At every step, `RobustBoost` solves an optimization problem to find a positive step in time Δt and a corresponding positive change in the average margin for training data Δm. `RobustBoost` stops training and exits if at least one of these three conditions is true:

- Time t reaches 1.

- `RobustBoost` cannot find a solution to the optimization problem with positive updates Δt and Δm.
- `RobustBoost` grows as many learners as you requested.

Results from `RobustBoost` can be usable for any termination condition. Estimate the classification accuracy by cross validation or by using an independent test set.

To get better classification accuracy from `RobustBoost`, you can adjust three parameters in `fitensemble`: `RobustErrorGoal`, `RobustMaxMargin`, and `RobustMarginSigma`. Start by varying values for `RobustErrorGoal` from 0 to 1. The maximal allowed value for `RobustErrorGoal` depends on the two other parameters. If you pass a value that is too high, `fitensemble` produces an error message showing the allowed range for `RobustErrorGoal`.

For examples using `RobustBoost`, see "Example: Tuning RobustBoost" on page 13-92

For references related to `RobustBoost`, see Freund [5].

LSBoost

You can use least squares boosting (`LSBoost`) to fit regression ensembles. At every step, the ensemble fits a new learner to the difference between the observed response and the aggregated prediction of all learners grown previously. The ensemble fits to minimize mean-squared error.

You can use `LSBoost` with shrinkage by passing in `LearnRate` parameter. By default this parameter is set to `1`, and the ensemble learns at the maximal speed. If you set `LearnRate` to a value from `0` to `1`, the ensemble fits every new learner to $y_n - \eta f(x_n)$, where

- y_n is the observed response.
- $f(x_n)$ is the aggregated prediction from all weak learners grown so far for observation x_n.
- η is the learning rate.

For examples using `LSBoost`, see "Creating a Regression Ensemble" on page 13-59, "Example: Regularizing a Regression Ensemble" on page 13-82

For references related to `LSBoost`, see Hastie, Tibshirani, and Friedman [9], Chapters 7 (Model Assessment and Selection) and 15 (Random Forests).

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14

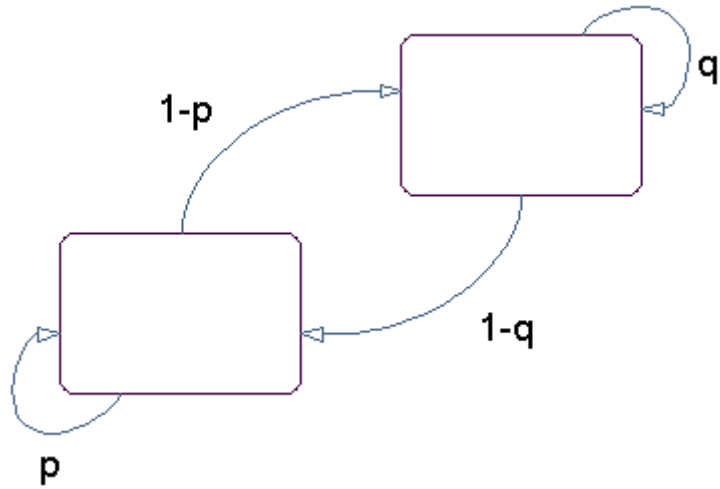
Markov Models

Introduction to Markov Models

Markov processes are examples of stochastic processes—processes that generate random sequences of outcomes or *states* according to certain probabilities. Markov processes are distinguished by being memoryless—their next state depends only on their current state, not on the history that led them there. Models of Markov processes are used in a wide variety of applications, from daily stock prices to the positions of genes in a chromosome.

Markov Chains

A Markov model is given visual representation with a *state diagram*, such as the one below.



State Diagram for a Markov Model

The rectangles in the diagram represent the possible states of the process you are trying to model, and the arrows represent transitions between states. The label on each arrow represents the probability of that transition. At each step of the process, the model may generate an output, or *emission*, depending on which state it is in, and then make a transition to another state. An important characteristic of Markov models is that the next state depends only on the current state, and not on the history of transitions that lead to the current state.

For example, for a sequence of coin tosses the two states are heads and tails. The most recent coin toss determines the current state of the model and each subsequent toss determines the transition to the next state. If the coin is fair, the transition probabilities are all 1/2. The emission might simply be the current state. In more complicated models, random processes at each state will generate emissions. You could, for example, roll a die to determine the emission at any step.

Markov chains are mathematical descriptions of Markov models with a discrete set of states. Markov chains are characterized by:

- A set of states {1, 2, ..., *M*}
- An *M*-by-*M transition matrix T* whose *i*,*j* entry is the probability of a transition from state *i* to state *j*. The sum of the entries in each row of *T* must be 1, because this is the sum of the probabilities of making a transition from a given state to each of the other states.
- A set of possible outputs, or *emissions*, $\{s_1, s_2, \ldots, s_N\}$. By default, the set of emissions is {1, 2, ... , *N*}, where *N* is the number of possible emissions, but you can choose a different set of numbers or symbols.
- An *M*-by-*N emission matrix E* whose *i*,*k* entry gives the probability of emitting symbol s_k given that the model is in state *i*.

Markov chains begin in an *initial state* i_0 at step 0. The chain then transitions to state i_1 with probability T_{1i_1}, and emits an output s_{k_1} with probability $E_{i_1k_1}$. Consequently, the probability of observing the sequence of states $i_1 i_2 \ldots i_r$ and the sequence of emissions $s_{k_1} s_{k_2} \ldots s_{k_r}$ in the first *r* steps, is

$$T_{1i_1} E_{i_1k_1} T_{i_1i_2} E_{i_2k_2} \ldots T_{i_{r-1}i_r} E_{i_rk}$$

Hidden Markov Models (HMM)

In this section...

Introduction to Hidden Markov Models (HMM)

A *hidden Markov model* (HMM) is one in which you observe a sequence of emissions, but do not know the sequence of states the model went through to generate the emissions. Analyses of hidden Markov models seek to recover the sequence of states from the observed data.

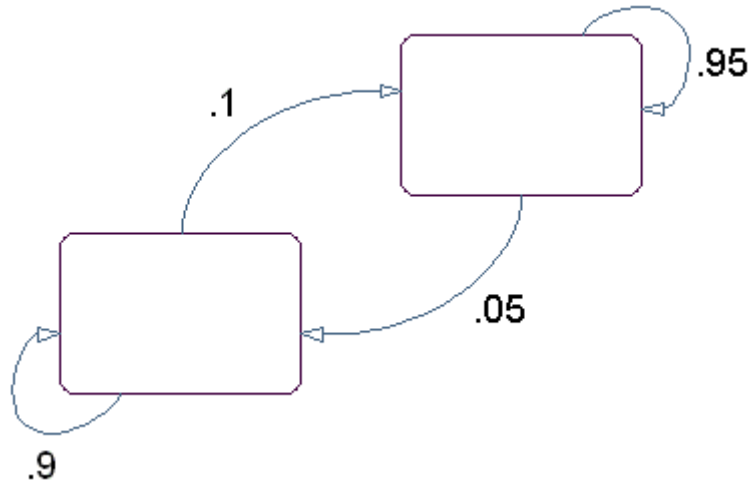
As an example, consider a Markov model with two states and six possible emissions. The model uses:

- A red die, having six sides, labeled 1 through 6.
- A green die, having twelve sides, five of which are labeled 2 through 6, while the remaining seven sides are labeled 1.
- A weighted red coin, for which the probability of heads is .9 and the probability of tails is .1.
- A weighted green coin, for which the probability of heads is .95 and the probability of tails is .05.

The model creates a sequence of numbers from the set {1, 2, 3, 4, 5, 6} with the following rules:

- Begin by rolling the red die and writing down the number that comes up, which is the emission.
- Toss the red coin and do one of the following:
  - If the result is heads, roll the red die and write down the result.
  - If the result is tails, roll the green die and write down the result.
- At each subsequent step, you flip the coin that has the same color as the die you rolled in the previous step. If the coin comes up heads, roll the same die as in the previous step. If the coin comes up tails, switch to the other die.

The state diagram for this model has two states, red and green, as shown in the following figure.



You determine the emission from a state by rolling the die with the same color as the state. You determine the transition to the next state by flipping the coin with the same color as the state.

The transition matrix is:

$$T = \begin{bmatrix} 0.9 & 0.1 \\ 0.05 & 0.95 \end{bmatrix}$$

The emissions matrix is:

$$E = \begin{bmatrix} \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} \\ \frac{7}{12} & \frac{1}{12} & \frac{1}{12} & \frac{1}{12} & \frac{1}{12} & \frac{1}{12} \end{bmatrix}$$

The model is not hidden because you know the sequence of states from the colors of the coins and dice. Suppose, however, that someone else is generating

the emissions without showing you the dice or the coins. All you see is the sequence of emissions. If you start seeing more 1s than other numbers, you might suspect that the model is in the green state, but you cannot be sure because you cannot see the color of the die being rolled.

Hidden Markov models raise the following questions:

- Given a sequence of emissions, what is the most likely state path?
- Given a sequence of emissions, how can you estimate transition and emission probabilities of the model?
- What is the *forward probability* that the model generates a given sequence?
- What is the *posterior probability* that the model is in a particular state at any point in the sequence?

Analyzing Hidden Markov Models

Statistics Toolbox functions related to hidden Markov models are:

- `hmmgenerate` — Generates a sequence of states and emissions from a Markov model
- `hmmestimate` — Calculates maximum likelihood estimates of transition and emission probabilities from a sequence of emissions and a known sequence of states
- `hmmtrain` — Calculates maximum likelihood estimates of transition and emission probabilities from a sequence of emissions
- `hmmviterbi` — Calculates the most probable state path for a hidden Markov model

- `hmmdecode` — Calculates the posterior state probabilities of a sequence of emissions

This section shows how to use these functions to analyze hidden Markov models.

Generating a Test Sequence

The following commands create the transition and emission matrices for the model described in the "Introduction to Hidden Markov Models (HMM)" on page 14-5:

```
TRANS = [.9 .1; .05 .95;];

EMIS = [1/6, 1/6, 1/6, 1/6, 1/6, 1/6;...
7/12, 1/12, 1/12, 1/12, 1/12, 1/12];
```

To generate a random sequence of states and emissions from the model, use `hmmgenerate`:

```
[seq,states] = hmmgenerate(1000,TRANS,EMIS);
```

The output `seq` is the sequence of emissions and the output `states` is the sequence of states.

`hmmgenerate` begins in state 1 at step 0, makes the transition to state i_1 at step 1, and returns i_1 as the first entry in `states`. To change the initial state, see "Changing the Initial State Distribution" on page 14-12.

Estimating the State Sequence

Given the transition and emission matrices `TRANS` and `EMIS`, the function `hmmviterbi` uses the Viterbi algorithm to compute the most likely sequence of states the model would go through to generate a given sequence `seq` of emissions:

```
likelystates = hmmviterbi(seq, TRANS, EMIS);
```

`likelystates` is a sequence the same length as `seq`.

To test the accuracy of `hmmviterbi`, compute the percentage of the actual sequence `states` that agrees with the sequence `likelystates`.

```
sum(states==likelystates)/1000
ans =
   0.8200
```

In this case, the most likely sequence of states agrees with the random sequence 82% of the time.

Estimating Transition and Emission Matrices

- "Using hmmestimate" on page 14-9
- "Using hmmtrain" on page 14-10

The functions `hmmestimate` and `hmmtrain` estimate the transition and emission matrices `TRANS` and `EMIS` given a sequence `seq` of emissions.

Using hmmestimate. The function `hmmestimate` requires that you know the sequence of states `states` that the model went through to generate `seq`.

The following takes the emission and state sequences and returns estimates of the transition and emission matrices:

```
[TRANS_EST, EMIS_EST] = hmmestimate(seq, states)

TRANS_EST =
0.8989    0.1011
0.0585    0.9415

EMIS_EST =
0.1721    0.1721    0.1749    0.1612    0.1803    0.1393
0.5836    0.0741    0.0804    0.0789    0.0726    0.1104
```

You can compare the outputs with the original transition and emission matrices, `TRANS` and `EMIS`:

```
TRANS
TRANS =
0.9000    0.1000
0.0500    0.9500

EMIS
```

```
EMIS =
0.1667    0.1667    0.1667    0.1667    0.1667    0.1667
0.5833    0.0833    0.0833    0.0833    0.0833    0.0833
```

Using hmmtrain. If you do not know the sequence of states `states`, but you have initial guesses for `TRANS` and `EMIS`, you can still estimate `TRANS` and `EMIS` using `hmmtrain`.

Suppose you have the following initial guesses for `TRANS` and `EMIS`.

```
TRANS_GUESS = [.85 .15; .1 .9];
EMIS_GUESS = [.17 .16 .17 .16 .17 .17;.6 .08 .08 .08 .08 08];
```

You estimate `TRANS` and `EMIS` as follows:

```
[TRANS_EST2, EMIS_EST2] = hmmtrain(seq, TRANS_GUESS, EMIS_GUESS)

TRANS_EST2 =
0.2286    0.7714
0.0032    0.9968

EMIS_EST2 =
0.1436    0.2348    0.1837    0.1963    0.2350    0.0066
0.4355    0.1089    0.1144    0.1082    0.1109    0.1220
```

`hmmtrain` uses an iterative algorithm that alters the matrices `TRANS_GUESS` and `EMIS_GUESS` so that at each step the adjusted matrices are more likely to generate the observed sequence, `seq`. The algorithm halts when the matrices in two successive iterations are within a small tolerance of each other.

If the algorithm fails to reach this tolerance within a maximum number of iterations, whose default value is `100`, the algorithm halts. In this case, `hmmtrain` returns the last values of `TRANS_EST` and `EMIS_EST` and issues a warning that the tolerance was not reached.

If the algorithm fails to reach the desired tolerance, increase the default value of the maximum number of iterations with the command:

```
hmmtrain(seq,TRANS_GUESS,EMIS_GUESS,'maxiterations',maxiter)
```

where `maxiter` is the maximum number of steps the algorithm executes.

Change the default value of the tolerance with the command:

```
hmmtrain(seq, TRANS_GUESS, EMIS_GUESS, 'tolerance', tol)
```

where `tol` is the desired value of the tolerance. Increasing the value of `tol` makes the algorithm halt sooner, but the results are less accurate.

Two factors reduce the reliability of the output matrices of `hmmtrain`:

- The algorithm converges to a local maximum that does not represent the true transition and emission matrices. If you suspect this, use different initial guesses for the matrices `TRANS_EST` and `EMIS_EST`.
- The sequence `seq` may be too short to properly train the matrices. If you suspect this, use a longer sequence for `seq`.

Estimating Posterior State Probabilities

The posterior state probabilities of an emission sequence `seq` are the conditional probabilities that the model is in a particular state when it generates a symbol in `seq`, given that `seq` is emitted. You compute the posterior state probabilities with `hmmdecode`:

```
PSTATES = hmmdecode(seq,TRANS,EMIS)
```

The output `PSTATES` is an M-by-L matrix, where M is the number of states and L is the length of `seq`. `PSTATES(i,j)` is the conditional probability that the model is in state `i` when it generates the `j`th symbol of `seq`, given that `seq` is emitted.

`hmmdecode` begins with the model in state 1 at step 0, prior to the first emission. `PSTATES(i,1)` is the probability that the model is in state i at the following step 1. To change the initial state, see “Changing the Initial State Distribution” on page 14-12.

To return the logarithm of the probability of the sequence `seq`, use the second output argument of `hmmdecode`:

```
[PSTATES,logpseq] = hmmdecode(seq,TRANS,EMIS)
```

The probability of a sequence tends to 0 as the length of the sequence increases, and the probability of a sufficiently long sequence becomes less

than the smallest positive number your computer can represent. `hmmdecode` returns the logarithm of the probability to avoid this problem.

Changing the Initial State Distribution

By default, Statistics Toolbox hidden Markov model functions begin in state 1. In other words, the distribution of initial states has all of its probability mass concentrated at state 1. To assign a different distribution of probabilities, $p = [p_1, p_2, ..., p_M]$, to the M initial states, do the following:

1. Create an M+1-by-M+1 augmented transition matrix, $\hat{T}$ of the following form:

   $$\hat{T} = \begin{bmatrix} 0 & p \\ 0 & T \end{bmatrix}$$

   where T is the true transition matrix. The first column of $\hat{T}$ contains M+1 zeros. p must sum to 1.

2. Create an M+1-by-N augmented emission matrix, $\hat{E}$, that has the following form:

   $$\hat{E} = \begin{bmatrix} 0 \\ E \end{bmatrix}$$

If the transition and emission matrices are `TRANS` and `EMIS`, respectively, you create the augmented matrices with the following commands:

```
TRANS_HAT = [0 p; zeros(size(TRANS,1),1) TRANS];

EMIS_HAT = [zeros(1,size(EMIS,2)); EMIS];
```

15

Design of Experiments

Introduction to Design of Experiments

Passive data collection leads to a number of problems in statistical modeling. Observed changes in a response variable may be correlated with, but not caused by, observed changes in individual *factors* (process variables). Simultaneous changes in multiple factors may produce interactions that are difficult to separate into individual effects. Observations may be dependent, while a model of the data considers them to be independent.

Designed experiments address these problems. In a designed experiment, the data-producing process is actively manipulated to improve the quality of information and to eliminate redundant data. A common goal of all experimental designs is to collect data as parsimoniously as possible while providing sufficient information to accurately estimate model parameters.

For example, a simple model of a response y in an experiment with two controlled factors x_1 and x_2 might look like this:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_1 x_2 + \varepsilon$$

Here ε includes both experimental error and the effects of any uncontrolled factors in the experiment. The terms $\beta_1 x_1$ and $\beta_2 x_2$ are *main effects* and the term $\beta_3 x_1 x_2$ is a two-way *interaction effect*. A designed experiment would systematically manipulate x_1 and x_2 while measuring y, with the objective of accurately estimating β_0, β_1, β_2, and β_3.

Full Factorial Designs

In this section...

Multilevel Designs

To systematically vary experimental factors, assign each factor a discrete set of *levels*. Full factorial designs measure response variables using every *treatment* (combination of the factor levels). A full factorial design for n factors with N_1, ..., N_n levels requires $N_1 \times ... \times N_n$ experimental runs—one for each treatment. While advantageous for separating individual effects, full factorial designs can make large demands on data collection.

As an example, suppose a machine shop has three machines and four operators. If the same operator always uses the same machine, it is impossible to determine if a machine or an operator is the cause of variation in production. By allowing every operator to use every machine, effects are separated. A full factorial list of treatments is generated by the Statistics Toolbox function `fullfact`:

```
dFF = fullfact([3,4])
dFF =
     1     1
     2     1
     3     1
     1     2
     2     2
     3     2
     1     3
     2     3
     3     3
     1     4
     2     4
     3     4
```

Each of the 3×4 = 12 rows of `dFF` represent one machine/operator combination.

Two-Level Designs

Many experiments can be conducted with two-level factors, using *two-level designs*. For example, suppose the machine shop in the previous example always keeps the same operator on the same machine, but wants to measure production effects that depend on the composition of the day and night shifts. The Statistics Toolbox function `ff2n` generates a full factorial list of treatments:

```
dFF2 = ff2n(4)
dFF2 =
     0     0     0     0
     0     0     0     1
     0     0     1     0
     0     0     1     1
     0     1     0     0
     0     1     0     1
     0     1     1     0
     0     1     1     1
     1     0     0     0
     1     0     0     1
     1     0     1     0
     1     0     1     1
     1     1     0     0
     1     1     0     1
     1     1     1     0
     1     1     1     1
```

Each of the $2^4 = 16$ rows of `dFF2` represent one schedule of operators for the day (0) and night (1) shifts.

Fractional Factorial Designs

In this section...

Introduction to Fractional Factorial Designs

Two-level designs are sufficient for evaluating many production processes. Factor levels of ±1 can indicate categorical factors, normalized factor extremes, or simply "up" and "down" from current factor settings. Experimenters evaluating process *changes* are interested primarily in the factor directions that lead to process improvement.

For experiments with many factors, two-level full factorial designs can lead to large amounts of data. For example, a two-level full factorial design with 10 factors requires $2^{10} = 1024$ runs. Often, however, individual factors or their interactions have no distinguishable effects on a response. This is especially true of higher order interactions. As a result, a well-designed experiment can use fewer runs for estimating model parameters.

Fractional factorial designs use a fraction of the runs required by full factorial designs. A subset of experimental treatments is selected based on an evaluation (or assumption) of which factors and interactions have the most significant effects. Once this selection is made, the experimental design must separate these effects. In particular, significant effects should not be *confounded*, that is, the measurement of one should not depend on the measurement of another.

Plackett-Burman Designs

Plackett-Burman designs are used when only main effects are considered significant. Two-level Plackett-Burman designs require a number of experimental runs that are a multiple of 4 rather than a power of 2. The MATLAB function `hadamard` generates these designs:

```
dPB = hadamard(8)
```

```
dPB =
     1     1     1     1     1     1     1     1
     1    -1     1    -1     1    -1     1    -1
     1     1    -1    -1     1     1    -1    -1
     1    -1    -1     1     1    -1    -1     1
     1     1     1     1    -1    -1    -1    -1
     1    -1     1    -1    -1     1    -1     1
     1     1    -1    -1    -1    -1     1     1
     1    -1    -1     1    -1     1     1    -1
```

Binary factor levels are indicated by ±1. The design is for eight runs (the rows of `dPB`) manipulating seven two-level factors (the last seven columns of `dPB`). The number of runs is a fraction $8/2^7 = 0.0625$ of the runs required by a full factorial design. Economy is achieved at the expense of confounding main effects with any two-way interactions.

General Fractional Designs

At the cost of a larger fractional design, you can specify which interactions you wish to consider significant. A design of *resolution R* is one in which no n-factor interaction is confounded with any other effect containing less than $R - n$ factors. Thus, a resolution III design does not confound main effects with one another but may confound them with two-way interactions (as in "Plackett-Burman Designs" on page 15-5), while a resolution IV design does not confound either main effects or two-way interactions but may confound two-way interactions with each other.

Specify general fractional factorial designs using a full factorial design for a selected subset of *basic factors* and *generators* for the remaining factors. Generators are products of the basic factors, giving the levels for the remaining factors. Use the Statistics Toolbox function `fracfact` to generate these designs:

```
dfF = fracfact('a b c d bcd acd')
dfF =
    -1    -1    -1    -1    -1    -1
    -1    -1    -1     1     1     1
    -1    -1     1    -1     1     1
    -1    -1     1     1    -1    -1
    -1     1    -1    -1     1    -1
```

```
    -1     1    -1     1    -1     1
    -1     1     1    -1    -1     1
    -1     1     1     1     1    -1
     1    -1    -1    -1    -1     1
     1    -1    -1     1     1    -1
     1    -1     1    -1     1    -1
     1    -1     1     1    -1     1
     1     1    -1    -1     1     1
     1     1    -1     1    -1    -1
     1     1     1    -1    -1    -1
     1     1     1     1     1     1
```

This is a six-factor design in which four two-level basic factors (`a`, `b`, `c`, and `d` in the first four columns of `dfF`) are measured in every combination of levels, while the two remaining factors (in the last three columns of `dfF`) are measured only at levels defined by the generators `bcd` and `acd`, respectively. Levels in the generated columns are products of corresponding levels in the columns that make up the generator.

The challenge of creating a fractional factorial design is to choose basic factors and generators so that the design achieves a specified resolution in a specified number of runs. Use the Statistics Toolbox function `fracfactgen` to find appropriate generators:

```
generators = fracfactgen('a b c d e f',4,4)
generators =
    'a'
    'b'
    'c'
    'd'
    'bcd'
    'acd'
```

These are generators for a six-factor design with factors `a` through `f`, using $2^4 = 16$ runs to achieve resolution IV. The `fracfactgen` function uses an efficient search algorithm to find generators that meet the requirements.

An optional output from `fracfact` displays the *confounding pattern* of the design:

```
[dfF,confounding] = fracfact(generators);
```

```
confounding
confounding =
    'Term'     'Generator'    'Confounding'
    'X1'       'a'            'X1'
    'X2'       'b'            'X2'
    'X3'       'c'            'X3'
    'X4'       'd'            'X4'
    'X5'       'bcd'          'X5'
    'X6'       'acd'          'X6'
    'X1*X2'    'ab'           'X1*X2 + X5*X6'
    'X1*X3'    'ac'           'X1*X3 + X4*X6'
    'X1*X4'    'ad'           'X1*X4 + X3*X6'
    'X1*X5'    'abcd'         'X1*X5 + X2*X6'
    'X1*X6'    'cd'           'X1*X6 + X2*X5 + X3*X4'
    'X2*X3'    'bc'           'X2*X3 + X4*X5'
    'X2*X4'    'bd'           'X2*X4 + X3*X5'
    'X2*X5'    'cd'           'X1*X6 + X2*X5 + X3*X4'
    'X2*X6'    'abcd'         'X1*X5 + X2*X6'
    'X3*X4'    'cd'           'X1*X6 + X2*X5 + X3*X4'
    'X3*X5'    'bd'           'X2*X4 + X3*X5'
    'X3*X6'    'ad'           'X1*X4 + X3*X6'
    'X4*X5'    'bc'           'X2*X3 + X4*X5'
    'X4*X6'    'ac'           'X1*X3 + X4*X6'
    'X5*X6'    'ab'           'X1*X2 + X5*X6'
```

The confounding pattern shows that main effects are effectively separated by the design, but two-way interactions are confounded with various other two-way interactions.

Response Surface Designs

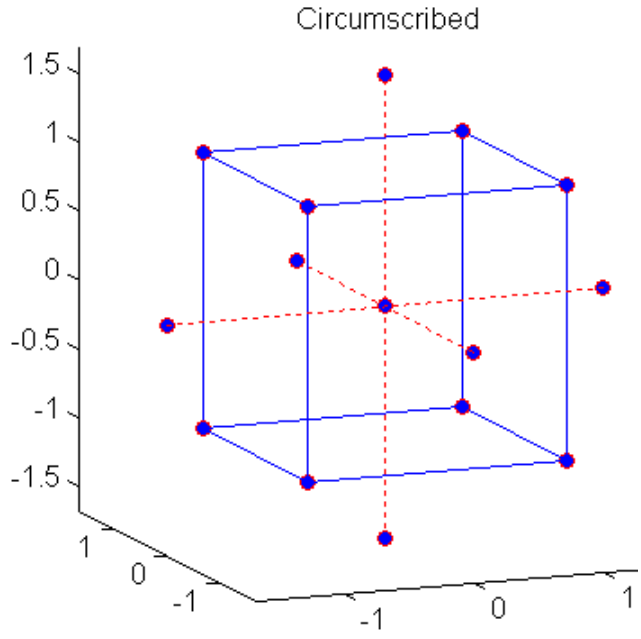
In this section...

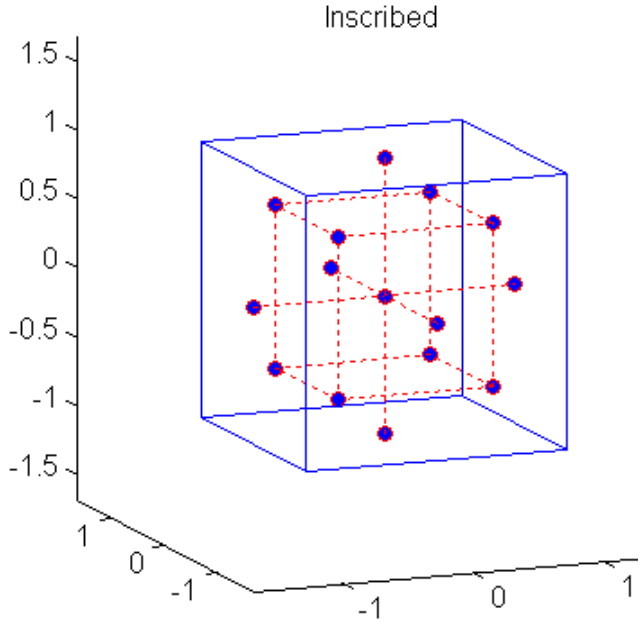
Introduction to Response Surface Designs

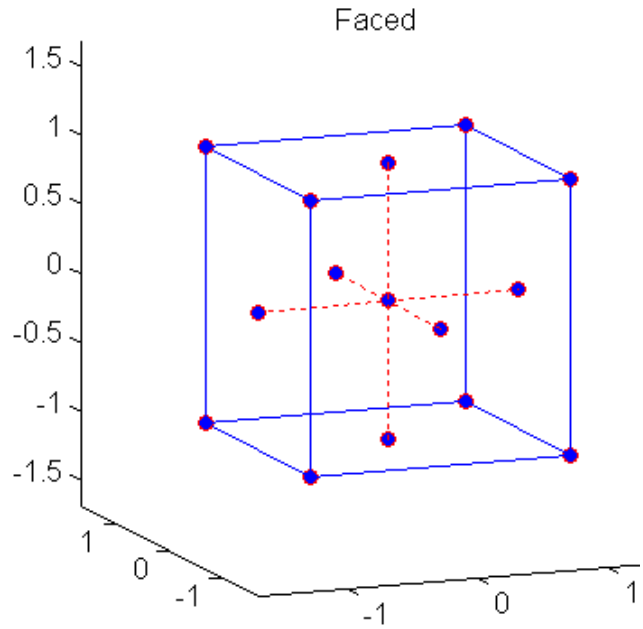
As discussed in "Response Surface Models" on page 9-59, quadratic response surfaces are simple models that provide a maximum or minimum without making additional assumptions about the form of the response. Quadratic models can be calibrated using full factorial designs with three or more levels for each factor, but these designs generally require more runs than necessary to accurately estimate model parameters. This section discusses designs for calibrating quadratic models that are much more efficient, using three or five levels for each factor, but not using all combinations of levels.

Central Composite Designs

Central composite designs (CCDs), also known as Box-Wilson designs, are appropriate for calibrating the full quadratic models described in "Response Surface Models" on page 9-59. There are three types of CCDs—circumscribed, inscribed, and faced—pictured below:


Circumscribed
1.5
1
0.5
0
-0.5
-1
-1.5
1
0
-1
-1
0
1


Inscribed
1.5
1
0.5
0
-0.5
-1
-1.5
1
0
-1
-1
0
1



Each design consists of a factorial design (the corners of a cube) together with *center* and *star* points that allow for estimation of second-order effects. For a full quadratic model with n factors, CCDs have enough design points to estimate the $(n+2)(n+1)/2$ coefficients in a full quadratic model with n factors.

The type of CCD used (the position of the factorial and star points) is determined by the number of factors and by the desired properties of the design. The following table summarizes some important properties. A design is *rotatable* if the prediction variance depends only on the distance of the design point from the center of the design.

Design	Rotatable	Factor Levels	Uses Points Outside ±1	Accuracy of Estimates
Circumscribed (CCC)	Yes	5	Yes	Good over entire design space
Inscribed (CCI)	Yes	5	No	Good over central subset of design space
Faced (CCF)	No	3	No	Fair over entire design space; poor for pure quadratic coefficients

Generate CCDs with the Statistics Toolbox function `ccdesign`:

```
dCC = ccdesign(3,'type','circumscribed')
dCC =
   -1.0000   -1.0000   -1.0000
   -1.0000   -1.0000    1.0000
   -1.0000    1.0000   -1.0000
   -1.0000    1.0000    1.0000
    1.0000   -1.0000   -1.0000
    1.0000   -1.0000    1.0000
    1.0000    1.0000   -1.0000
    1.0000    1.0000    1.0000
   -1.6818         0         0
    1.6818         0         0
         0   -1.6818         0
         0    1.6818         0
         0         0   -1.6818
         0         0    1.6818
         0         0         0
         0         0         0
         0         0         0
         0         0         0
         0         0         0
         0         0         0
         0         0         0
         0         0         0
         0         0         0
```

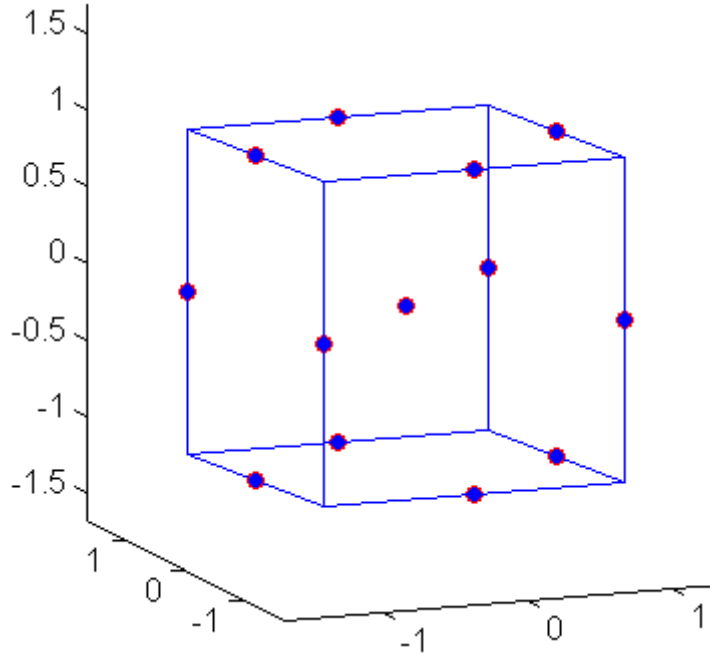
```
     0     0     0
```

The repeated center point runs allow for a more uniform estimate of the prediction variance over the entire design space.

Box-Behnken Designs

Like the designs described in “Central Composite Designs” on page 15-9, Box-Behnken designs are used to calibrate full quadratic models. Box-Behnken designs are rotatable and, for a small number of factors (four or less), require fewer runs than CCDs. By avoiding the corners of the design space, they allow experimenters to work around extreme factor combinations. Like an inscribed CCD, however, extremes are then poorly estimated.

The geometry of a Box-Behnken design is pictured in the following figure.



Design points are at the midpoints of edges of the design space and at the center, and do not contain an embedded factorial design.

Generate Box-Behnken designs with the Statistics Toolbox function `bbdesign`:

```
dBB = bbdesign(3)
dBB =
     -1     -1      0
     -1      1      0
      1     -1      0
      1      1      0
     -1      0     -1
     -1      0      1
      1      0     -1
      1      0      1
      0     -1     -1
      0     -1      1
      0      1     -1
      0      1      1
      0      0      0
      0      0      0
      0      0      0
```

Again, the repeated center point runs allow for a more uniform estimate of the prediction variance over the entire design space.

D-Optimal Designs

In this section...

Introduction to D-Optimal Designs

Traditional experimental designs ("Full Factorial Designs" on page 15-3, "Fractional Factorial Designs" on page 15-5, and "Response Surface Designs" on page 15-9) are appropriate for calibrating linear models in experimental settings where factors are relatively unconstrained in the region of interest. In some cases, however, models are necessarily nonlinear. In other cases, certain treatments (combinations of factor levels) may be expensive or infeasible to measure. *D-optimal designs* are model-specific designs that address these limitations of traditional designs.

A *D*-optimal design is generated by an iterative search algorithm and seeks to minimize the covariance of the parameter estimates for a specified model. This is equivalent to maximizing the determinant $D = |X^TX|$, where X is the design matrix of model terms (the columns) evaluated at specific treatments in the design space (the rows). Unlike traditional designs, *D*-optimal designs do not require orthogonal design matrices, and as a result, parameter estimates may be correlated. Parameter estimates may also be locally, but not globally, *D*-optimal.

There are several Statistics Toolbox functions for generating *D*-optimal designs:

Function	Description
`candexch`	Uses a row-exchange algorithm to generate a *D*-optimal design with a specified number of runs for a specified model and a specified candidate set. This is the second component of the algorithm used by `rowexch`.
`candgen`	Generates a candidate set for a specified model. This is the first component of the algorithm used by `rowexch`.
`cordexch`	Uses a coordinate-exchange algorithm to generate a *D*-optimal design with a specified number of runs for a specified model.
`daugment`	Uses a coordinate-exchange algorithm to augment an existing *D*-optimal design with additional runs to estimate additional model terms.
`dcovary`	Uses a coordinate-exchange algorithm to generate a *D*-optimal design with fixed covariate factors.
`rowexch`	Uses a row-exchange algorithm to generate a *D*-optimal design with a specified number of runs for a specified model. The algorithm calls `candgen` and then `candexch`. (Call `candexch` separately to specify a candidate set.)

The following sections explain how to use these functions to generate *D*-optimal designs.

Note The Statistics Toolbox function `rsmdemo` generates simulated data for experimental settings specified by either the user or by a *D*-optimal design generated by `cordexch`. It uses the `rstool` interface to visualize response surface models fit to the data, and it uses the `nlintool` interface to visualize a nonlinear model fit to the data.

Generating D-Optimal Designs

Two Statistics Toolbox algorithms generate *D*-optimal designs:

- The `cordexch` function uses a coordinate-exchange algorithm
- The `rowexch` function uses a row-exchange algorithm

Both `cordexch` and `rowexch` use iterative search algorithms. They operate by incrementally changing an initial design matrix X to increase $D = |X^TX|$ at each step. In both algorithms, there is randomness built into the selection of the initial design and into the choice of the incremental changes. As a result, both algorithms may return locally, but not globally, D-optimal designs. Run each algorithm multiple times and select the best result for your final design. Both functions have a `'tries'` parameter that automates this repetition and comparison.

At each step, the row-exchange algorithm exchanges an entire row of X with a row from a design matrix C evaluated at a *candidate set* of feasible treatments. The `rowexch` function automatically generates a C appropriate for a specified model, operating in two steps by calling the `candgen` and `candexch` functions in sequence. Provide your own C by calling `candexch` directly. In either case, if C is large, its static presence in memory can affect computation.

The coordinate-exchange algorithm, by contrast, does not use a candidate set. (Or rather, the candidate set is the entire design space.) At each step, the coordinate-exchange algorithm exchanges a single element of X with a new element evaluated at a neighboring point in design space. The absence of a candidate set reduces demands on memory, but the smaller scale of the search means that the coordinate-exchange algorithm is more likely to become trapped in a local minimum than the row-exchange algorithm.

For example, suppose you want a design to estimate the parameters in the following three-factor, seven-term interaction model:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_{12} x_1 x_2 + \beta_{13} x_1 x_3 + \beta_{23} x_2 x_3 + \varepsilon$$

Use `cordexch` to generate a D-optimal design with seven runs:

```
nfactors = 3;
nruns = 7;
[dCE,X] = cordexch(nfactors,nruns,'interaction','tries',10)
dCE =
     -1      1      1
     -1     -1     -1
      1      1      1
     -1      1     -1
      1     -1      1
```

```
     1    -1    -1
    -1    -1     1
X =
     1    -1     1     1    -1    -1     1
     1    -1    -1    -1     1     1     1
     1     1     1     1     1     1     1
     1    -1     1    -1    -1     1    -1
     1     1    -1     1    -1     1    -1
     1     1    -1    -1    -1    -1     1
     1    -1    -1     1     1    -1    -1
```

Columns of the design matrix `X` are the model terms evaluated at each row of the design `dCE`. The terms appear in order from left to right:

1. Constant term
2. Linear terms (1, 2, 3)
3. Interaction terms (12, 13, 23)

Use `X` to fit the model, as described in "Linear Regression" on page 9-3, to response data measured at the design points in `dCE`.

Use `rowexch` in a similar fashion to generate an equivalent design:

```
[dRE,X] = rowexch(nfactors,nruns,'interaction','tries',10)
dRE =
    -1    -1     1
     1    -1     1
     1    -1    -1
     1     1     1
    -1    -1    -1
    -1     1    -1
    -1     1     1
X =
     1    -1    -1     1     1    -1    -1
     1     1    -1     1    -1     1    -1
     1     1    -1    -1    -1    -1     1
     1     1     1     1     1     1     1
     1    -1    -1    -1     1     1     1
     1    -1     1    -1    -1     1    -1
```

```
     1    -1     1     1    -1    -1     1
```

Augmenting D-Optimal Designs

In practice, you may want to add runs to a completed experiment to learn more about a process and estimate additional model coefficients. The `daugment` function uses a coordinate-exchange algorithm to augment an existing *D*-optimal design.

For example, the following eight-run design is adequate for estimating main effects in a four-factor model:

```
dCEmain = cordexch(4,8)
dCEmain =
     1    -1    -1     1
    -1    -1     1     1
    -1     1    -1     1
     1     1     1    -1
     1     1     1     1
    -1     1    -1    -1
     1    -1    -1    -1
    -1    -1     1    -1
```

To estimate the six interaction terms in the model, augment the design with eight additional runs:

```
dCEinteraction = daugment(dCEmain,8,'interaction')
dCEinteraction =
     1    -1    -1     1
    -1    -1     1     1
    -1     1    -1     1
     1     1     1    -1
     1     1     1     1
    -1     1    -1    -1
     1    -1    -1    -1
    -1    -1     1    -1
    -1     1     1     1
    -1    -1    -1    -1
     1    -1     1    -1
     1     1    -1     1
    -1     1     1    -1
```

```
     1     1    -1    -1
     1    -1     1     1
     1     1     1    -1
```

The augmented design is full factorial, with the original eight runs in the first eight rows.

The `'start'` parameter of the `candexch` function provides the same functionality as `daugment`, but uses a row exchange algorithm rather than a coordinate-exchange algorithm.

Specifying Fixed Covariate Factors

In many experimental settings, certain factors and their covariates are constrained to a fixed set of levels or combinations of levels. These cannot be varied when searching for an optimal design. The `dcovary` function allows you to specify fixed covariate factors in the coordinate exchange algorithm.

For example, suppose you want a design to estimate the parameters in a three-factor linear additive model, with eight runs that necessarily occur at different times. If the process experiences temporal linear drift, you may want to include the run time as a variable in the model. Produce the design as follows:

```
time = linspace(-1,1,8)';
[dCV,X] = dcovary(3,time,'linear')
dCV =
   -1.0000    1.0000    1.0000   -1.0000
    1.0000   -1.0000   -1.0000   -0.7143
   -1.0000   -1.0000   -1.0000   -0.4286
    1.0000   -1.0000    1.0000   -0.1429
    1.0000    1.0000   -1.0000    0.1429
   -1.0000    1.0000   -1.0000    0.4286
    1.0000    1.0000    1.0000    0.7143
   -1.0000   -1.0000    1.0000    1.0000
X =
    1.0000   -1.0000    1.0000    1.0000   -1.0000
    1.0000    1.0000   -1.0000   -1.0000   -0.7143
    1.0000   -1.0000   -1.0000   -1.0000   -0.4286
    1.0000    1.0000   -1.0000    1.0000   -0.1429
```

```
    1.0000    1.0000    1.0000   -1.0000    0.1429
    1.0000   -1.0000    1.0000   -1.0000    0.4286
    1.0000    1.0000    1.0000    1.0000    0.7143
    1.0000   -1.0000   -1.0000    1.0000    1.0000
```

The column vector `time` is a fixed factor, normalized to values between ±1. The number of rows in the fixed factor specifies the number of runs in the design. The resulting design `dCV` gives factor settings for the three controlled model factors at each time.

Specifying Categorical Factors

Categorical factors take values in a discrete set of levels. Both `cordexch` and `rowexch` have a `'categorical'` parameter that allows you to specify the indices of categorical factors and a `'levels'` parameter that allows you to specify a number of levels for each factor.

For example, the following eight-run design is for a linear additive model with five factors in which the final factor is categorical with three levels:

```
dCEcat = cordexch(5,8,'linear','categorical',5,'levels',3)
dCEcat =
    -1    -1     1     1     2
    -1    -1    -1    -1     3
     1     1     1     1     3
     1     1    -1    -1     2
     1    -1    -1     1     3
    -1     1    -1     1     1
    -1     1     1    -1     3
     1    -1     1    -1     1
```

Specifying Candidate Sets

The row-exchange algorithm exchanges rows of an initial design matrix X with rows from a design matrix C evaluated at a candidate set of feasible treatments. The `rowexch` function automatically generates a C appropriate for a specified model, operating in two steps by calling the `candgen` and `candexch` functions in sequence. Provide your own C by calling `candexch` directly.

For example, the following uses `rowexch` to generate a five-run design for a two-factor pure quadratic model using a candidate set that is produced internally:

```
dRE1 = rowexch(2,5,'purequadratic','tries',10)
dRE1 =
    -1     1
     0     0
     1    -1
     1     0
     1     1
```

The same thing can be done using `candgen` and `candexch` in sequence:

```
[dC,C] = candgen(2,'purequadratic') % Candidate set, C
dC =
    -1    -1
     0    -1
     1    -1
    -1     0
     0     0
     1     0
    -1     1
     0     1
     1     1
C =
     1    -1    -1     1     1
     1     0    -1     0     1
     1     1    -1     1     1
     1    -1     0     1     0
     1     0     0     0     0
     1     1     0     1     0
     1    -1     1     1     1
     1     0     1     0     1
     1     1     1     1     1
treatments = candexch(C,5,'tries',10) % D-opt subset
treatments =
     2
     1
     7
     3
```

```
     4
dRE2 = dC(treatments,:) % Display design
dRE2 =
     0    -1
    -1    -1
    -1     1
     1    -1
    -1     0
```

You can replace `C` in this example with a design matrix evaluated at your own candidate set. For example, suppose your experiment is constrained so that the two factors cannot have extreme settings simultaneously. The following produces a restricted candidate set:

```
constraint = sum(abs(dC),2) < 2; % Feasible treatments
my_dC = dC(constraint,:)
my_dC =
     0    -1
    -1     0
     0     0
     1     0
     0     1
```

Use the `x2fx` function to convert the candidate set to a design matrix:

```
my_C = x2fx(my_dC,'purequadratic')
my_C =
     1     0    -1     0     1
     1    -1     0     1     0
     1     0     0     0     0
     1     1     0     1     0
     1     0     1     0     1
```

Find the required design in the same manner:

```
my_treatments = candexch(my_C,5,'tries',10) % D-opt subset
my_treatments =
     2
     4
     5
     1
```

```
     3
my_dRE = my_dC(my_treatments,:) % Display design
my_dRE =
    -1     0
     1     0
     0     1
     0    -1
     0     0
```

16

Statistical Process Control

Introduction to Statistical Process Control

Statistical process control (SPC) refers to a number of different methods for monitoring and assessing the quality of manufactured goods. Combined with methods from the Chapter 15, “Design of Experiments”, SPC is used in programs that define, measure, analyze, improve, and control development and production processes. These programs are often implemented using “Design for Six Sigma” methodologies.

Control Charts

A control chart displays measurements of process samples over time. The measurements are plotted together with user-defined *specification limits* and process-defined *control limits*. The process can then be compared with its specifications—to see if it is *in control* or *out of control*.

The chart is just a monitoring tool. Control activity might occur if the chart indicates an undesirable, systematic change in the process. The control chart is used to discover the variation, so that the process can be adjusted to reduce it.

Control charts are created with the `controlchart` function. Any of the following chart types may be specified:

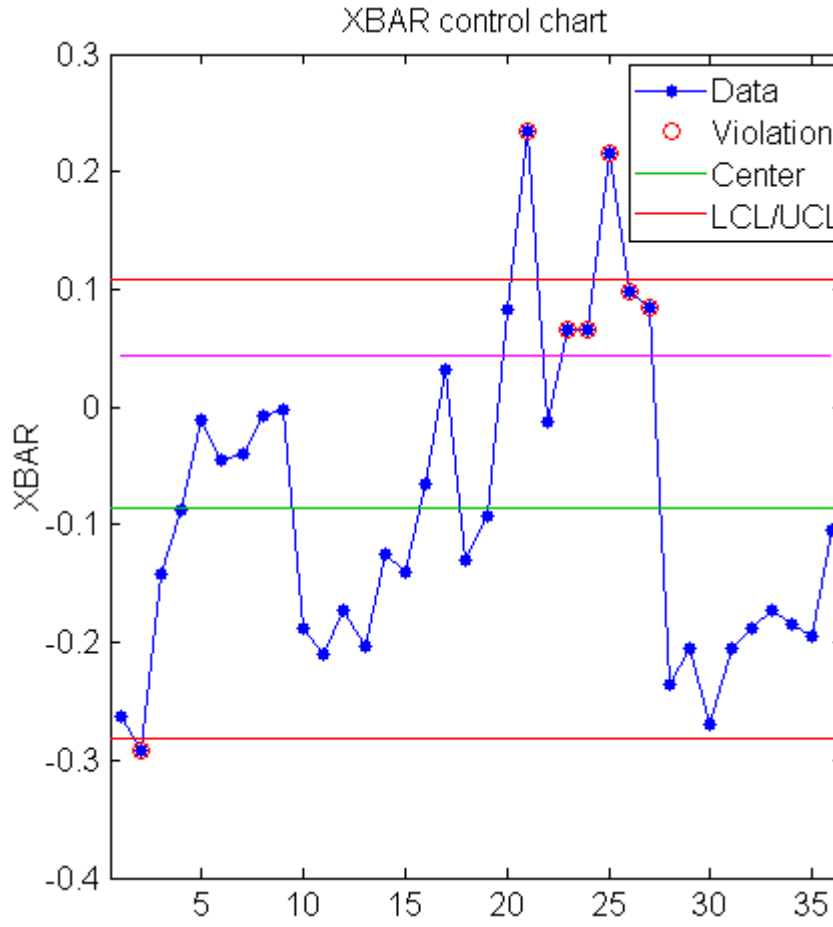
- Xbar or mean
- Standard deviation
- Range
- Exponentially weighted moving average
- Individual observation
- Moving range of individual observations
- Moving average of individual observations
- Proportion defective
- Number of defectives
- Defects per unit
- Count of defects

Control rules are specified with the `controlrules` function.

For example, the following commands create an xbar chart, using the "Western Electric 2" rule (2 of 3 points at least 2 standard errors above the center line) to mark out of control measurements:

```
load parts;
st = controlchart(runout,'rules','we2');
```

```
x = st.mean;
cl = st.mu;
se = st.sigma./sqrt(st.n);
hold on
plot(cl+2*se,'m')
```



Measurements that violate the control rule can then be identified:

```
R = controlrules('we2',x,cl,se);
I = find(R)
```

```
I =
    21
    23
    24
    25
    26
    27
```

Capability Studies

Before going into production, many manufacturers run a *capability study* to determine if their process will run within specifications enough of the time. *Capability indices* produced by such a study are used to estimate expected percentages of defective parts.

Capability studies are conducted with the `capability` function. The following capability indices are produced:

- `mu` — Sample mean
- `sigma` — Sample standard deviation
- `P` — Estimated probability of being within the lower (`L`) and upper (`U`) specification limits
- `Pl` — Estimated probability of being below `L`
- `Pu` — Estimated probability of being above `U`
- `Cp` — `(U-L)/(6*sigma)`
- `Cpl` — `(mu-L)./(3.*sigma)`
- `Cpu` — `(U-mu)./(3.*sigma)`
- `Cpk` — `min(Cpl,Cpu)`

As an example, simulate a sample from a process with a mean of 3 and a standard deviation of 0.005:

```
data = normrnd(3,0.005,100,1);
```

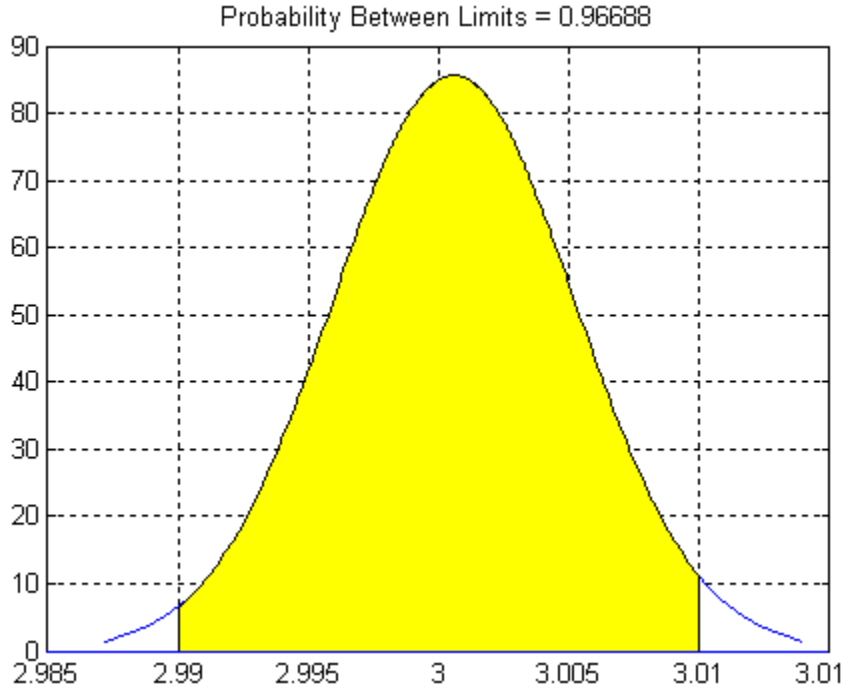
Compute capability indices if the process has an upper specification limit of 3.01 and a lower specification limit of 2.99:

```
S = capability(data,[2.99 3.01])
S =
       mu: 3.0006
    sigma: 0.0047
        P: 0.9669
       Pl: 0.0116
       Pu: 0.0215
```

```
 Cp: 0.7156
Cpl: 0.7567
Cpu: 0.6744
Cpk: 0.6744
```

Visualize the specification and process widths:

```
capaplot(data,[2.99 3.01]);
grid on
```



17

Parallel Statistics

Quick Start Parallel Computing for Statistics Toolbox

Note To use parallel computing as described in this chapter, you must have a Parallel Computing Toolbox license.

In this section...

What Is Parallel Statistics Functionality?

You can use any of the Statistics Toolbox functions with Parallel Computing Toolbox constructs such as `parfor` and `spmd`. However, some functions, such as those with interactive displays, can lose functionality in parallel. In particular, displays and interactive usage are not effective on workers (see "Vocabulary for Parallel Computation" on page 17-7).

Additionally, the following functions are enhanced to use parallel computing internally. These functions use `parfor` internally to parallelize calculations.

- `bootci`
- `bootstrp`
- `candexch`
- `cordexch`
- `crossval`
- `daugment`
- `dcovary`
- `jackknife`
- `nnmf`
- `plsregress`

- `rowexch`
- `sequentialfs`
- `TreeBagger`
- `TreeBagger.growTrees`

This chapter gives the simplest way to use these enhanced functions in parallel. For more advanced topics, including the issues of reproducibility and nested `parfor` loops, see the other sections in this chapter.

For information on parallel statistical computing at the command line, enter

```
help parallelstats
```

How To Compute in Parallel

To have a function compute in parallel:

1. "Open matlabpool" on page 17-3
2. "Set the UseParallel Option to 'always'" on page 17-5
3. "Call the Function Using the Options Structure" on page 17-5

Open matlabpool

To run a statistical computation in parallel, first set up a parallel environment.

Note Setting up a parallel environment can take several seconds.

Multicore. For a multicore machine, enter the following at the MATLAB command line:

```
matlabpool open n
```

n is the number of workers you want to use.

Network. If you have multiple processors on a network, use Parallel Computing Toolbox functions and MATLAB® Distributed Computing Server™ software to establish parallel computation. Make sure that your system is configured properly for parallel computing. Check with your system administrator, or refer to the Parallel Computing Toolbox documentation, or the Administrator Guide documentation for MATLAB Distributed Computing Server.

Many parallel statistical functions call a function that can be one you define in a file. For example, `jackknife` calls a function (`jackfun`) that can be a built-in MATLAB function such as `corr`, but can also be a function you define. Built-in functions are available to all workers. However, you must take extra steps to enable workers to access a function file that you define.

To place a function file on the path of all workers, and check that it is accessible:

1. At the command line, enter

   ```
   matlabpool open conf
   ```

   or

   ```
   matlabpool open conf n
   ```

   where *`conf`* is your configuration, and *`n`* is the number of processors you want to use.

2. If *`network_file_path`* is the network path to your function file, enter

   ```
   pctRunOnAll('addpath network_file_path')
   ```

   so the worker processors can access your function file.

3. Check whether the file is on the path of every worker by entering:

   ```
   pctRunOnAll('which filename')
   ```

   If any worker does not have a path to the file, it reports:

   ```
   filename not found.
   ```

Set the UseParallel Option to 'always'

Create an options structure with the `statset` function. To run in parallel, set the `UseParallel` option to `'always'`:

```
paroptions = statset('UseParallel','always');
```

Call the Function Using the Options Structure

Call your function with syntax that uses the options structure. For example:

```
% Run crossval in parallel
cvMse = crossval('mse',x,y,'predfun',regf,'Options',paroptions);

% Run bootstrp in parallel
sts = bootstrp(100,@(x)[mean(x) std(x)],y,'Options',paroptions);

% Run TreeBagger in parallel
b = TreeBagger(50,meas,spec,'OOBPred','on','Options',paroptions);
```

For more complete examples of parallel statistical functions, see "Example: Parallel Treebagger" on page 17-5 and "Examples of Parallel Statistical Functions" on page 17-19.

After you have finished computing in parallel, close the parallel environment:

```
matlabpool close
```

Tip To save time, keep the pool open if you expect to compute in parallel again soon.

Example: Parallel Treebagger

To run the example "Workflow Example: Regression of Insurance Risk Rating for Car Imports with TreeBagger" on page 13-97 in parallel:

1 Set up the parallel environment to use two cores:

```
matlabpool open 2

Starting matlabpool using the 'local' configuration ...
```

```
connected to 2 labs.
```

2 Set the options to use parallel processing:

```
paroptions = statset('UseParallel','always');
```

3 Load the problem data and separate it into input and response:

```
load imports-85;
Y = X(:,1);
X = X(:,2:end);
```

4 Estimate feature importance using leaf size 1 and 1000 trees in parallel. Time the function for comparison purposes:

```
tic
b = TreeBagger(1000,X,Y,'Method','r','OOBVarImp','on',...
    'cat',16:25,'MinLeaf',1,'Options',paroptions);
toc

Elapsed time is 37.357930 seconds.
```

5 Perform the same computation in serial for timing comparison:

```
tic
b = TreeBagger(1000,X,Y,'Method','r','OOBVarImp','on',...
    'cat',16:25,'MinLeaf',1); % No options gives serial
toc

Elapsed time is 63.921864 seconds.
```

Computing in parallel took less than 60% of the time of computing serially.

Concepts of Parallel Computing in Statistics Toolbox

In this section...

Subtleties in Parallel Computing

There are two main subtleties in parallel computations:

- Nested parallel evaluations (see "No Nested parfor Loops" on page 17-11). Only the outermost `parfor` loop runs in parallel, the others run serially.
- Reproducible results when using random numbers (see "Reproducibility in Parallel Statistical Computations" on page 17-13). How can you get exactly the same results when repeatedly running a parallel computation that uses random numbers?

Vocabulary for Parallel Computation

- *worker* — An independent MATLAB session that runs code distributed by the *client*.
- *client* — The MATLAB session with which you interact, and that distributes jobs to workers.
- `parfor` — A Parallel Computing Toolbox function that distributes independent code segments to workers (see "Working with parfor" on page 17-10).
- *random stream* — A pseudorandom number generator, and the sequence of values it generates. MATLAB implements random streams with the `RandStream` class.
- *reproducible computation* — A computation that can be exactly replicated, even in the presence of random numbers (see "Reproducibility in Parallel Statistical Computations" on page 17-13).

When to Run Statistical Functions in Parallel

In this section...

Why Run in Parallel?

The main reason to run statistical computations in parallel is to gain speed, meaning to reduce the execution time of your program or functions. "Factors Affecting Speed" on page 17-8 discusses the main items affecting the speed of programs or functions. "Factors Affecting Results" on page 17-9 discusses details that can cause a parallel run to give different results than a serial run.

Factors Affecting Speed

Some factors that can affect the speed of execution of parallel processing are:

- Parallel environment setup. It takes time to run `matlabpool` to begin computing in parallel. If your computation is fast, the setup time can exceed any time saved by computing in parallel.
- Parallel overhead. There is overhead in communication and coordination when running in parallel. If function evaluations are fast, this overhead could be an appreciable part of the total computation time. Thus, solving a problem in parallel can be slower than solving the problem serially. For an example, see Improving Optimization Performance with Parallel Computing in MATLAB Digest, March 2009.
- No nested `parfor` loops. This is described in "Working with parfor" on page 17-10. `parfor` does not work in parallel when called from within another `parfor` loop. If you have programmed your custom functions to take advantage of parallel processing, the limitation of no nested `parfor` loops can cause a parallel function to run slower than expected.
- When executing serially, `parfor` loops run slightly slower than `for` loops.
- Passing parameters. Parameters are automatically passed to worker sessions during the execution of parallel computations. If there are many

parameters, or they take a large amount of memory, passing parameters can slow the execution of your computation.

- Contention for resources: network and computing. If the pool of workers has low bandwidth or high latency, parallel computation can be slow.

Factors Affecting Results

Some factors can affect results when using parallel processing. There are several caveats related to `parfor` listed in "Limitations" in the Parallel Computing Toolbox documentation. Some important factors are:

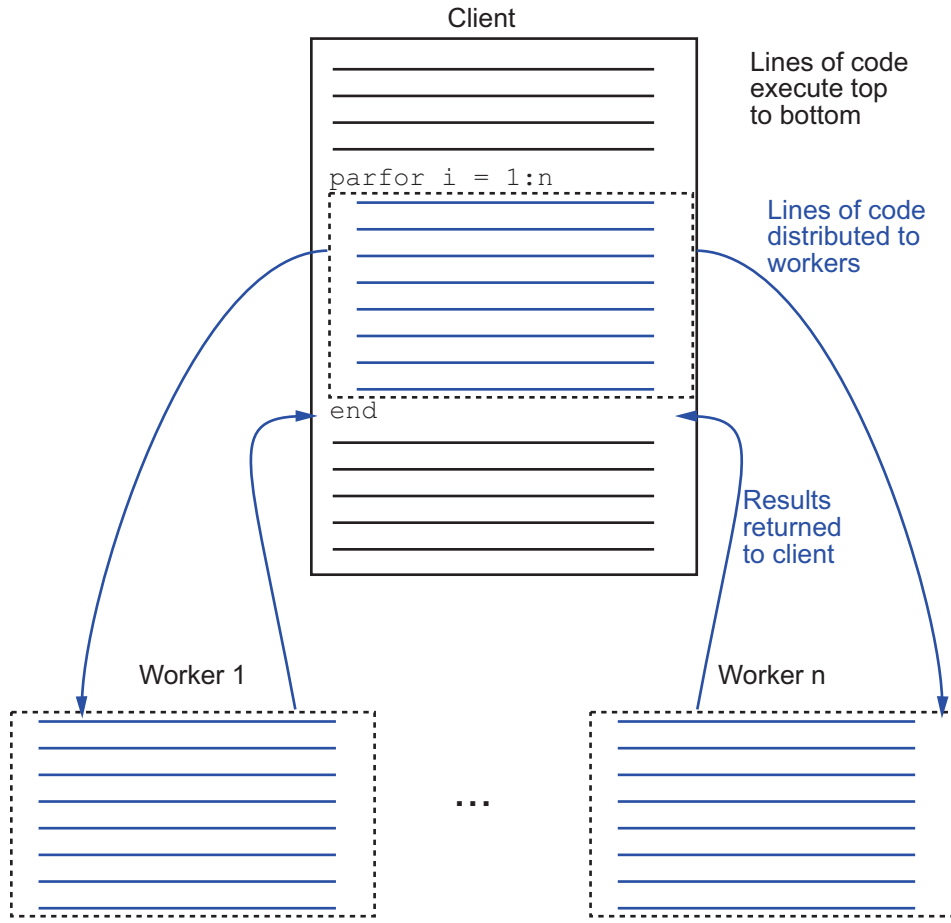
- Persistent or global variables. If any functions use persistent or global variables, these variables can take different values on different worker processors. Furthermore, they might not be cleared properly on the worker processors.
- Accessing external files. External files can be accessed unpredictably during a parallel computation. The order of computations is not guaranteed during parallel processing, so external files can be accessed in unpredictable order, leading to unpredictable results. Furthermore, if multiple processors try to read an external file simultaneously, the file can become locked, leading to a read error, and halting function execution.
- Noncomputational functions, such as `input`, `plot`, and `keyboard`, can behave badly when used in your custom functions. When called in a `parfor` loop, these functions are executed on worker machines. This can cause a worker to become nonresponsive, since it is waiting for input.
- `parfor` does not allow `break` or `return` statements.
- The random numbers you use can affect the results of your computations. See "Reproducibility in Parallel Statistical Computations" on page 17-13.

Working with parfor

In this section...

How Statistical Functions Use parfor

`parfor` is a Parallel Computing Toolbox function similar to a `for` loop. Parallel statistical functions call `parfor` internally. `parfor` distributes computations to worker processors.



Characteristics of parfor

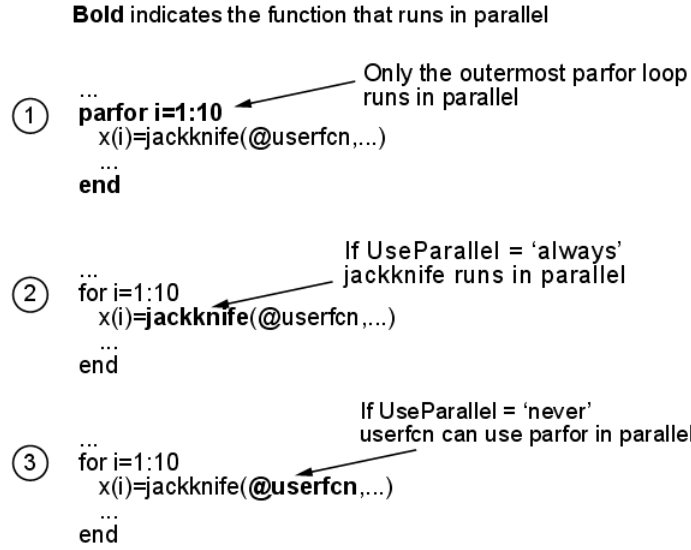
More caveats related to `parfor` appear in "Limitations" in the Parallel Computing Toolbox documentation.

No Nested parfor Loops

`parfor` does not work in parallel when called from within another `parfor` loop, or from an `spmd` block. Parallelization occurs only at the outermost level.

Suppose, for example, you want to apply `jackknife` to your function `userfcn`, which calls `parfor`, and you want to call `jackknife` in a loop. The following figure shows three cases:

1. The outermost loop is `parfor`. Only that loop runs in parallel.
2. The outermost `parfor` loop is in `jackknife`. Only `jackknife` runs in parallel.
3. The outermost `parfor` loop is in `userfcn`. `userfcn` uses `parfor` in parallel.



When parfor Runs in Parallel

Reproducibility in Parallel Statistical Computations

In this section...

Issues and Considerations in Reproducing Parallel Computations

A *reproducible* computation is one that gives the same results every time it runs. Reproducibility is important for:

- Debugging — To correct an anomalous result, you need to reproduce the result.
- Confidence — When you can reproduce results, you can investigate and understand them.
- Modifying existing code — When you change existing code, you want to ensure that you do not break anything.

Generally, you do not need to ensure reproducibility for your computation. Often, when you want reproducibility, the simplest technique is to run in serial instead of in parallel. In serial computation you can simply call the `rng` function as follows:

```
s = rng % Obtain the current state of the random stream
% run the statistical function
rng(s) % Reset the stream to the previous state
% run the statistical function again, obtain identical results
```

This section addresses the case when your function uses random numbers, and you want reproducible results in parallel. This section also addresses the case when you want the same results in parallel as in serial.

Running Reproducible Parallel Computations

To run a Statistics Toolbox function reproducibly:

1. Set the `UseSubstreams` option to `'always'`.
2. Set the `Streams` option to a type that supports substreams: `'mlfg6331_64'` or `'mrg32k3a'`. For information on these streams, see "Choosing a Random Number Generator" in the MATLAB Mathematics documentation.
3. To compute in parallel, set the `UseParallel` option to `'always'`.
4. Call the function with the options structure.
5. To reproduce the computation, reset the stream, then call the function again.

To understand why this technique gives reproducibility, see "How Substreams Enable Reproducible Parallel Computations" on page 17-15.

For example, to use the `'mlfg6331_64'` stream for reproducible computation:

1. Create an appropriate options structure:

```
s = RandStream('mlfg6331_64');
options = statset('UseParallel','always', ...
    'Streams',s,'UseSubstreams','always');
```

2. Run your parallel computation. For instructions, see "Quick Start Parallel Computing for Statistics Toolbox" on page 17-2.
3. Reset the random stream:

```
reset(s);
```

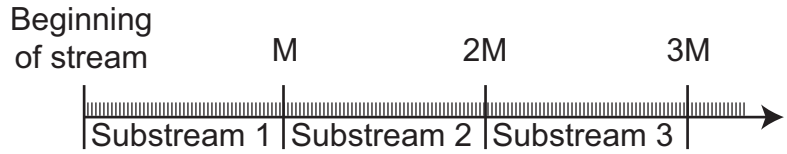
4. Rerun your parallel computation. You obtain identical results.

For an example of a parallel computation run this reproducible way, see "Reproducible Parallel Bootstrap" on page 17-23.

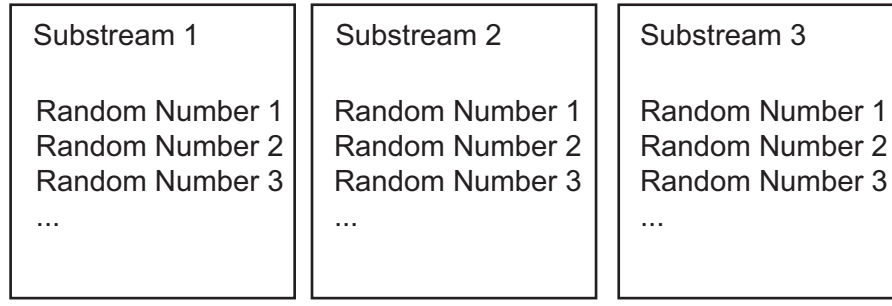
Subtleties in Parallel Statistical Computation Using Random Numbers

What Are Substreams?

A *substream* is a portion of a random stream that `RandStream` can access quickly. There is a number `M` such that for any positive integer `k`, `RandStream` can go the `k`Mth pseudorandom number in the stream. From that point, `RandStream` can generate the subsequent entries in the stream. Currently, `RandStream` has $M = 2^{72}$, about 5e21, or more.



The entries in different substreams have good statistical properties, similar to the properties of entries in a single stream: independence, and lack of k-way correlation at various lags. The substreams are so long that you can view the substreams as being independent streams, as in the following picture.



Two `RandStream` stream types support substreams: `'mlfg6331_64'` and `'mrg32k3a'`.

How Substreams Enable Reproducible Parallel Computations

When MATLAB performs computations in parallel with `parfor`, each worker receives loop iterations in an unpredictable order. Therefore, you cannot

predict which worker gets which iteration, so cannot determine the random numbers associated with each iteration.

Substreams allow MATLAB to tie each iteration to a particular sequence of random numbers. `parfor` gives each iteration an index. The iteration uses the index as the substream number. Since the random numbers are associated with the iterations, not with the workers, the entire computation is reproducible.

To obtain reproducible results, simply reset the stream, and all the substreams generate identical random numbers when called again. This method succeeds when all the workers use the same stream, and the stream supports substreams. This concludes the discussion of how the procedure in "Running Reproducible Parallel Computations" on page 17-14 gives reproducible parallel results.

Random Numbers on the Client or Workers

A few functions generate random numbers on the client before distributing them to parallel workers. The workers do not use random numbers, so operate purely deterministically. For these functions, you can run a parallel computation reproducibly using any random stream type.

The functions that operate this way include:

- `crossval`
- `plsregress`
- `sequentialfs`

To obtain identical results, reset the random stream on the client, or the random stream you pass to the client. For example:

```
s = rng % Obtain the current state of the random stream
% run the statistical function
rng(s) % Reset the stream to the previous state
% run the statistical function again, obtain identical results
```

While this method enables you to run reproducibly in parallel, the results can differ from a serial computation. The reason for the difference is `parfor` loops run in reverse order from `for` loops. Therefore, a serial computation can

generate random numbers in a different order than a parallel computation. For unequivocal reproducibility, use the technique in "Running Reproducible Parallel Computations" on page 17-14.

Distributing Streams Explicitly

For testing or comparison using particular random number algorithms, you must set the random number generators. How do you set these generators in parallel, or initialize streams on each worker in a particular way? Or you might want to run a computation using a different sequence of random numbers than any other you have run. How can you ensure the sequence you use is statistically independent?

Parallel Statistics Toolbox functions allow you to set random streams on each worker explicitly. For information on *creating* multiple streams, enter `help RandStream/create` at the command line. To create four independent streams using the `'mrg32k3a'` generator:

```
s = RandStream.create('mrg32k3a','NumStreams',4,...
    'CellOutput',true);
```

Pass these streams to a statistical function using the `Streams` option. For example:

```
matlabpool open 4 % if you have at least 4 cores
s = RandStream.create('mrg32k3a','NumStreams',4,...
    'CellOutput',true); % create 4 independent streams
paroptions = statset('UseParallel','always',...
    'Streams',s); % set the 4 different streams
x = [randn(700,1); 4 + 2*randn(300,1)];
latt = -4:0.01:12;
myfun = @(X) ksdensity(X,latt);
pdfestimate = myfun(x);
B = bootstrp(200,myfun,x,'Options',paroptions);
```

See "Example: Parallel Bootstrap" on page 17-21 for a plot of the results of this computation.

This method of distributing streams gives each worker a different stream for the computation. However, it does not allow for a reproducible computation, because the workers perform the 200 bootstraps in an unpredictable order. If

you want to perform a reproducible computation, use substreams as described in “Running Reproducible Parallel Computations” on page 17-14.

If you set the `UseSubstreams` option to `'always'`, then set the `Streams` option to a single random stream of the type that supports substreams (`'mlfg6331_64'` or `'mrg32k3a'`). This setting gives reproducible computations.

Examples of Parallel Statistical Functions

In this section...

Example: Parallel Jackknife

This example is from the `jackknife` function reference page, but runs in parallel.

```
matlabpool open
opts = statset('UseParallel','always');
sigma = 5;
y = normrnd(0,sigma,100,1);
m = jackknife(@var, y,1,'Options',opts);
n = length(y);
bias = -sigma^2 / n % known bias formula
jbias = (n - 1)*(mean(m)-var(y,1)) % jackknife bias estimate

bias =
   -0.2500

jbias =
   -0.2698
```

This simple example is not a good candidate for parallel computation:

```
% How long to compute in serial?
tic;m = jackknife(@var,y,1);toc
Elapsed time is 0.023852 seconds.

% How long to compute in parallel?
tic;m = jackknife(@var,y,1,'Options',opts);toc
Elapsed time is 1.911936 seconds.
```

`jackknife` does not use random numbers, so gives the same results every time, whether run in parallel or serial.

Example: Parallel Cross Validation

Simple Parallel Cross Validation

This example is the same as the first in the `crossval` function reference page, but runs in parallel.

```
matlabpool open
opts = statset('UseParallel','always');

load('fisheriris');
y = meas(:,1);
X = [ones(size(y,1),1),meas(:,2:4)];
regf=@(XTRAIN,ytrain,XTEST)(XTEST*regress(ytrain,XTRAIN));

cvMse = crossval('mse',X,y,'Predfun',regf,'Options',opts)

cvMse =
    0.0999
```

This simple example is not a good candidate for parallel computation:

```
% How long to compute in serial?
tic;cvMse = crossval('mse',X,y,'Predfun',regf);toc
Elapsed time is 0.046005 seconds.

% How long to compute in parallel?
tic;cvMse = crossval('mse',X,y,'Predfun',regf,...
    'Options',opts);toc
Elapsed time is 1.333021 seconds.
```

Reproducible Parallel Cross Validation

To run `crossval` in parallel in a reproducible fashion, set the options and reset the random stream appropriately (see "Running Reproducible Parallel Computations" on page 17-14).

```
matlabpool open
```

```
s = RandStream('mlfg6331_64');
options = statset('UseParallel','always',...
    'Streams',s,'UseSubstreams','always');

load('fisheriris');
y = meas(:,1);
X = [ones(size(y,1),1),meas(:,2:4)];
regf=@(XTRAIN,ytrain,XTEST)(XTEST*regress(ytrain,XTRAIN));

cvMse = crossval('mse',X,y,'Predfun',regf,'Options',opts)

cvMse =
    0.1020
```

Reset the stream and the result is identical:

```
reset(s)
cvMse = crossval('mse',X,y,'Predfun',regf,'Options',opts)

cvMse =
    0.1020
```

Example: Parallel Bootstrap

Bootstrap in Serial and Parallel

Here is an example timing a bootstrap in parallel versus in serial. The example generates data from a mixture of two Gaussians, constructs a nonparametric estimate of the resulting data, and uses a bootstrap to get a sense of the sampling variability.

1 Generate the data:

```
% Generate a random sample of size 1000,
% from a mixture of two Gaussian distributions
x = [randn(700,1); 4 + 2*randn(300,1)];
```

2 Construct a nonparametric estimate of the density from the data:

```
latt = -4:0.01:12;
myfun = @(X) ksdensity(X,latt);
pdfestimate = myfun(x);
```

3 Bootstrap the estimate to get a sense of its sampling variability. Run the bootstrap in serial for timing comparison.

```
tic;B = bootstrp(200,myfun,x);toc

Elapsed time is 17.455586 seconds.
```

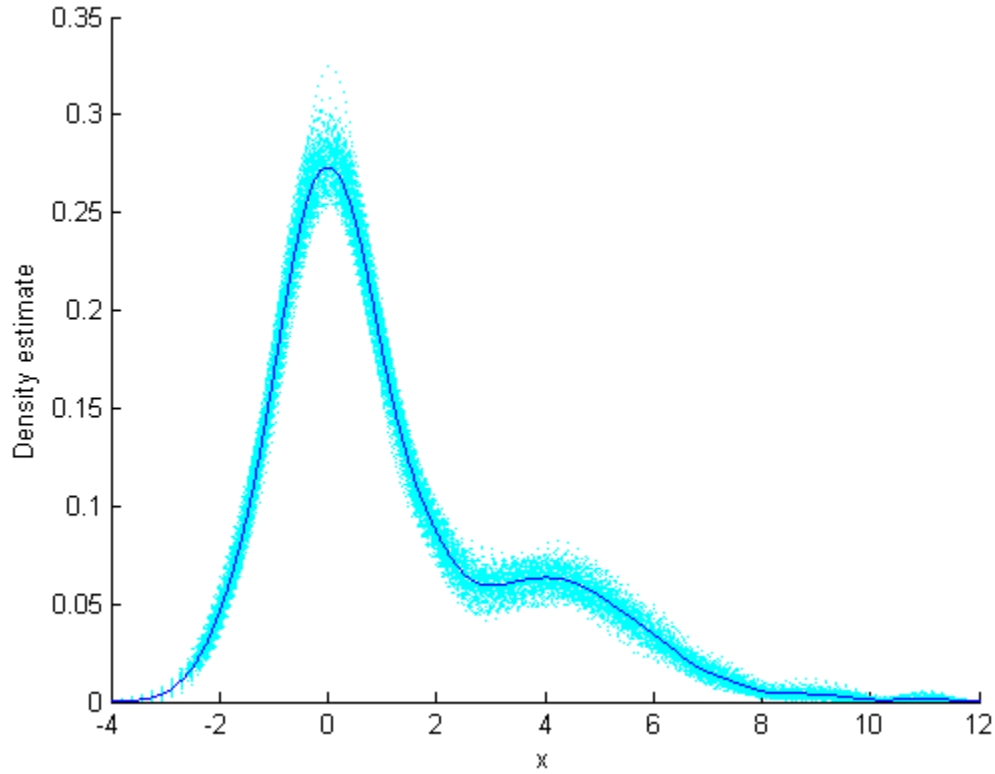
4 Run the bootstrap in parallel for timing comparison:

```
matlabpool open
Starting matlabpool using the 'local' configuration ...
connected to 2 labs.

opt = statset('UseParallel','always');
tic;B = bootstrp(200,myfun,x,'Options',opt);toc

Elapsed time is 9.984345 seconds.
```

Computing in parallel is nearly twice as fast as computing in serial for this example.

Overlay the `ksdensity` density estimate with the 200 bootstrapped estimates obtained in the parallel bootstrap. You can get a sense of how to assess the accuracy of the density estimate from this plot.

```
hold on
for i=1:size(B,1),
    plot(latt,B(i,:),'c:')
end
plot(latt,pdfestimate);
xlabel('x');ylabel('Density estimate')
```



Reproducible Parallel Bootstrap

To run the example in parallel in a reproducible fashion, set the options appropriately (see "Running Reproducible Parallel Computations" on page 17-14). First set up the problem and parallel environment as in "Bootstrap in Serial and Parallel" on page 17-21. Then set the options to use substreams along with a stream that supports substreams.

```
s = RandStream('mlfg6331_64'); % has substreams
opts = statset('UseParallel','always',...
    'Streams',s,'UseSubstreams','always');
B2 = bootstrp(200,myfun,x,'Options',opts);
```

To rerun the bootstrap and get the same result:

```
reset(s) % set the stream to initial state
B3 = bootstrp(200,myfun,x,'Options',opts);
isequal(B2,B3) % check if same results

ans =
     1
```

Function Reference

File I/O

caseread	Read case names from file
casewrite	Write case names to file
tblread	Read tabular data from file
tblwrite	Write tabular data to file
tdfread	Read tab-delimited file
xptread	Create dataset array from data stored in SAS XPORT format file

Data Organization

Categorical Arrays

addlevels (categorical)	Add levels to categorical array
cat (categorical)	Concatenate categorical arrays
categorical	Create categorical array
cellstr (categorical)	Convert categorical array to cell array of strings
char (categorical)	Convert categorical array to character array
circshift (categorical)	Shift categorical array circularly
ctranspose (categorical)	Transpose categorical matrix
double (categorical)	Convert categorical array to double array
droplevels (categorical)	Drop levels
end (categorical)	Last index in indexing expression for categorical array
flipdim (categorical)	Flip categorical array along specified dimension
fliplr (categorical)	Flip categorical matrix in left/right direction
flipud (categorical)	Flip categorical matrix in up/down direction
getlabels (categorical)	Access categorical array labels
getlevels (categorical)	Get categorical array levels

hist (categorical)	Plot histogram of categorical data
horzcat (categorical)	Horizontal concatenation for categorical arrays
int16 (categorical)	Convert categorical array to signed 16-bit integer array
int32 (categorical)	Convert categorical array to signed 32-bit integer array
int64 (categorical)	Convert categorical array to signed 64-bit integer array
int8 (categorical)	Convert categorical array to signed 8-bit integer array
intersect (categorical)	Set intersection for categorical arrays
ipermute (categorical)	Inverse permute dimensions of categorical array
isempty (categorical)	True for empty categorical array
isequal (categorical)	True if categorical arrays are equal
islevel (categorical)	Test for levels
ismember (categorical)	True for elements of categorical array in set
ismember (ordinal)	Test for membership
isscalar (categorical)	True if categorical array is scalar
isundefined (categorical)	Test for undefined elements
isvector (categorical)	True if categorical array is vector
length (categorical)	Length of categorical array
levelcounts (categorical)	Element counts by level
mergelevels (ordinal)	Merge levels
ndims (categorical)	Number of dimensions of categorical array
nominal	Construct nominal categorical array

numel (categorical)	Number of elements in categorical array
ordinal	Construct ordinal categorical array
permute (categorical)	Permute dimensions of categorical array
reorderlevels (categorical)	Reorder levels
repmat (categorical)	Replicate and tile categorical array
reshape (categorical)	Resize categorical array
rot90 (categorical)	Rotate categorical matrix 90 degrees
setdiff (categorical)	Set difference for categorical arrays
setlabels (categorical)	Label levels
setxor (categorical)	Set exclusive-or for categorical arrays
shiftdim (categorical)	Shift dimensions of categorical array
single (categorical)	Convert categorical array to single array
size (categorical)	Size of categorical array
sort (ordinal)	Sort elements of ordinal array
sortrows (ordinal)	Sort rows
squeeze (categorical)	Squeeze singleton dimensions from categorical array
summary (categorical)	Summary statistics for categorical array
times (categorical)	Product of categorical arrays
transpose (categorical)	Transpose categorical matrix
uint16 (categorical)	Convert categorical array to unsigned 16-bit integers
uint32 (categorical)	Convert categorical array to unsigned 32-bit integers

uint64 (categorical)	Convert categorical array to unsigned 64-bit integers
uint8 (categorical)	Convert categorical array to unsigned 8-bit integers
union (categorical)	Set union for categorical arrays
unique (categorical)	Unique values in categorical array
vertcat (categorical)	Vertical concatenation for categorical arrays

Dataset Arrays

cat (dataset)	Concatenate dataset arrays
cellstr (dataset)	Create cell array of strings from dataset array
dataset	Construct dataset array
datasetfun (dataset)	Apply function to dataset array variables
double (dataset)	Convert dataset variables to double array
end (dataset)	Last index in indexing expression for dataset array
export (dataset)	Write dataset array to file
get (dataset)	Access dataset array properties
grpstats (dataset)	Summary statistics by group for dataset arrays
horzcat (dataset)	Horizontal concatenation for dataset arrays
isempty (dataset)	True for empty dataset array
join (dataset)	Merge observations
length (dataset)	Length of dataset array

ndims (dataset)	Number of dimensions of dataset array
numel (dataset)	Number of elements in dataset array
replacedata (dataset)	Replace dataset variables
set (dataset)	Set and display properties
single (dataset)	Convert dataset variables to single array
size (dataset)	Size of dataset array
sortrows (dataset)	Sort rows of dataset array
stack (dataset)	Stack data from multiple variables into single variable
summary (dataset)	Print summary of dataset array
unique (dataset)	Unique observations in dataset array
unstack (dataset)	Unstack data from single variable into multiple variables
vertcat (dataset)	Vertical concatenation for dataset arrays

Grouped Data

gplotmatrix	Matrix of scatter plots by group
grp2idx	Create index vector from grouping variable
grpstats	Summary statistics by group
gscatter	Scatter plot by group

Descriptive Statistics

Summaries

crosstab	Cross-tabulation
grpstats	Summary statistics by group
summary (categorical)	Summary statistics for categorical array
tabulate	Frequency table

Measures of Central Tendency

geomean	Geometric mean
harmmean	Harmonic mean
trimmean	Mean excluding outliers

Measures of Dispersion

iqr	Interquartile range
mad	Mean or median absolute deviation

moment	Central moments
range	Range of values

Measures of Shape

kurtosis	Kurtosis
moment	Central moments
prctile	Calculate percentile values
quantile	Quantiles
skewness	Skewness
zscore	Standardized *z*-scores

Statistics Resampling

bootci	Bootstrap confidence interval
bootstrp	Bootstrap sampling
jackknife	Jackknife sampling

Data with Missing Values

nancov	Covariance ignoring `NaN` values
nanmax	Maximum ignoring `NaN` values
nanmean	Mean ignoring `NaN` values
nanmedian	Median ignoring `NaN` values
nanmin	Minimum ignoring `NaN` values
nanstd	Standard deviation ignoring `NaN` values
nansum	Sum ignoring `NaN` values
nanvar	Variance, ignoring `NaN` values

Data Correlation

canoncorr	Canonical correlation
cholcov	Cholesky-like covariance decomposition
cophenet	Cophenetic correlation coefficient
corr	Linear or rank correlation
corrcov	Convert covariance matrix to correlation matrix
partialcorr	Linear or rank partial correlation coefficients
tiedrank	Rank adjusted for ties

Statistical Visualization

Distribution Plots

boxplot	Box plot
cdfplot	Empirical cumulative distribution function plot
dfittool	Interactive distribution fitting
disttool	Interactive density and distribution plots
ecdfhist	Empirical cumulative distribution function histogram
fsurfht	Interactive contour plot
hist3	Bivariate histogram
histfit	Histogram with normal fit
normplot	Normal probability plot
normspec	Normal density plot between specifications
pareto	Pareto chart
probplot	Probability plots

qqplot	Quantile-quantile plot
randtool	Interactive random number generation
scatterhist	Scatter plot with marginal histograms
surfht	Interactive contour plot
wblplot	Weibull probability plot

Scatter Plots

gline	Interactively add line to plot
gname	Add case names to plot
gplotmatrix	Matrix of scatter plots by group
gscatter	Scatter plot by group
lsline	Add least-squares line to scatter plot
refcurve	Add reference curve to plot
refline	Add reference line to plot
scatterhist	Scatter plot with marginal histograms

ANOVA Plots

anova1	One-way analysis of variance
aoctool	Interactive analysis of covariance
manovacluster	Dendrogram of group mean clusters following MANOVA
multcompare	Multiple comparison test

Regression Plots

addedvarplot	Added-variable plot
gline	Interactively add line to plot
lassoPlot	Trace plot of lasso fit
lsline	Add least-squares line to scatter plot
polytool	Interactive polynomial fitting
rcoplot	Residual case order plot
refcurve	Add reference curve to plot
refline	Add reference line to plot
robustdemo	Interactive robust regression
rsmdemo	Interactive response surface demonstration
rstool	Interactive response surface modeling
view (classregtree)	Plot tree

Multivariate Plots

andrewsplot	Andrews plot
biplot	Biplot
glyphplot	Glyph plot
parallelcoords	Parallel coordinates plot

Cluster Plots

dendrogram	Dendrogram plot
manovacluster	Dendrogram of group mean clusters following MANOVA
silhouette	Silhouette plot

Classification Plots

perfcurve	Compute Receiver Operating Characteristic (ROC) curve or other performance curve for classifier output
view (classregtree)	Plot tree

DOE Plots

interactionplot	Interaction plot for grouped data
maineffectsplot	Main effects plot for grouped data
multivarichart	Multivari chart for grouped data
rsmdemo	Interactive response surface demonstration
rstool	Interactive response surface modeling

SPC Plots

capaplot	Process capability plot
controlchart	Shewhart control charts
histfit	Histogram with normal fit
normspec	Normal density plot between specifications

Probability Distributions

Distribution Objects

cdf (ProbDist)	Return cumulative distribution function (CDF) for ProbDist object
fitdist	Fit probability distribution to data
icdf (ProbDistUnivKernel)	Return inverse cumulative distribution function (ICDF) for ProbDistUnivKernel object
icdf (ProbDistUnivParam)	Return inverse cumulative distribution function (ICDF) for ProbDistUnivParam object
iqr (ProbDistUnivKernel)	Return interquartile range (IQR) for ProbDistUnivKernel object
iqr (ProbDistUnivParam)	Return interquartile range (IQR) for ProbDistUnivParam object

mean (ProbDistUnivParam)	Return mean of ProbDistUnivParam object
median (ProbDistUnivKernel)	Return median of ProbDistUnivKernel object
median (ProbDistUnivParam)	Return median of ProbDistUnivParam object
paramci (ProbDistUnivParam)	Return parameter confidence intervals of ProbDistUnivParam object
pdf (ProbDist)	Return probability density function (PDF) for ProbDist object
ProbDistUnivKernel	Construct ProbDistUnivKernel object
ProbDistUnivParam	Construct ProbDistUnivParam object
random (ProbDist)	Generate random number drawn from ProbDist object
std (ProbDistUnivParam)	Return standard deviation of ProbDistUnivParam object
var (ProbDistUnivParam)	Return variance of ProbDistUnivParam object

Distribution Plots

boxplot	Box plot
cdfplot	Empirical cumulative distribution function plot
dfittool	Interactive distribution fitting
disttool	Interactive density and distribution plots
ecdfhist	Empirical cumulative distribution function histogram

fsurfht	Interactive contour plot
hist3	Bivariate histogram
histfit	Histogram with normal fit
normplot	Normal probability plot
normspec	Normal density plot between specifications
pareto	Pareto chart
probplot	Probability plots
qqplot	Quantile-quantile plot
randtool	Interactive random number generation
scatterhist	Scatter plot with marginal histograms
surfht	Interactive contour plot
wblplot	Weibull probability plot

Probability Density

betapdf	Beta probability density function
binopdf	Binomial probability density function
chi2pdf	Chi-square probability density function
copulapdf	Copula probability density function
disttool	Interactive density and distribution plots
evpdf	Extreme value probability density function
exppdf	Exponential probability density function

fpdf	*F* probability density function
gampdf	Gamma probability density function
geopdf	Geometric probability density function
gevpdf	Generalized extreme value probability density function
gppdf	Generalized Pareto probability density function
hygepdf	Hypergeometric probability density function
ksdensity	Kernel smoothing density estimate
lognpdf	Lognormal probability density function
mnpdf	Multinomial probability density function
mvnpdf	Multivariate normal probability density function
mvtpdf	Multivariate *t* probability density function
nbinpdf	Negative binomial probability density function
ncfpdf	Noncentral *F* probability density function
nctpdf	Noncentral *t* probability density function
ncx2pdf	Noncentral chi-square probability density function
normpdf	Normal probability density function
pdf	Probability density functions
pdf (gmdistribution)	Probability density function for Gaussian mixture distribution

pdf (piecewisedistribution)	Probability density function for piecewise distribution
poisspdf	Poisson probability density function
random (piecewisedistribution)	Random numbers from piecewise distribution
raylpdf	Rayleigh probability density function
tpdf	Student's *t* probability density function
unidpdf	Discrete uniform probability density function
unifpdf	Continuous uniform probability density function
wblpdf	Weibull probability density function

Cumulative Distribution

betacdf	Beta cumulative distribution function
binocdf	Binomial cumulative distribution function
cdf	Cumulative distribution functions
cdf (gmdistribution)	Cumulative distribution function for Gaussian mixture distribution
cdf (piecewisedistribution)	Cumulative distribution function for piecewise distribution
cdfplot	Empirical cumulative distribution function plot
chi2cdf	Chi-square cumulative distribution function
copulacdf	Copula cumulative distribution function

disttool	Interactive density and distribution plots
ecdf	Empirical cumulative distribution function
ecdfhist	Empirical cumulative distribution function histogram
evcdf	Extreme value cumulative distribution function
expcdf	Exponential cumulative distribution function
fcdf	*F* cumulative distribution function
gamcdf	Gamma cumulative distribution function
geocdf	Geometric cumulative distribution function
gevcdf	Generalized extreme value cumulative distribution function
gpcdf	Generalized Pareto cumulative distribution function
hygecdf	Hypergeometric cumulative distribution function
logncdf	Lognormal cumulative distribution function
mvncdf	Multivariate normal cumulative distribution function
mvtcdf	Multivariate *t* cumulative distribution function
ncfcdf	Noncentral *F* cumulative distribution function
nctcdf	Noncentral *t* cumulative distribution function

ncx2cdf	Noncentral chi-square cumulative distribution function
normcdf	Normal cumulative distribution function
poisscdf	Poisson cumulative distribution function
raylcdf	Rayleigh cumulative distribution function
tcdf	Student's *t* cumulative distribution function
unidcdf	Discrete uniform cumulative distribution function
unifcdf	Continuous uniform cumulative distribution function
wblcdf	Weibull cumulative distribution function

Inverse Cumulative Distribution

betainv	Beta inverse cumulative distribution function
binoinv	Binomial inverse cumulative distribution function
chi2inv	Chi-square inverse cumulative distribution function
evinv	Extreme value inverse cumulative distribution function
expinv	Exponential inverse cumulative distribution function
finv	*F* inverse cumulative distribution function

gaminv	Gamma inverse cumulative distribution function
geoinv	Geometric inverse cumulative distribution function
gevinv	Generalized extreme value inverse cumulative distribution function
gpinv	Generalized Pareto inverse cumulative distribution function
hygeinv	Hypergeometric inverse cumulative distribution function
icdf	Inverse cumulative distribution functions
icdf (piecewisedistribution)	Inverse cumulative distribution function for piecewise distribution
logninv	Lognormal inverse cumulative distribution function
nbininv	Negative binomial inverse cumulative distribution function
ncfinv	Noncentral *F* inverse cumulative distribution function
nctinv	Noncentral *t* inverse cumulative distribution function
ncx2inv	Noncentral chi-square inverse cumulative distribution function
norminv	Normal inverse cumulative distribution function
poissinv	Poisson inverse cumulative distribution function
raylinv	Rayleigh inverse cumulative distribution function
tinv	Student's *t* inverse cumulative distribution function

unidinv	Discrete uniform inverse cumulative distribution function
unifinv	Continuous uniform inverse cumulative distribution function
wblinv	Weibull inverse cumulative distribution function

Distribution Statistics

betastat	Beta mean and variance
binostat	Binomial mean and variance
chi2stat	Chi-square mean and variance
copulastat	Copula rank correlation
evstat	Extreme value mean and variance
expstat	Exponential mean and variance
fstat	*F* mean and variance
gamstat	Gamma mean and variance
geostat	Geometric mean and variance
gevstat	Generalized extreme value mean and variance
gpstat	Generalized Pareto mean and variance
hygestat	Hypergeometric mean and variance
lognstat	Lognormal mean and variance
nbinstat	Negative binomial mean and variance
ncfstat	Noncentral *F* mean and variance
nctstat	Noncentral *t* mean and variance
ncx2stat	Noncentral chi-square mean and variance

normstat	Normal mean and variance
poisstat	Poisson mean and variance
raylstat	Rayleigh mean and variance
tstat	Student's *t* mean and variance
unidstat	Discrete uniform mean and variance
unifstat	Continuous uniform mean and variance
wblstat	Weibull mean and variance

Distribution Fitting

Supported Distributions

betafit	Beta parameter estimates
binofit	Binomial parameter estimates
copulafit	Fit copula to data
copulaparam	Copula parameters as function of rank correlation
dfittool	Interactive distribution fitting
evfit	Extreme value parameter estimates
expfit	Exponential parameter estimates
fit (gmdistribution)	Gaussian mixture parameter estimates
gamfit	Gamma parameter estimates
gevfit	Generalized extreme value parameter estimates

gpfit	Generalized Pareto parameter estimates
histfit	Histogram with normal fit
johnsrnd	Johnson system random numbers
lognfit	Lognormal parameter estimates
mle	Maximum likelihood estimates
mlecov	Asymptotic covariance of maximum likelihood estimators
nbinfit	Negative binomial parameter estimates
normfit	Normal parameter estimates
normplot	Normal probability plot
pearsrnd	Pearson system random numbers
poissfit	Poisson parameter estimates
raylfit	Rayleigh parameter estimates
unifit	Continuous uniform parameter estimates
wblfit	Weibull parameter estimates
wblplot	Weibull probability plot

Piecewise Distributions

boundary (piecewisedistribution)	Piecewise distribution boundaries
lowerparams (paretotails)	Lower Pareto tails parameters
nsegments (piecewisedistribution)	Number of segments
paretotails	Construct Pareto tails object
piecewisedistribution	Create piecewise distribution object
segment (piecewisedistribution)	Segments containing values
upperparams (paretotails)	Upper Pareto tails parameters

Negative Log-Likelihood

betalike	Beta negative log-likelihood
evlike	Extreme value negative log-likelihood
explike	Exponential negative log-likelihood
gamlike	Gamma negative log-likelihood
gevlike	Generalized extreme value negative log-likelihood
gplike	Generalized Pareto negative log-likelihood
lognlike	Lognormal negative log-likelihood
mvregresslike	Negative log-likelihood for multivariate regression
normlike	Normal negative log-likelihood
wbllike	Weibull negative log-likelihood

Random Number Generators

betarnd	Beta random numbers
binornd	Binomial random numbers
chi2rnd	Chi-square random numbers
copularnd	Copula random numbers
datasample	Randomly sample from data, with or without replacement
evrnd	Extreme value random numbers
exprnd	Exponential random numbers
frnd	*F* random numbers
gamrnd	Gamma random numbers
geornd	Geometric random numbers

gevrnd	Generalized extreme value random numbers
gprnd	Generalized Pareto random numbers
hygernd	Hypergeometric random numbers
iwishrnd	Inverse Wishart random numbers
johnsrnd	Johnson system random numbers
lhsdesign	Latin hypercube sample
lhsnorm	Latin hypercube sample from normal distribution
lognrnd	Lognormal random numbers
mhsample	Metropolis-Hastings sample
mnrnd	Multinomial random numbers
mvnrnd	Multivariate normal random numbers
mvtrnd	Multivariate *t* random numbers
nbinrnd	Negative binomial random numbers
ncfrnd	Noncentral *F* random numbers
nctrnd	Noncentral *t* random numbers
ncx2rnd	Noncentral chi-square random numbers
normrnd	Normal random numbers
pearsrnd	Pearson system random numbers
poissrnd	Poisson random numbers
randg	Gamma random numbers
random	Random numbers
random (gmdistribution)	Random numbers from Gaussian mixture distribution
random (piecewisedistribution)	Random numbers from piecewise distribution

randsample	Random sample
randtool	Interactive random number generation
raylrnd	Rayleigh random numbers
slicesample	Slice sampler
trnd	Student's *t* random numbers
unidrnd	Discrete uniform random numbers
unifrnd	Continuous uniform random numbers
wblrnd	Weibull random numbers
wishrnd	Wishart random numbers

Quasi-Random Numbers

addlistener (qrandstream)	Add listener for event
delete (qrandstream)	Delete handle object
end (qrandset)	Last index in indexing expression for point set
eq (qrandstream)	Test handle equality
findobj (qrandstream)	Find objects matching specified conditions
findprop (qrandstream)	Find property of MATLAB handle object
ge (qrandstream)	Greater than or equal relation for handles
gt (qrandstream)	Greater than relation for handles
haltonset	Construct Halton quasi-random point set
isvalid (qrandstream)	Test handle validity

le (qrandstream)	Less than or equal relation for handles
length (qrandset)	Length of point set
lt (qrandstream)	Less than relation for handles
ndims (qrandset)	Number of dimensions in matrix
ne (qrandstream)	Not equal relation for handles
net (qrandset)	Generate quasi-random point set
notify (qrandstream)	Notify listeners of event
qrand (qrandstream)	Generate quasi-random points from stream
qrandset	Abstract quasi-random point set class
qrandstream	Construct quasi-random number stream
rand (qrandstream)	Generate quasi-random points from stream
reset (qrandstream)	Reset state
scramble (qrandset)	Scramble quasi-random point set
size (qrandset)	Number of dimensions in matrix
sobolset	Construct Sobol quasi-random point set

Piecewise Distributions

boundary (piecewisedistribution)	Piecewise distribution boundaries
cdf (piecewisedistribution)	Cumulative distribution function for piecewise distribution
icdf (piecewisedistribution)	Inverse cumulative distribution function for piecewise distribution
lowerparams (paretotails)	Lower Pareto tails parameters

nsegments (piecewisedistribution)	Number of segments
paretotails	Construct Pareto tails object
pdf (piecewisedistribution)	Probability density function for piecewise distribution
piecewisedistribution	Create piecewise distribution object
random (piecewisedistribution)	Random numbers from piecewise distribution
segment (piecewisedistribution)	Segments containing values
upperparams (paretotails)	Upper Pareto tails parameters

Hypothesis Tests

ansaribradley	Ansari-Bradley test
barttest	Bartlett's test
canoncorr	Canonical correlation
chi2gof	Chi-square goodness-of-fit test
dwtest	Durbin-Watson test
friedman	Friedman's test
jbtest	Jarque-Bera test
kruskalwallis	Kruskal-Wallis test
kstest	One-sample Kolmogorov-Smirnov test
kstest2	Two-sample Kolmogorov-Smirnov test
lillietest	Lilliefors test
linhyptest	Linear hypothesis test
ranksum	Wilcoxon rank sum test
runstest	Run test for randomness
sampsizepwr	Sample size and power of test
signrank	Wilcoxon signed rank test
signtest	Sign test
ttest	One-sample and paired-sample *t*-test
ttest2	Two-sample *t*-test
vartest	Chi-square variance test
vartest2	Two-sample *F*-test for equal variances
vartestn	Bartlett multiple-sample test for equal variances

zscore	Standardized *z*-scores
ztest	*z*-test

Analysis of Variance

ANOVA Plots

anova1	One-way analysis of variance
aoctool	Interactive analysis of covariance
manovacluster	Dendrogram of group mean clusters following MANOVA
multcompare	Multiple comparison test

ANOVA Operations

anova1	One-way analysis of variance
anova2	Two-way analysis of variance
anovan	*N*-way analysis of variance
aoctool	Interactive analysis of covariance
dummyvar	Create dummy variables
friedman	Friedman's test
kruskalwallis	Kruskal-Wallis test
manova1	One-way multivariate analysis of variance

manovacluster	Dendrogram of group mean clusters following MANOVA
multcompare	Multiple comparison test

Parametric Regression Analysis

Regression Plots

addedvarplot	Added-variable plot
gline	Interactively add line to plot
lassoPlot	Trace plot of lasso fit
lsline	Add least-squares line to scatter plot
polytool	Interactive polynomial fitting
rcoplot	Residual case order plot
refcurve	Add reference curve to plot
refline	Add reference line to plot
robustdemo	Interactive robust regression
rsmdemo	Interactive response surface demonstration
rstool	Interactive response surface modeling
view (classregtree)	Plot tree

Linear Regression

coxphfit	Cox proportional hazards regression
dummyvar	Create dummy variables
glmfit	Generalized linear model regression
glmval	Generalized linear model values
invpred	Inverse prediction
lasso	Regularized least-squares regression using lasso or elastic net algorithms
leverage	Leverage
mnrfit	Multinomial logistic regression
mnrval	Multinomial logistic regression values
mvregress	Multivariate linear regression
mvregresslike	Negative log-likelihood for multivariate regression
plsregress	Partial least-squares regression
polyconf	Polynomial confidence intervals
polytool	Interactive polynomial fitting
regress	Multiple linear regression
regstats	Regression diagnostics
ridge	Ridge regression
robustdemo	Interactive robust regression
robustfit	Robust regression
rsmdemo	Interactive response surface demonstration
rstool	Interactive response surface modeling
stepwise	Interactive stepwise regression

stepwisefit	Stepwise regression
x2fx	Convert predictor matrix to design matrix

Nonlinear Regression

dummyvar	Create dummy variables
hougen	Hougen-Watson model
nlinfit	Nonlinear regression
nlintool	Interactive nonlinear regression
nlmefit	Nonlinear mixed-effects estimation
nlmefitsa	Fit nonlinear mixed effects model with stochastic EM algorithm
nlparci	Nonlinear regression parameter confidence intervals
nlpredci	Nonlinear regression prediction confidence intervals

Multivariate Methods

Multivariate Plots

andrewsplot	Andrews plot
biplot	Biplot
glyphplot	Glyph plot
parallelcoords	Parallel coordinates plot

Multidimensional Scaling

cmdscale	Classical multidimensional scaling
mahal	Mahalanobis distance
mdscale	Nonclassical multidimensional scaling
pdist	Pairwise distance between pairs of objects
squareform	Format distance matrix

Procrustes Analysis

procrustes	Procrustes analysis

Feature Selection

sequentialfs	Sequential feature selection

Feature Transformation

Nonnegative Matrix Factorization (p. 18-37)

Principal Component Analysis (p. 18-37)

Factor Analysis (p. 18-37)

Nonnegative Matrix Factorization

nnmf	Nonnegative matrix factorization

Principal Component Analysis

barttest	Bartlett's test
pareto	Pareto chart
pcacov	Principal component analysis on covariance matrix
pcares	Residuals from principal component analysis
princomp	Principal component analysis (PCA) on data

Factor Analysis

factoran	Factor analysis

Cluster Analysis

Cluster Plots

dendrogram	Dendrogram plot
manovacluster	Dendrogram of group mean clusters following MANOVA
silhouette	Silhouette plot

Hierarchical Clustering

cluster	Construct agglomerative clusters from linkages
clusterdata	Agglomerative clusters from data
cophenet	Cophenetic correlation coefficient
inconsistent	Inconsistency coefficient
linkage	Agglomerative hierarchical cluster tree
pdist	Pairwise distance between pairs of objects
squareform	Format distance matrix

K-Means Clustering

kmeans	*K*-means clustering
mahal	Mahalanobis distance

Gaussian Mixture Models

cdf (gmdistribution)	Cumulative distribution function for Gaussian mixture distribution
cluster (gmdistribution)	Construct clusters from Gaussian mixture distribution
fit (gmdistribution)	Gaussian mixture parameter estimates
gmdistribution	Construct Gaussian mixture distribution
mahal (gmdistribution)	Mahalanobis distance to component means
pdf (gmdistribution)	Probability density function for Gaussian mixture distribution
posterior (gmdistribution)	Posterior probabilities of components
random (gmdistribution)	Random numbers from Gaussian mixture distribution

Model Assessment

confusionmat	Confusion matrix
crossval	Loss estimate using cross-validation
cvpartition	Create cross-validation partition for data
repartition (cvpartition)	Repartition data for cross-validation

test (cvpartition)	Test indices for cross-validation
training (cvpartition)	Training indices for cross-validation

Parametric Classification

Discriminant Analysis

ClassificationDiscriminant	Discriminant analysis classification
ClassificationPartitionedModel	Cross-validated classification model
classify	Discriminant analysis
compact (ClassificationDiscriminant)	Compact discriminant analysis classifier
CompactClassificationDiscriminant	Compact discriminant analysis class
crossval (ClassificationDiscriminant)	Cross-validated discriminant analysis classifier
edge (CompactClassificationDiscriminant)	Classification edge
fit (ClassificationDiscriminant)	Fit discriminant analysis classifier
kfoldEdge (ClassificationPartitionedModel)	Classification edge for observations not used for training
kfoldfun (ClassificationPartitionedModel)	Cross validate function
kfoldLoss (ClassificationPartitionedModel)	Classification loss for observations not used for training

kfoldMargin (ClassificationPartitionedModel)	Classification margins for observations not used for training
kfoldPredict (ClassificationPartitionedModel)	Predict response for observations not used for training
loss (CompactClassificationDiscriminant)	Classification error
mahal (CompactClassificationDiscriminant)	Mahalanobis distance to class means
make (ClassificationDiscriminant)	Construct discriminant analysis classifier from parameters
margin (CompactClassificationDiscriminant)	Classification margins
predict (CompactClassificationDiscriminant)	Predict classification
resubEdge (ClassificationDiscriminant)	Classification edge by resubstitution
resubLoss (ClassificationDiscriminant)	Classification error by resubstitution
resubMargin (ClassificationDiscriminant)	Classification margins by resubstitution
resubPredict (ClassificationDiscriminant)	Predict resubstitution response of classifier

Naive Bayes Classification

fit (NaiveBayes)	Create Naive Bayes classifier object by fitting training data
NaiveBayes	Create NaiveBayes object
posterior (NaiveBayes)	Compute posterior probability of each class for test data
predict (NaiveBayes)	Predict class label for test data

Classification Plots

perfcurve	Compute Receiver Operating Characteristic (ROC) curve or other performance curve for classifier output
view (classregtree)	Plot tree

Nonparametric Supervised Learning

Distance Computation and Nearest Neighbor Search

createns	Create object to use in *k*-nearest neighbors search
knnsearch	Find *k*-nearest neighbors using data
knnsearch (ExhaustiveSearcher)	Find *k*-nearest neighbors using `ExhaustiveSearcher` object
knnsearch (KDTreeSearcher)	Find *k*-nearest neighbors using `KDTreeSearcher` object
pdist	Pairwise distance between pairs of objects
pdist2	Pairwise distance between two sets of observations
rangesearch	Find all neighbors within specified distance
rangesearch (ExhaustiveSearcher)	Find all neighbors within specified distance using object
rangesearch (KDTreeSearcher)	Find all neighbors within specified distance using object
relieff	Importance of attributes (predictors) using ReliefF algorithm

Classification Trees

catsplit (classregtree)	Categorical splits used for branches in decision tree
children (classregtree)	Child nodes
classcount (classregtree)	Class counts
ClassificationPartitionedModel	Cross-validated classification model

ClassificationTree	Binary decision tree for classification
classname (classregtree)	Class names for classification decision tree
classprob (classregtree)	Class probabilities
classregtree	Construct classification and regression trees
classregtree	Classification and regression trees
compact (ClassificationTree)	Compact tree
CompactClassificationTree	Compact classification tree
crossval (ClassificationTree)	Cross-validated decision tree
cutcategories (classregtree)	Cut categories
cutpoint (classregtree)	Decision tree cut point values
cuttype (classregtree)	Cut types
cutvar (classregtree)	Cut variable names
cvloss (ClassificationTree)	Classification error by cross validation
edge (CompactClassificationTree)	Classification edge
eval (classregtree)	Predicted responses
fit (ClassificationTree)	Fit classification tree
isbranch (classregtree)	Test node for branch
kfoldEdge (ClassificationPartitionedModel)	Classification edge for observations not used for training
kfoldfun (ClassificationPartitionedModel)	Cross validate function
kfoldLoss (ClassificationPartitionedModel)	Classification loss for observations not used for training
kfoldMargin (ClassificationPartitionedModel)	Classification margins for observations not used for training
kfoldPredict (ClassificationPartitionedModel)	Predict response for observations not used for training

loss (CompactClassificationTree)	Classification error
margin (CompactClassificationTree)	Classification margins
meansurrvarassoc (classregtree)	Mean predictive measure of association for surrogate splits in decision tree
meanSurrVarAssoc (CompactClassificationTree)	Mean predictive measure of association for surrogate splits in decision tree
nodeclass (classregtree)	Class values of nodes of classification tree
nodeerr (classregtree)	Return vector of node errors
nodeprob (classregtree)	Node probabilities
nodesize (classregtree)	Return node size
numnodes (classregtree)	Number of nodes
parent (classregtree)	Parent node
predict (CompactClassificationTree)	Predict classification
predictorImportance (CompactClassificationTree)	Estimates of predictor importance
prune (ClassificationTree)	Produce sequence of subtrees by pruning
prune (classregtree)	Prune tree
prunelist (classregtree)	Pruning levels for decision tree nodes
resubEdge (ClassificationTree)	Classification edge by resubstitution
resubLoss (ClassificationTree)	Classification error by resubstitution
resubMargin (ClassificationTree)	Classification margins by resubstitution
resubPredict (ClassificationTree)	Predict resubstitution response of tree
risk (classregtree)	Node risks

surrcutcategories (classregtree)	Categories used for surrogate splits in decision tree
surrcutflip (classregtree)	Numeric cutpoint assignments used for surrogate splits in decision tree
surrcutpoint (classregtree)	Cutpoints used for surrogate splits in decision tree
surrcuttype (classregtree)	Types of surrogate splits used at branches in decision tree
surrcutvar (classregtree)	Variables used for surrogate splits in decision tree
surrvarassoc (classregtree)	Predictive measure of association for surrogate splits in decision tree
template (ClassificationTree)	Create classification template
test (classregtree)	Error rate
type (classregtree)	Tree type
varimportance (classregtree)	Compute embedded estimates of input feature importance
view (classregtree)	Plot tree
view (CompactClassificationTree)	View tree

Regression Trees

catsplit (classregtree)	Categorical splits used for branches in decision tree
children (classregtree)	Child nodes
classregtree	Construct classification and regression trees
classregtree	Classification and regression trees
compact (RegressionTree)	Compact regression tree
CompactRegressionTree	Compact regression tree

crossval (RegressionTree)	Cross-validated decision tree
cutcategories (classregtree)	Cut categories
cutpoint (classregtree)	Decision tree cut point values
cuttype (classregtree)	Cut types
cutvar (classregtree)	Cut variable names
cvloss (RegressionTree)	Regression error by cross validation
eval (classregtree)	Predicted responses
fit (RegressionTree)	Binary decision tree for regression
isbranch (classregtree)	Test node for branch
kfoldfun (RegressionPartitionedModel)	Cross validate function
kfoldLoss (RegressionPartitionedModel)	Cross-validation loss of partitioned regression model
kfoldPredict (RegressionPartitionedModel)	Predict response for observations not used for training.
loss (CompactRegressionTree)	Regression error
meansurrvarassoc (classregtree)	Mean predictive measure of association for surrogate splits in decision tree
meanSurrVarAssoc (CompactRegressionTree)	Mean predictive measure of association for surrogate splits in decision tree
nodeerr (classregtree)	Return vector of node errors
nodemean (classregtree)	Mean values of nodes of regression tree
nodeprob (classregtree)	Node probabilities
nodesize (classregtree)	Return node size
numnodes (classregtree)	Number of nodes
parent (classregtree)	Parent node
predict (CompactRegressionTree)	Predict response of regression tree

predictorImportance (CompactRegressionTree)	Estimates of predictor importance
prune (classregtree)	Prune tree
prune (RegressionTree)	Produce sequence of subtrees by pruning
prunelist (classregtree)	Pruning levels for decision tree nodes
RegressionPartitionedModel	Cross-validated regression model
RegressionTree	Regression tree
resubLoss (RegressionTree)	Regression error by resubstitution
resubPredict (RegressionTree)	Predict resubstitution response of tree
risk (classregtree)	Node risks
surrcutcategories (classregtree)	Categories used for surrogate splits in decision tree
surrcutflip (classregtree)	Numeric cutpoint assignments used for surrogate splits in decision tree
surrcutpoint (classregtree)	Cutpoints used for surrogate splits in decision tree
surrcuttype (classregtree)	Types of surrogate splits used at branches in decision tree
surrcutvar (classregtree)	Variables used for surrogate splits in decision tree
surrvarassoc (classregtree)	Predictive measure of association for surrogate splits in decision tree
template (RegressionTree)	Create regression template
test (classregtree)	Error rate
type (classregtree)	Tree type
varimportance (classregtree)	Compute embedded estimates of input feature importance

view (classregtree)	Plot tree
view (CompactRegressionTree)	View tree

Ensemble Methods — Classification

append (TreeBagger)	Append new trees to ensemble
ClassificationBaggedEnsemble	Classification ensemble grown by resampling
ClassificationEnsemble	Ensemble classifier
ClassificationPartitionedEnsemble	Cross-validated classification ensemble
combine (CompactTreeBagger)	Combine two ensembles
compact (ClassificationEnsemble)	Compact classification ensemble
compact (TreeBagger)	Compact ensemble of decision trees
CompactClassificationEnsemble	Compact classification ensemble class
CompactTreeBagger	Compact ensemble of decision trees grown by bootstrap aggregation
crossval (ClassificationEnsemble)	Cross validate ensemble
edge (CompactClassificationEnsemble)	Classification edge
error (CompactTreeBagger)	Error (misclassification probability or MSE)
error (TreeBagger)	Error (misclassification probability or MSE)
fillProximities (TreeBagger)	Proximity matrix for training data
fitensemble	Fitted ensemble for classification or regression
growTrees (TreeBagger)	Train additional trees and add to ensemble

kfoldEdge (ClassificationPartitionedEnsemble)	Classification edge for observations not used for training
kfoldfun (ClassificationPartitionedModel)	Cross validate function
kfoldLoss (ClassificationPartitionedEnsemble)	Classification loss for observations not used for training
kfoldMargin (ClassificationPartitionedModel)	Classification margins for observations not used for training
kfoldPredict (ClassificationPartitionedModel)	Predict response for observations not used for training
loss (CompactClassificationEnsemble)	Classification error
margin (CompactClassificationEnsemble)	Classification margins
margin (CompactTreeBagger)	Classification margin
margin (TreeBagger)	Classification margin
mdsProx (CompactTreeBagger)	Multidimensional scaling of proximity matrix
mdsProx (TreeBagger)	Multidimensional scaling of proximity matrix
meanMargin (CompactTreeBagger)	Mean classification margin
meanMargin (TreeBagger)	Mean classification margin
oobEdge (ClassificationBaggedEnsemble)	Out-of-bag classification edge
oobError (TreeBagger)	Out-of-bag error
oobLoss (ClassificationBaggedEnsemble)	Out-of-bag classification error
oobMargin (ClassificationBaggedEnsemble)	Out-of-bag classification margins
oobMargin (TreeBagger)	Out-of-bag margins
oobMeanMargin (TreeBagger)	Out-of-bag mean margins

oobPredict (ClassificationBaggedEnsemble)	Predict out-of-bag response of ensemble
oobPredict (TreeBagger)	Ensemble predictions for out-of-bag observations
outlierMeasure (CompactTreeBagger)	Outlier measure for data
predict (CompactClassificationEnsemble)	Predict classification
predict (CompactTreeBagger)	Predict response
predict (TreeBagger)	Predict response
predictorImportance (CompactClassificationEnsemble)	Estimates of predictor importance
proximity (CompactTreeBagger)	Proximity matrix for data
resubEdge (ClassificationEnsemble)	Classification edge by resubstitution
resubLoss (ClassificationEnsemble)	Classification error by resubstitution
resubMargin (ClassificationEnsemble)	Classification margins by resubstitution
resubPredict (ClassificationEnsemble)	Predict ensemble response by resubstitution
resume (ClassificationEnsemble)	Resume training ensemble
resume (ClassificationPartitionedEnsemble)	Resume training learners on cross-validation folds
SetDefaultYfit (CompactTreeBagger)	Set default value for `predict`
TreeBagger	Bootstrap aggregation for ensemble of decision trees

Ensemble Methods — Regression

append (TreeBagger)	Append new trees to ensemble
combine (CompactTreeBagger)	Combine two ensembles

compact (RegressionEnsemble)	Create compact regression ensemble
compact (TreeBagger)	Compact ensemble of decision trees
CompactRegressionEnsemble	Compact regression ensemble class
CompactTreeBagger	Compact ensemble of decision trees grown by bootstrap aggregation
crossval (RegressionEnsemble)	Cross validate ensemble
cvshrink (RegressionEnsemble)	Cross validate shrinking (pruning) ensemble
error (CompactTreeBagger)	Error (misclassification probability or MSE)
error (TreeBagger)	Error (misclassification probability or MSE)
fillProximities (TreeBagger)	Proximity matrix for training data
fitensemble	Fitted ensemble for classification or regression
growTrees (TreeBagger)	Train additional trees and add to ensemble
kfoldfun (RegressionPartitionedModel)	Cross validate function
kfoldLoss (RegressionPartitionedEnsemble)	Cross-validation loss of partitioned regression ensemble
kfoldPredict (RegressionPartitionedModel)	Predict response for observations not used for training.
loss (CompactRegressionEnsemble)	Regression error
mdsProx (CompactTreeBagger)	Multidimensional scaling of proximity matrix
mdsProx (TreeBagger)	Multidimensional scaling of proximity matrix
meanMargin (CompactTreeBagger)	Mean classification margin
oobError (TreeBagger)	Out-of-bag error

oobLoss (RegressionBaggedEnsemble)	Out-of-bag regression error
oobPredict (RegressionBaggedEnsemble)	Predict out-of-bag response of ensemble
oobPredict (TreeBagger)	Ensemble predictions for out-of-bag observations
outlierMeasure (CompactTreeBagger)	Outlier measure for data
predict (CompactRegressionEnsemble)	Predict response of ensemble
predict (CompactTreeBagger)	Predict response
predict (TreeBagger)	Predict response
predictorImportance (CompactRegressionEnsemble)	Estimates of predictor importance
proximity (CompactTreeBagger)	Proximity matrix for data
RegressionBaggedEnsemble	Regression ensemble grown by resampling
RegressionEnsemble	Ensemble regression
RegressionPartitionedEnsemble	Cross-validated regression ensemble
regularize (RegressionEnsemble)	Find weights to minimize resubstitution error plus penalty term
resubLoss (RegressionEnsemble)	Regression error by resubstitution
resubPredict (RegressionEnsemble)	Predict response of ensemble by resubstitution
resume (RegressionEnsemble)	Resume training ensemble
resume (RegressionPartitionedEnsemble)	Resume training ensemble
SetDefaultYfit (CompactTreeBagger)	Set default value for `predict`

shrink (RegressionEnsemble)	Prune ensemble
TreeBagger	Bootstrap aggregation for ensemble of decision trees

Hidden Markov Models

hmmdecode	Hidden Markov model posterior state probabilities
hmmestimate	Hidden Markov model parameter estimates from emissions and states
hmmgenerate	Hidden Markov model states and emissions
hmmtrain	Hidden Markov model parameter estimates from emissions
hmmviterbi	Hidden Markov model most probable state path

Design of Experiments

DOE Plots

interactionplot	Interaction plot for grouped data
maineffectsplot	Main effects plot for grouped data
multivarichart	Multivari chart for grouped data
rsmdemo	Interactive response surface demonstration
rstool	Interactive response surface modeling

Full Factorial Designs

ff2n	Two-level full factorial design
fullfact	Full factorial design

Fractional Factorial Designs

fracfact	Fractional factorial design
fracfactgen	Fractional factorial design generators

Response Surface Designs

bbdesign	Box-Behnken design
ccdesign	Central composite design

D-Optimal Designs

candexch	*D*-optimal design from candidate set using row exchanges
candgen	Candidate set generation
cordexch	Coordinate exchange
daugment	*D*-optimal augmentation
dcovary	*D*-optimal design with fixed covariates
rowexch	Row exchange
rsmdemo	Interactive response surface demonstration

Latin Hypercube Designs

lhsdesign	Latin hypercube sample
lhsnorm	Latin hypercube sample from normal distribution

Quasi-Random Designs

addlistener (qrandstream)	Add listener for event
delete (qrandstream)	Delete handle object
end (qrandset)	Last index in indexing expression for point set
eq (qrandstream)	Test handle equality
findobj (qrandstream)	Find objects matching specified conditions
findprop (qrandstream)	Find property of MATLAB handle object
ge (qrandstream)	Greater than or equal relation for handles
gt (qrandstream)	Greater than relation for handles
haltonset	Construct Halton quasi-random point set
isvalid (qrandstream)	Test handle validity
le (qrandstream)	Less than or equal relation for handles
length (qrandset)	Length of point set
lt (qrandstream)	Less than relation for handles
ndims (qrandset)	Number of dimensions in matrix
ne (qrandstream)	Not equal relation for handles
net (qrandset)	Generate quasi-random point set
notify (qrandstream)	Notify listeners of event
qrand (qrandstream)	Generate quasi-random points from stream
qrandset	Abstract quasi-random point set class
qrandstream	Construct quasi-random number stream

rand (qrandstream)	Generate quasi-random points from stream
reset (qrandstream)	Reset state
scramble (qrandset)	Scramble quasi-random point set
size (qrandset)	Number of dimensions in matrix
sobolset	Construct Sobol quasi-random point set

Statistical Process Control

SPC Plots

capaplot	Process capability plot
controlchart	Shewhart control charts
histfit	Histogram with normal fit
normspec	Normal density plot between specifications

SPC Functions

capability	Process capability indices
controlrules	Western Electric and Nelson control rules
gagerr	Gage repeatability and reproducibility study

GUIs

aoctool	Interactive analysis of covariance
dfittool	Interactive distribution fitting
disttool	Interactive density and distribution plots
fsurfht	Interactive contour plot
polytool	Interactive polynomial fitting
randtool	Interactive random number generation
regstats	Regression diagnostics
robustdemo	Interactive robust regression
rsmdemo	Interactive response surface demonstration
rstool	Interactive response surface modeling
surfht	Interactive contour plot

Utilities

combnk	Enumeration of combinations
perms	Enumeration of permutations
statget	Access values in statistics options structure
statset	Create statistics options structure
zscore	Standardized *z*-scores

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Class Reference

Data Organization

In this section...

Categorical Arrays

categorical	Arrays for categorical data
nominal	Arrays for nominal categorical data
ordinal	Arrays for ordinal categorical data

Dataset Arrays

dataset	Arrays for statistical data

Probability Distributions

In this section...

Distribution Objects

ProbDist	Object representing probability distribution
ProbDistKernel	Object representing nonparametric probability distribution defined by kernel smoothing
ProbDistParametric	Object representing parametric probability distribution
ProbDistUnivKernel	Object representing univariate kernel probability distribution
ProbDistUnivParam	Object representing univariate parametric probability distribution

Quasi-Random Numbers

haltonset	Halton quasi-random point sets
qrandset	Quasi-random point sets
qrandstream	Quasi-random number streams
sobolset	Sobol quasi-random point sets

Piecewise Distributions

paretotails	Empirical distributions with Pareto tails
piecewisedistribution	Piecewise-defined distributions

Gaussian Mixture Models

gmdistribution	Gaussian mixture models

Model Assessment

cvpartition	Data partitions for cross-validation

Parametric Classification

In this section...

Discriminant Analysis

ClassificationDiscriminant	Discriminant analysis classification
ClassificationPartitionedModel	Cross-validated classification model
CompactClassificationDiscriminant	Compact discriminant analysis class

Naive Bayes Classification

NaiveBayes	Naive Bayes classifier

Distance Classifiers

ExhaustiveSearcher	Nearest neighbors search using exhaustive search
KDTreeSearcher	Nearest neighbors search using *k*d-tree
NeighborSearcher	Nearest neighbor search object

Supervised Learning

In this section...

Classification Trees

ClassificationPartitionedModel	Cross-validated classification model
ClassificationTree	Binary decision tree for classification
classregtree	Classification and regression trees
CompactClassificationTree	Compact classification tree

Classification Ensemble Classes

ClassificationBaggedEnsemble	Classification ensemble grown by resampling
ClassificationEnsemble	Ensemble classifier
ClassificationPartitionedEnsemble	Cross-validated classification ensemble
CompactClassificationEnsemble	Compact classification ensemble class
CompactTreeBagger	Compact ensemble of decision trees grown by bootstrap aggregation
TreeBagger	Bootstrap aggregation for ensemble of decision trees

Regression Trees

classregtree	Classification and regression trees
CompactRegressionTree	Compact regression tree
RegressionPartitionedModel	Cross-validated regression model
RegressionTree	Regression tree

Regression Ensemble Classes

CompactRegressionEnsemble	Compact regression ensemble class
CompactTreeBagger	Compact ensemble of decision trees grown by bootstrap aggregation
RegressionBaggedEnsemble	Regression ensemble grown by resampling
RegressionEnsemble	Ensemble regression
RegressionPartitionedEnsemble	Cross-validated regression ensemble
TreeBagger	Bootstrap aggregation for ensemble of decision trees

Quasi-Random Design of Experiments

haltonset	Halton quasi-random point sets
qrandset	Quasi-random point sets
qrandstream	Quasi-random number streams
sobolset	Sobol quasi-random point sets

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Functions — Alphabetical List

addedvarplot

Purpose

Added-variable plot

Syntax

```
addedvarplot(X,y,num,inmodel)
addedvarplot(X,y,num,inmodel,stats)
```

Description

`addedvarplot(X,y,num,inmodel)` displays an added variable plot using the predictive terms in `X`, the response values in `y`, the added term in column `num` of `X`, and the model with current terms specified by `inmodel`. `X` is an n-by-p matrix of n observations of p predictive terms. `y` is vector of n response values. `num` is a scalar index specifying the column of `X` with the term to be added. `inmodel` is a logical vector of p elements specifying the columns of `X` in the current model. By default, all elements of `inmodel` are `false`.

Note `addedvarplot` automatically includes a constant term in all models. Do not enter a column of 1s directly into `X`.

`addedvarplot(X,y,num,inmodel,stats)` uses the `stats` output from the `stepwisefit` function to improve the efficiency of repeated calls to `addedvarplot`. Otherwise, this syntax is equivalent to the previous syntax.

Added variable plots are used to determine the unique effect of adding a new term to a multilinear model. The plot shows the relationship between the part of the response unexplained by terms already in the model and the part of the new term unexplained by terms already in the model. The "unexplained" parts are measured by the residuals of the respective regressions. A scatter of the residuals from the two regressions forms the added variable plot.

In addition to the scatter of residuals, the plot produced by `addedvarplot` shows 95% confidence intervals on predictions from the fitted line. The fitted line has intercept zero because, under typical linear model assumptions, both of the plotted variables have mean zero. The slope of the fitted line is the coefficient that the new term would have if it were added to the model with terms `inmodel`.

Added variable plots are sometimes known as partial regression leverage plots.

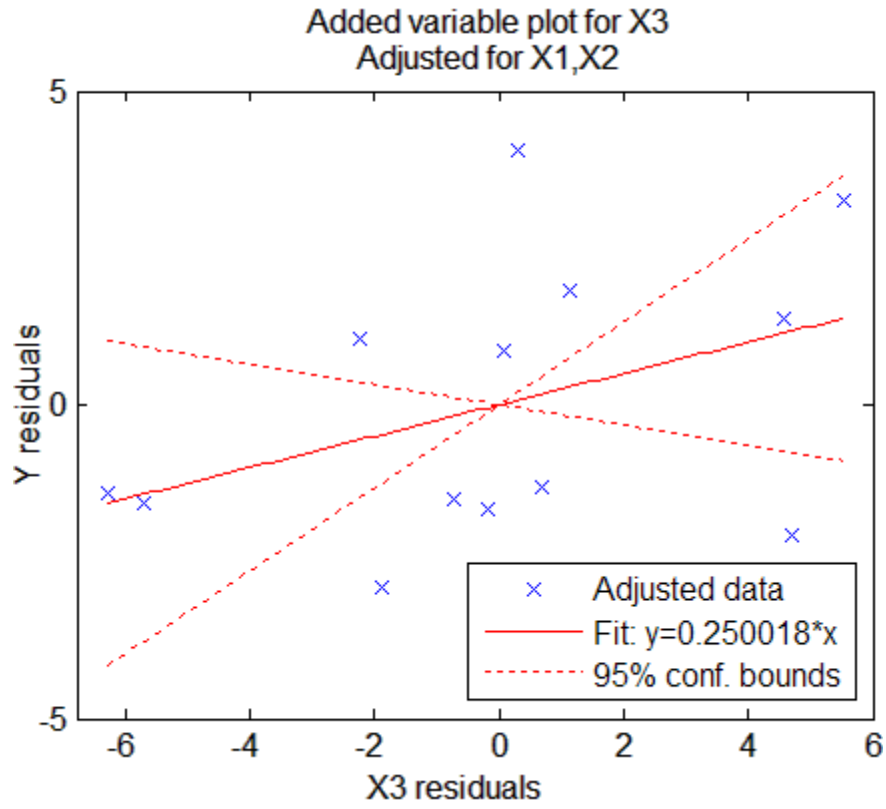
Examples

Load the data in `hald.mat`, which contains observations of the heat of reaction of various cement mixtures:

```
load hald
whos
  Name          Size    Bytes   Class   Attributes

  Description   22x58   2552    char
  hald          13x5     520    double
  heat          13x1     104    double
  ingredients   13x4     416    double
```

Create an added variable plot to investigate the addition of the third column of `ingredients` to a model consisting of the first two columns:

```
inmodel = [true true false false];
addedvarplot(ingredients,heat,3,inmodel)
```



The wide scatter and the low slope of the fitted line are evidence against the statistical significance of adding the third column to the model.

See Also

`stepwisefit` | `stepwise`

Purpose

Add levels to categorical array

Syntax

```
B = addlevels(A,newlevels)
```

Description

`B = addlevels(A,newlevels)` adds new levels to the categorical array `A`. `newlevels` is a cell array of strings or a 2-D character matrix that specifies the levels to add. `addlevels` adds the new levels at the end of the list of possible categorical levels in `A`, but does not modify the value of any element. `B` does not contain elements at the new levels.

Examples

Example 1

Add levels for additional species in Fisher's iris data:

```
load fisheriris
species = nominal(species,...
                  {'Species1','Species2','Species3'},...
                  {'setosa','versicolor','virginica'});
species = addlevels(species,{'Species4','Species5'});
getlabels(species)
ans =
 'Species1' 'Species2' 'Species3' 'Species4' 'Species5'
```

Example 2

1. Load patient data from the CSV file `hospital.dat` and store the information in a dataset array with observation names given by the first column in the data (patient identification):

   ```
   patients = dataset('file','hospital.dat',...
                      'delimiter',',',...
                      'ReadObsNames',true);
   ```

2. Make the {0,1}-valued variable `smoke` nominal, and change the labels to `'No'` and `'Yes'`:

   ```
   patients.smoke = nominal(patients.smoke,{'No','Yes'});
   ```

3 Add new levels to `smoke` as placeholders for more detailed histories of smokers:

```
patients.smoke = addlevels(patients.smoke,...
                 {'0-5 Years','5-10 Years','LongTerm'});
```

4 Assuming the nonsmokers have never smoked, relabel the `'No'` level:

```
patients.smoke = setlabels(patients.smoke,'Never','No');
```

5 Drop the undifferentiated `'Yes'` level from `smoke`:

```
patients.smoke = droplevels(patients.smoke,'Yes');

Warning: OLDLEVELS contains categorical levels that
were present in A, caused some array elements to have
undefined levels.
```

Note that smokers now have an undefined level.

6 Set each smoker to one of the new levels, by observation name:

```
patients.smoke('YPL-320') = '5-10 Years';
```

See Also

`droplevels` | `getlabels` | `islevel` | `mergelevels` | `reorderlevels`

Purpose

Add listener for event

Syntax

```
el = addlistener(hsource,'eventname',callback)
el = addlistener(hsource,property,'eventname',callback)
```

Description

`el = addlistener(hsource,'eventname',callback)` creates a listener for the event named `eventname`, the source of which is handle object `hsource`. If `hsource` is an array of source handles, the listener responds to the named event on any handle in the array. `callback` is a function handle that is invoked when the event is triggered.

`el = addlistener(hsource,property,'eventname',callback)` adds a listener for a property event. `eventname` must be one of the strings `'PreGet'`, `'PostGet'`, `'PreSet'`, and `'PostSet'`. `property` must be either a property name or cell array of property names, or a `meta.property` or array of `meta.property`. The properties must belong to the class of `hsource`. If `hsource` is scalar, `property` can include dynamic properties.

For all forms, `addlistener` returns an `event.listener`. To remove a listener, delete the object returned by `addlistener`. For example, `delete(el)` calls the handle class delete method to remove the listener and delete it from the workspace.

See Also

`delete` | `dynamicprops` | `event.listener` | `events` | `meta.property` | `notify` | `qrandstream` | `reset`

gmdistribution.AIC property

Purpose

Akaike Information Criterion

Description

The Akaike Information Criterion: `2*NlogL+2*m`, where `m` is the number of estimated parameters.

Note This property applies only to gmdistribution objects constructed with `fit`.

Purpose

Andrews plot

Syntax

```
andrewsplot(X)
andrewsplot(X,...,'Standardize',standopt)
andrewsplot(X,...,'Quantile',alpha)
andrewsplot(X,...,'Group',group)
andrewsplot(X,...,'PropName',PropVal,...)
h = andrewsplot(X,...)
```

Description

`andrewsplot(X)` creates an Andrews plot of the multivariate data in the matrix `X`. The rows of `X` correspond to observations, the columns to variables. Andrews plots represent each observation by a function $f(t)$ of a continuous dummy variable t over the interval [0,1]. $f(t)$ is defined for the i th observation in `X` as

$$f(t) = X(i,1)/\sqrt{2} + X(i,2)\sin(2\pi t) + X(i,3)\cos(2\pi t) + \ldots$$

`andrewsplot` treats `NaN` values in `X` as missing values and ignores the corresponding rows.

`andrewsplot(X,...,'Standardize',standopt)` creates an Andrews plot where *`standopt`* is one of the following:

- `'on'` — scales each column of `X` to have mean `0` and standard deviation `1` before making the plot.
- `'PCA'` — creates an Andrews plot from the principal component scores of `X`, in order of decreasing eigenvalue. (See `princomp`.)
- `'PCAStd'` — creates an Andrews plot using the standardized principal component scores. (See `princomp`.)

`andrewsplot(X,...,'Quantile',alpha)` plots only the median and the `alpha` and (1 – `alpha`) quantiles of $f(t)$ at each value of t. This is useful if `X` contains many observations.

`andrewsplot(X,...,'Group',group)` plots the data in different groups with different colors. Groups are defined by `group`, a numeric array containing a group index for each observation. `group` can also be a

categorical array, character matrix, or cell array of strings containing a group name for each observation. (See “Grouped Data” on page 2-34.)

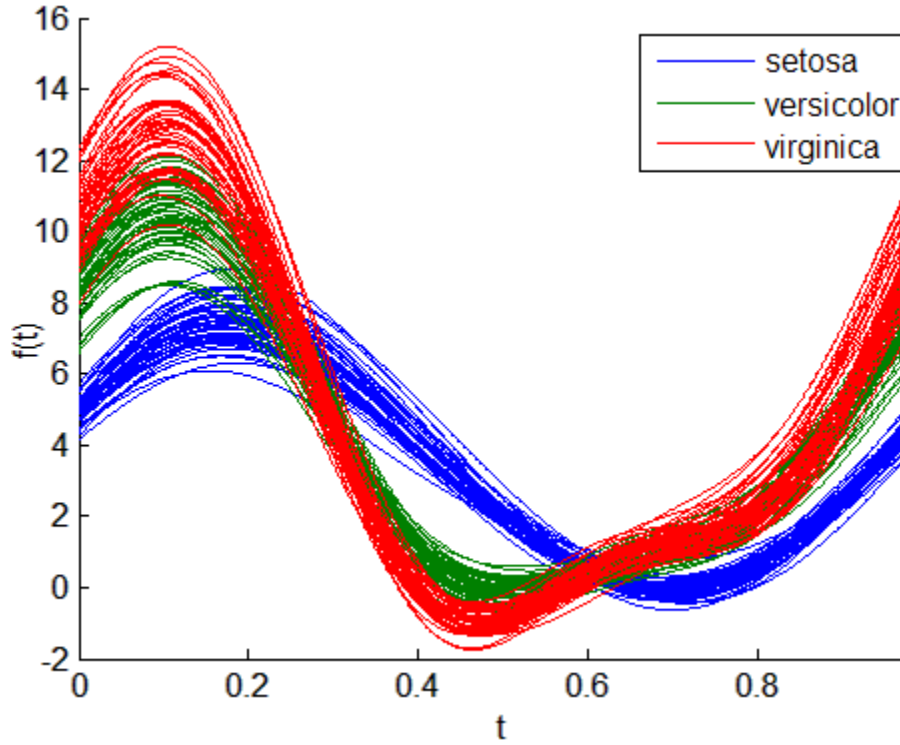
`andrewsplot(X,...,'PropName',PropVal,...)` sets optional lineseries object properties to the specified values for all lineseries objects created by `andrewsplot`. (See Lineseries Properties.)

`h = andrewsplot(X,...)` returns a column vector of handles to the lineseries objects created by `andrewsplot`, one handle per row of `X`. If you use the `'Quantile'` input parameter, `h` contains one handle for each of the three lineseries objects created. If you use both the `'Quantile'` and the `'Group'` input parameters, `h` contains three handles for each group.

Examples

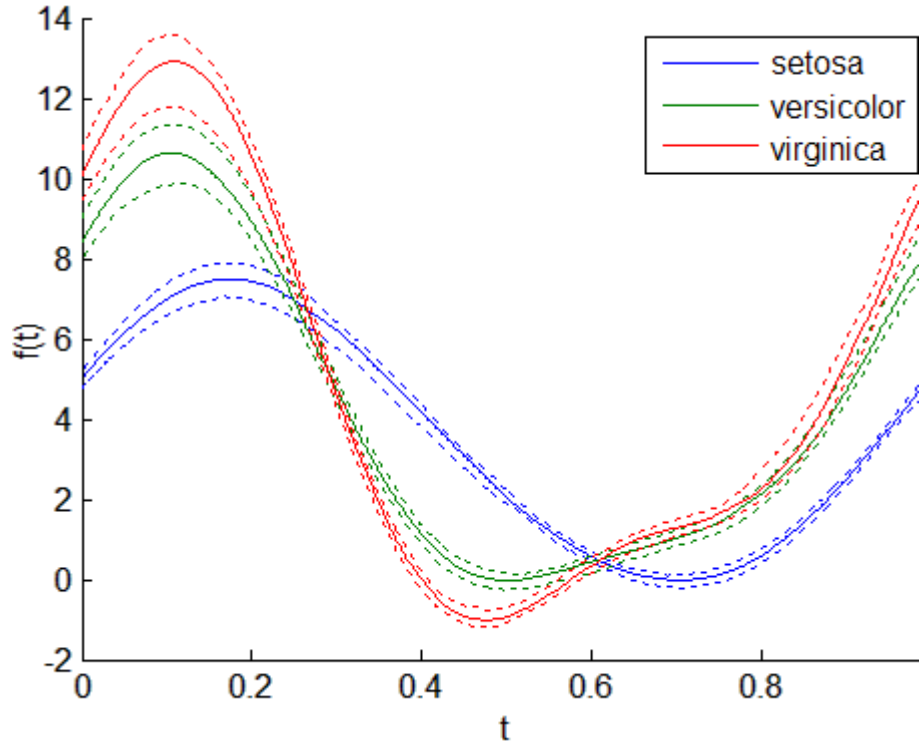
Make a grouped plot of the Fisher iris data:

```
load fisheriris
andrewsplot(meas,'group',species)
```



Plot only the median and quartiles of each group:

```
andrewsplot(meas,'group',species,'quantile',.25)
```



See Also `parallelcoords` | `glyphplot`

How To

- “Grouped Data” on page 2-34

Purpose

One-way analysis of variance

Syntax

```
p = anova1(X)
p = anova1(X,group)
p = anova1(X,group,displayopt)
[p,table] = anova1(...)
[p,table,stats] = anova1(...)
```

Description

`p = anova1(X)` performs balanced one-way ANOVA for comparing the means of two or more columns of data in the matrix `X`, where each column represents an independent sample containing mutually independent observations. The function returns the *p* value under the null hypothesis that all samples in `X` are drawn from populations with the same mean.

If `p` is near zero, it casts doubt on the null hypothesis and suggests that at least one sample mean is significantly different than the other sample means. Common significance levels are 0.05 or 0.01.

The `anova1` function displays two figures, the standard ANOVA table and a box plot of the columns of `X`.

The standard ANOVA table divides the variability of the data into two parts:

- Variability due to the differences among the column means (variability *between* groups)
- Variability due to the differences between the data in each column and the column mean (variability *within* groups)

The standard ANOVA table has six columns:

1 The source of the variability.

2 The sum of squares (`SS`) due to each source.

3 The degrees of freedom (`df`) associated with each source.

4 The mean squares (MS) for each source, which is the ratio SS/df.

5 The *F*-statistic, which is the ratio of the mean squares.

6 The *p* value, which is derived from the cdf of *F*.

The box plot of the columns of X suggests the size of the *F*-statistic and the *p* value. Large differences in the center lines of the boxes correspond to large values of *F* and correspondingly small values of *p*.

anova1 treats NaN values as missing, and disregards them.

p = anova1(X,group) performs ANOVA by group. For more information on grouping variables, see "Grouped Data" on page 2-34.

If X is a matrix, anova1 treats each column as a separate group, and evaluates whether the population means of the columns are equal. This form of anova1 is appropriate when each group has the same number of elements (balanced ANOVA). group can be a character array or a cell array of strings, with one row per column of X, containing group names. Enter an empty array ([]) or omit this argument if you do not want to specify group names.

If X is a vector, group must be a categorical variable, vector, string array, or cell array of strings with one name for each element of X. X values corresponding to the same value of group are placed in the same group. This form of anova1 is appropriate when groups have different numbers of elements (unbalanced ANOVA).

If group contains empty or NaN-valued cells or strings, the corresponding observations in X are disregarded.

p = anova1(X,group,*displayopt*) enables the ANOVA table and box plot displays when *displayopt* is 'on' (default) and suppresses the displays when *displayopt* is 'off'. Notches in the boxplot provide a test of group medians (see boxplot) different from the *F* test for means in the ANOVA table.

[p,table] = anova1(...) returns the ANOVA table (including column and row labels) in the cell array table. Copy a text version of

the ANOVA table to the clipboard using the `Copy Text` item on the **Edit** menu.

`[p,table,stats] = anova1(...)` returns a structure `stats` used to perform a follow-up multiple comparison test. `anova1` evaluates the hypothesis that the samples all have the same mean against the alternative that the means are not all the same. Sometimes it is preferable to perform a test to determine which pairs of means are significantly different, and which are not. Use the `multcompare` function to perform such tests by supplying the `stats` structure as input.

Assumptions

The ANOVA test makes the following assumptions about the data in `X`:

- All sample populations are normally distributed.
- All sample populations have equal variance.
- All observations are mutually independent.

The ANOVA test is known to be robust with respect to modest violations of the first two assumptions.

Examples

Example 1

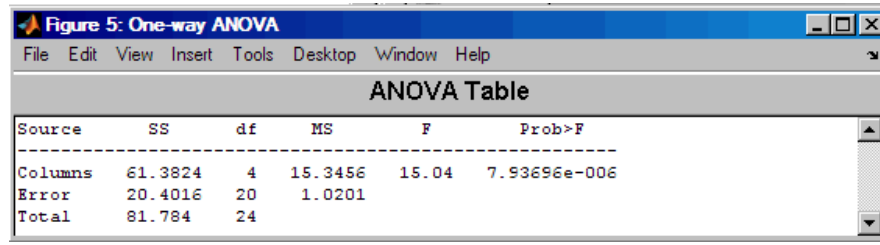
Create `X` with columns that are constants plus random normal disturbances with mean zero and standard deviation one:

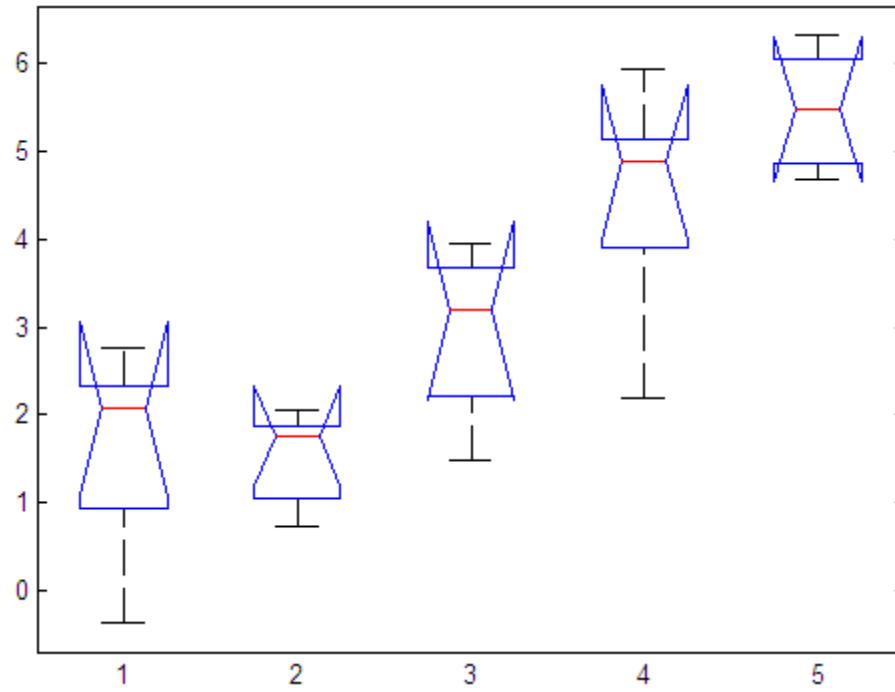
```
X = meshgrid(1:5)
X =
   1   2   3   4   5
   1   2   3   4   5
   1   2   3   4   5
   1   2   3   4   5
   1   2   3   4   5

X = X + normrnd(0,1,5,5)
X =
    1.3550    2.0662    2.4688    5.9447    5.4897
```

```
    2.0693    1.7611    1.4864    4.8826    6.3222
    2.1919    0.7276    3.1905    4.8768    4.6841
    2.7620    1.8179    3.9506    4.4678    4.9291
   -0.3626    1.1685    3.5742    2.1945    5.9465
```

Perform one-way ANOVA:

```
p = anova1(X)
p =
   7.9370e-006
```





The very small *p* value indicates that differences between column means are highly significant. The probability of this outcome under the null hypothesis (that samples drawn from the same population would have means differing by the amounts seen in `X`) is equal to the *p* value.

Example 2

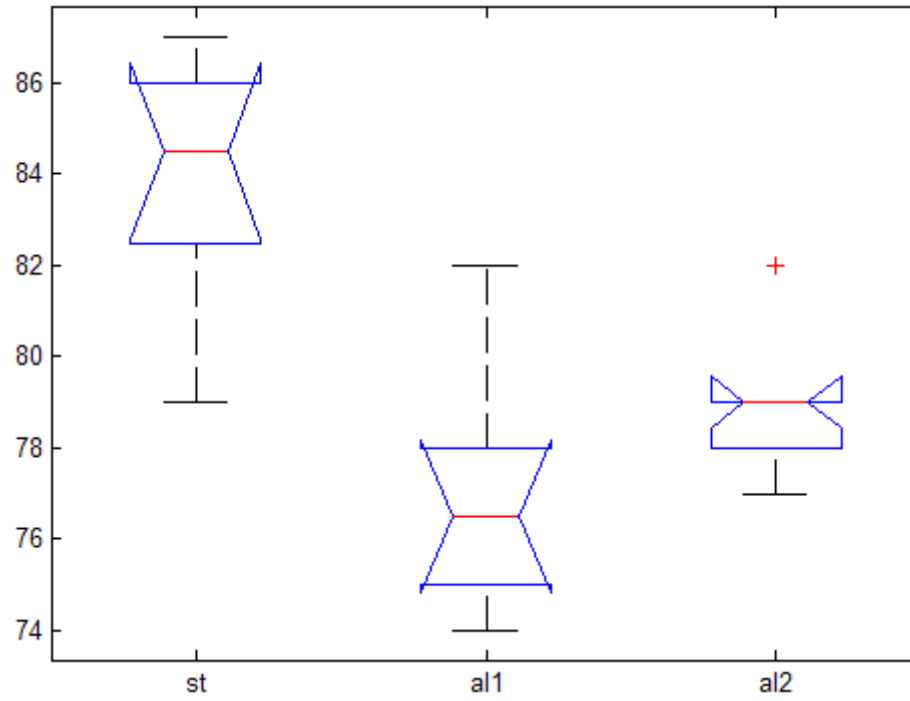
The following example is from a study of the strength of structural beams in Hogg. The vector `strength` measures deflections of beams in thousandths of an inch under 3,000 pounds of force. The vector `alloy` identifies each beam as steel (`'st'`), alloy 1 (`'al1'`), or alloy 2 (`'al2'`). (Although `alloy` is sorted in this example, grouping variables do not need to be sorted.) The null hypothesis is that steel beams are equal in strength to beams made of the two more expensive alloys.

```
strength = [82 86 79 83 84 85 86 87 74 82 ...
```

```
            78 75 76 77 79 79 77 78 82 79];

alloy = {'st','st','st','st','st','st','st','st',...
         'al1','al1','al1','al1','al1','al1',...
         'al2','al2','al2','al2','al2','al2'};

p = anova1(strength,alloy)
p =
  1.5264e-004
```

ANOVA Table

Source	SS	df	MS	F	Prob>F
Columns	184.8	2	92.4	15.4	0.0002
Error	102	17	6		
Total	286.8	19			



The *p* value suggests rejection of the null hypothesis. The box plot shows that steel beams deflect more than beams made of the more expensive alloys.

References

[1] Hogg, R. V., and J. Ledolter. *Engineering Statistics*. New York: MacMillan, 1987.

See Also

`anova2` | `anovan` | `boxplot` | `manova1` | `multcompare`

How To

- "Grouped Data" on page 2-34

anova2

Purpose

Two-way analysis of variance

Syntax

```
p = anova2(X,reps)
p = anova2(X,reps,displayopt)
[p,table] = anova2(...)
[p,table,stats] = anova2(...)
```

Description

`p = anova2(X,reps)` performs a balanced two-way ANOVA for comparing the means of two or more columns and two or more rows of the observations in `X`. The data in different columns represent changes in factor *A*. The data in different rows represent changes in factor *B*. If there is more than one observation for each combination of factors, input `reps` indicates the number of replicates in each position, which must be constant. (For unbalanced designs, use `anovan`.)

The matrix below shows the format for a set-up where column factor A has two levels, row factor B has three levels, and there are two replications (`reps = 2`). The subscripts indicate row, column, and replicate, respectively.

$$\begin{matrix} A=1 & A=2 \end{matrix}$$
$$\left.\begin{bmatrix} x_{111} & x_{121} \\ x_{112} & x_{122} \end{bmatrix}\right\} B=1$$
$$\left.\begin{bmatrix} x_{211} & x_{221} \\ x_{212} & x_{222} \end{bmatrix}\right\} B=2$$
$$\left.\begin{bmatrix} x_{311} & x_{321} \\ x_{312} & x_{322} \end{bmatrix}\right\} B=3$$

When `reps` is `1` (default), `anova2` returns two *p*-values in vector `p`:

1. The *p* value for the null hypothesis, H_{0A}, that all samples from factor A (i.e., all column-samples in `X`) are drawn from the same population
2. The *p* value for the null hypothesis, H_{0B}, that all samples from factor B (i.e., all row-samples in `X`) are drawn from the same population

When `reps` is greater than `1`, `anova2` returns a third *p* value in vector `p`:

3. The *p* value for the null hypothesis, H_{0AB}, that the effects due to factors A and B are *additive* (i.e., that there is no interaction between factors A and B)

If any *p* value is near zero, this casts doubt on the associated null hypothesis. A sufficiently small *p* value for H_{0A} suggests that at least one column-sample mean is significantly different that the other column-sample means; i.e., there is a main effect due to factor A. A sufficiently small *p* value for H_{0B} suggests that at least one row-sample mean is significantly different than the other row-sample means; i.e., there is a main effect due to factor B. A sufficiently small *p* value for H_{0AB} suggests that there is an interaction between factors A and B. The choice of a limit for the *p* value to determine whether a result is "statistically significant" is left to the researcher. It is common to declare a result significant if the *p* value is less than 0.05 or 0.01.

`anova2` also displays a figure showing the standard ANOVA table, which divides the variability of the data in `X` into three or four parts depending on the value of `reps`:

- The variability due to the differences among the column means
- The variability due to the differences among the row means
- The variability due to the interaction between rows and columns (if reps is greater than its default value of one)
- The remaining variability not explained by any systematic source

The ANOVA table has five columns:

- The first shows the source of the variability.
- The second shows the Sum of Squares (SS) due to each source.
- The third shows the degrees of freedom (df) associated with each source.

- The fourth shows the Mean Squares (MS), which is the ratio SS/df.
- The fifth shows the *F* statistics, which is the ratio of the mean squares.

`p = anova2(X,reps,displayopt)` enables the ANOVA table display when *`displayopt`* is `'on'` (default) and suppresses the display when *`displayopt`* is `'off'`.

`[p,table] = anova2(...)` returns the ANOVA table (including column and row labels) in cell array `table`. (Copy a text version of the ANOVA table to the clipboard by using the `Copy Text` item on the **Edit** menu.)

`[p,table,stats] = anova2(...)` returns a `stats` structure that you can use to perform a follow-up multiple comparison test.

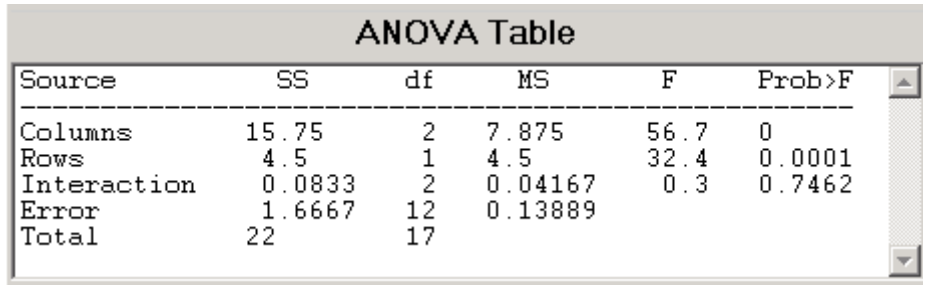
The `anova2` test evaluates the hypothesis that the row, column, and interaction effects are all the same, against the alternative that they are not all the same. Sometimes it is preferable to perform a test to determine *which pairs* of effects are significantly different, and which are not. Use the `multcompare` function to perform such tests by supplying the `stats` structure as input.

Examples

The data below come from a study of popcorn brands and popper type (Hogg 1987). The columns of the matrix `popcorn` are brands (Gourmet, National, and Generic). The rows are popper type (Oil and Air.) The study popped a batch of each brand three times with each popper. The values are the yield in cups of popped popcorn.

```
load popcorn

popcorn
popcorn =
  5.5000  4.5000  3.5000
  5.5000  4.5000  4.0000
  6.0000  4.0000  3.0000
  6.5000  5.0000  4.0000
  7.0000  5.5000  5.0000
```

```
   7.0000   5.0000   4.5000

p = anova2(popcorn,3)
p =
   0.0000   0.0001   0.7462
```



ANOVA Table

Source	SS	df	MS	F	Prob>F
Columns	15.75	2	7.875	56.7	0
Rows	4.5	1	4.5	32.4	0.0001
Interaction	0.0833	2	0.04167	0.3	0.7462
Error	1.6667	12	0.13889		
Total	22	17			

The vector p shows the *p*-values for the three brands of popcorn, 0.0000, the two popper types, 0.0001, and the interaction between brand and popper type, 0.7462. These values indicate that both popcorn brand and popper type affect the yield of popcorn, but there is no evidence of a synergistic (interaction) effect of the two.

The conclusion is that you can get the greatest yield using the Gourmet brand and an Air popper (the three values `popcorn(4:6,1)`).

References

[1] Hogg, R. V., and J. Ledolter. *Engineering Statistics*. New York: MacMillan, 1987.

See Also

`anova1` | `anovan`

Purpose

N-way analysis of variance

Syntax

```
p = anovan(y,group)
p = anovan(y,group,param,val)
[p,table] = anovan(y,group,param,val)
[p,table,stats] = anovan(y,group,param,val)
[p,table,stats,terms] = anovan(y,group,param,val)
```

Description

`p = anovan(y,group)` performs multiway (n-way) analysis of variance (ANOVA) for testing the effects of multiple factors on the mean of the vector `y`. (See "Grouped Data".) This test compares the variance explained by factors to the left over variance that cannot be explained. The factors and factor levels of the observations in `y` are assigned by the cell array `group`. Each of the cells in the cell array `group` contains a list of factor levels identifying the observations in `y` with respect to one of the factors. The list within each cell can be a categorical array, numeric vector, character matrix, or single-column cell array of strings, and must have the same number of elements as `y`. The fitted ANOVA model includes the main effects of each grouping variable. All grouping variables are treated as fixed effects by default. The result `p` is a vector of *p*-values, one per term. For an example, see "Example of Three-Way ANOVA" on page 20-28.

`p = anovan(y,group,param,val)` specifies one or more of the parameter name/value pairs described in the following table.

Parameter	Value
`'alpha'`	A number between 0 and 1 requesting 100(1 – *alpha*)% confidence bounds (default 0.05 for 95% confidence)
`'continuous'`	A vector of indices indicating which grouping variables should be treated as continuous predictors rather than as categorical predictors.
`'display'`	`'on'` displays an ANOVA table (the default) `'off'` omits the display

Parameter	Value
'model'	The type of model used. See "Model Type" on page 20-26 for a description of this parameter.
'nested'	A matrix M of 0's and 1's specifying the nesting relationships among the grouping variables. M(i,j) is 1 if variable i is nested in variable j.
'random'	A vector of indices indicating which grouping variables are random effects (all are fixed by default). See "ANOVA with Random Effects" on page 8-19 for an example of how to use 'random'.
'sstype'	1, 2, 3 (default), or h specifies the type of sum of squares. See "Sum of Squares" on page 20-27 for a description of this parameter.
'varnames'	A character matrix or a cell array of strings specifying names of grouping variables, one per grouping variable. When you do not specify 'varnames', the default labels 'X1', 'X2', 'X3', ..., 'XN' are used. See "ANOVA with Random Effects" on page 8-19 for an example of how to use 'varnames'.

`[p,table] = anovan(y,group,`*`param`*`,val)` returns the ANOVA table (including factor labels) in cell array `table`. (Copy a text version of the ANOVA table to the clipboard by using the `Copy Text` item on the **Edit** menu.)

`[p,table,stats] = anovan(y,group,`*`param`*`,val)` returns a `stats` structure that you can use to perform a follow-up multiple comparison test with the `multcompare` function. See "The Stats Structure" on page 20-31The Stats Structure for more information.

`[p,table,stats,terms] = anovan(y,group,`*`param`*`,val)` returns the main and interaction terms used in the ANOVA computations. The terms are encoded in the output matrix `terms` using the same format described above for input `'model'`. When you specify `'model'` itself in this matrix format, the matrix returned in `terms` is identical.

Model Type

This section explains how to use the argument `'model'` with the syntax:

```
[...]  = anovan(y,group,'model',modeltype)
```

The argument *`modeltype`*, which specifies the type of model the function uses, can be any one of the following:

- `'linear'` — The default `'linear'` model computes only the p-values for the null hypotheses on the N main effects.
- `'interaction'` — The `'interaction'` model computes the p-values for null hypotheses on the N main effects and the $\binom{N}{2}$ two-factor interactions.
- `'full'` — The `'full'` model computes the p-values for null hypotheses on the N main effects and interactions at all levels.
- An integer — For an integer value of `modeltype`, `k` (`k` ≤ `N`), `anovan` computes all interaction levels through the `k`th level. For example, the value `3` means main effects plus two- and three-factor interactions. The values `k = 1` and `k = 2` are equivalent to the `'linear'` and `'interaction'` specifications, respectively, while the value `k = N` is equivalent to the `'full'` specification.
- A matrix of term definitions having the same form as the input to the `x2fx` function. All entries must be `0` or `1` (no higher powers).

For more precise control over the main and interaction terms that `anovan` computes, `modeltype` can specify a matrix containing one row for each main or interaction term to include in the ANOVA model. Each row defines one term using a vector of N zeros and ones. The table below illustrates the coding for a 3-factor ANOVA.

Matrix Row	ANOVA Term
`[1 0 0]`	Main term A
`[0 1 0]`	Main term B

Matrix Row	ANOVA Term
`[0 0 1]`	Main term C
`[1 1 0]`	Interaction term AB
`[1 0 1]`	Interaction term AC
`[0 1 1]`	Interaction term BC
`[1 1 1]`	Interaction term ABC

For example, if *`modeltype`* is the matrix `[0 1 0;0 0 1;0 1 1]`, the output vector `p` contains the *p*-values for the null hypotheses on the main effects B and C and the interaction effect BC, in that order. A simple way to generate the *`modeltype`* matrix is to modify the `terms` output, which codes the terms in the current model using the format described above. If `anovan` returns `[0 1 0;0 0 1;0 1 1]` for `terms`, for example, and there is no significant result for interaction BC, you can recompute the ANOVA on just the main effects B and C by specifying `[0 1 0;0 0 1]` for *`modeltype`*.

Sum of Squares

This section explains how to use the argument `'sstype'` with the syntax:

```
[...]  = anovan(y,group,'sstype',type)
```

This syntax computes the ANOVA using the type of sum of squares specified by *`type`*, which can be `1`, `2`, `3`, or `h`. While the numbers `1` – `3` designate Type 1, Type 2, or Type 3 sum of squares, respectively, `h` represents a hierarchical model similar to type 2, but with continuous as well as categorical factors used to determine the hierarchy of terms. The default value is `3`. For a model containing main effects but no interactions, the value of *`type`* only influences computations on unbalanced data.

The sum of squares for any term is determined by comparing two models. The Type 1 sum of squares for a term is the reduction in residual sum of squares obtained by adding that term to a fit that already includes the terms listed before it. The Type 2 sum of squares is

the reduction in residual sum of squares obtained by adding that term to a model consisting of all other terms that do not contain the term in question. The Type 3 sum of squares is the reduction in residual sum of squares obtained by adding that term to a model containing all other terms, but with their effects constrained to obey the usual "sigma restrictions" that make models estimable.

Suppose you are fitting a model with two factors and their interaction, and that the terms appear in the order A, B, AB. Let $R(\cdot)$ represent the residual sum of squares for a model, so for example $R(A, B, AB)$ is the residual sum of squares fitting the whole model, $R(A)$ is the residual sum of squares fitting just the main effect of A, and $R(1)$ is the residual sum of squares fitting just the mean. The three types of sums of squares are as follows:

Term	Type 1 Sum of Squares	Type 2 Sum of Squares	Type 3 Sum of Squares
A	$R(1) - R(A)$	$R(B) - R(A, B)$	$R(B, AB) - R(A, B, AB)$
B	$R(A) - R(A, B)$	$R(A) - R(A, B)$	$R(A, AB) - R(A, B, AB)$
AB	$R(A, B) - R(A, B, AB)$	$R(A, B) - R(A, B, AB)$	$R(A, B) - R(A, B, AB)$

The models for Type 3 sum of squares have sigma restrictions imposed. This means, for example, that in fitting $R(B, AB)$, the array of AB effects is constrained to sum to 0 over A for each value of B, and over B for each value of A.

Example of Three-Way ANOVA

As an example of three-way ANOVA, consider the vector `y` and `group` inputs below.

```
y = [52.7 57.5 45.9 44.5 53.0 57.0 45.9 44.0]';
g1 = [1 2 1 2 1 2 1 2];
g2 = {'hi';'hi';'lo';'lo';'hi';'hi';'lo';'lo'};
g3 = {'may';'may';'may';'may';'june';'june';'june';'june'};
```

This defines a three-way ANOVA with two levels of each factor. Every observation in `y` is identified by a combination of factor levels. If the factors are A, B, and C, then observation `y(1)` is associated with

- Level 1 of factor A
- Level `'hi'` of factor B
- Level `'may'` of factor C

Similarly, observation `y(6)` is associated with

- Level 2 of factor A
- Level `'hi'` of factor B
- Level `'june'` of factor C

To compute the ANOVA, enter

```
p = anovan(y,{g1 g2 g3})
p =
  0.4174
  0.0028
  0.9140
```

Output vector `p` contains *p*-values for the null hypotheses on the N main effects. Element `p(1)` contains the *p* value for the null hypotheses, H_{0A}, that samples at all levels of factor A are drawn from the same population; element `p(2)` contains the *p* value for the null hypotheses, H_{0B}, that samples at all levels of factor B are drawn from the same population; and so on.

If any *p* value is near zero, this casts doubt on the associated null hypothesis. For example, a sufficiently small *p* value for H_{0A} suggests that at least one A-sample mean is significantly different from the other A-sample means; that is, there is a main effect due to factor A. You need to choose a bound for the *p* value to determine whether a result is statistically significant. It is common to declare a result significant if the *p* value is less than 0.05 or 0.01.

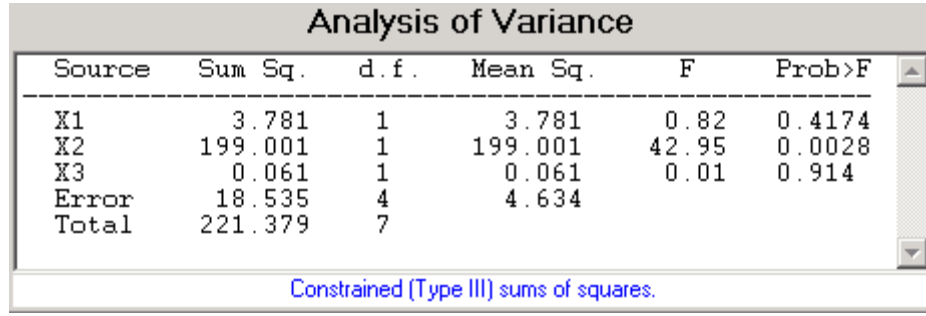
anovan also displays a figure showing the standard ANOVA table, which by default divides the variability of the data in x into

- The variability due to differences between the levels of each factor accounted for in the model (one row for each factor)
- The remaining variability not explained by any systematic source

The ANOVA table has six columns:

- The first shows the source of the variability.
- The second shows the sum of squares (SS) due to each source.
- The third shows the degrees of freedom (df) associated with each source.
- The fourth shows the mean squares (MS), which is the ratio SS/df.
- The fifth shows the *F* statistics, which are the ratios of the mean squares.
- The sixth shows the *p*-values for the *F* statistics.

The table is shown in the following figure:



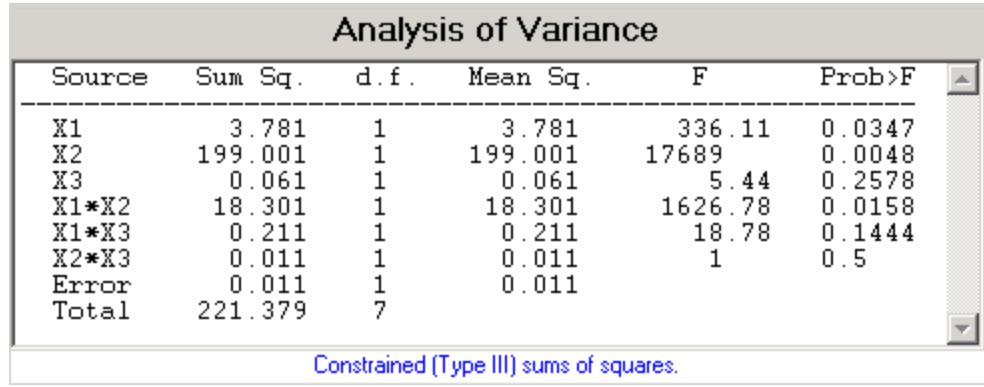
Two-Factor Interactions

By default, anovan computes *p*-values just for the three main effects. To also compute *p*-values for the two-factor interactions, X1*X2, X1*X3,

and `X2*X3`, add the name/value pair `'model', 'interaction'` as input arguments.

```
p = anovan(y,{g1 g2 g3},'model','interaction')
p =
  0.0347
  0.0048
  0.2578
  0.0158
  0.1444
  0.5000
```

The first three entries of p are the *p*-values for the main effects. The last three entries are the *p*-values for the two-factor interactions. You can determine the order in which the two-factor interactions occur from the ANOVAN table shown in the following figure.



The Stats Structure

The `anovan` test evaluates the hypothesis that the different levels of a factor (or more generally, a term) have the same effect, against the alternative that they do not all have the same effect. Sometimes it is preferable to perform a test to determine which pairs of levels are significantly different, and which are not. Use the `multcompare` function to perform such tests by supplying the `stats` structure as input.

The stats structure contains the fields listed below, in addition to a number of other fields required for doing multiple comparisons using the multcompare function:

Field	Description
coeffs	Estimated coefficients
coeffnames	Name of term for each coefficient
vars	Matrix of grouping variable values for each term
resid	Residuals from the fitted model

The stats structure also contains the following fields if there are random effects:

Field	Description
ems	Expected mean squares
denom	Denominator definition
rtnames	Names of random terms
varest	Variance component estimates (one per random term)
varci	Confidence intervals for variance components

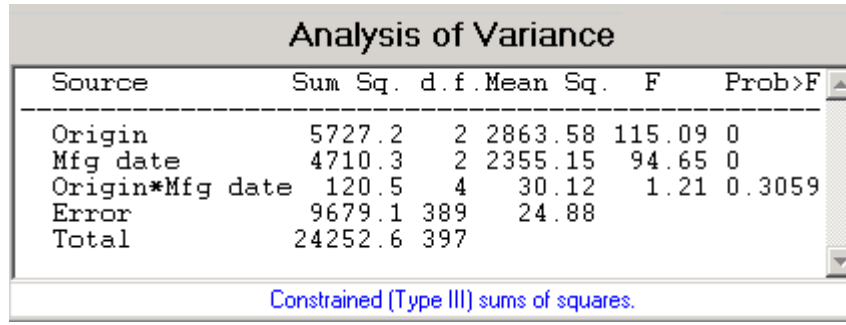
Examples

"Example: Two-Way ANOVA" on page 8-10 shows how to use anova2 to analyze the effects of two factors on a response in a balanced design. For a design that is not balanced, use anovan instead.

The data in carbig.mat gives measurements on 406 cars. Use anonvan to study how the mileage depends on where and when the cars were made:

```
load carbig

p = anovan(MPG,{org when},'model',2,'sstype',3,...
           'varnames',{'Origin';'Mfg date'})
p =
```

```
     0
     0
0.3059
```



The p value for the interaction term is not small, indicating little evidence that the effect of the year or manufacture (`when`) depends on where the car was made (`org`). The linear effects of those two factors, however, are significant.

References

[1] Hogg, R. V., and J. Ledolter. *Engineering Statistics*. New York: MacMillan, 1987.

See Also

`anova1` | `anova2` | `multcompare`

How To

- "Grouped Data" on page 2-34

ansaribradley

Purpose

Ansari-Bradley test

Syntax

```
h = ansaribradley(x,y)
h = ansaribradley(x,y,alpha)
h = ansaribradley(x,y,alpha,tail)
[h,p] = ansaribradley(...)
[h,p,stats] = ansaribradley(...)
[...] = ansaribradley(x,y,alpha,tail,exact)
[...] = ansaribradley(x,y,alpha,tail,exact,dim)
```

Description

`h = ansaribradley(x,y)` performs an Ansari-Bradley test of the hypothesis that two independent samples, in the vectors `x` and `y`, come from the same distribution, against the alternative that they come from distributions that have the same median and shape but different dispersions (e.g. variances). The result is `h = 0` if the null hypothesis of identical distributions cannot be rejected at the 5% significance level, or `h = 1` if the null hypothesis can be rejected at the 5% level. `x` and `y` can have different lengths.

`x` and `y` can also be matrices or *N*-dimensional arrays. For matrices, `ansaribradley` performs separate tests along each column, and returns a vector of results. `x` and `y` must have the same number of columns. For *N*-dimensional arrays, `ansaribradley` works along the first nonsingleton dimension. `x` and `y` must have the same size along all the remaining dimensions.

`h = ansaribradley(x,y,alpha)` performs the test at the significance level `(100*alpha)`, where `alpha` is a scalar.

`h = ansaribradley(x,y,alpha,tail)` performs the test against the alternative hypothesis specified by the string *`tail`*. *`tail`* is one of:

- `'both'` — Two-tailed test (dispersion parameters are not equal)
- `'right'` — Right-tailed test (dispersion of `X` is greater than dispersion of `Y`)
- `'left'` — Left-tailed test (dispersion of `X` is less than dispersion of `Y`)

`[h,p] = ansaribradley(...)` returns the *p* value, i.e., the probability of observing the given result, or one more extreme, by chance if the null hypothesis is true. Small values of `p` cast doubt on the validity of the null hypothesis.

`[h,p,stats] = ansaribradley(...)` returns a structure `stats` with the following fields:

- `W` — Value of the test statistic `W`, which is the sum of the Ansari-Bradley ranks for the `X` sample
- `Wstar` — Approximate normal statistic `W*`

`[...] = ansaribradley(x,y,alpha,tail,exact)` computes `p` using an exact calculation of the distribution of `W` with `exact = 'on'`. This can be time-consuming for large samples. `exact = 'off'` computes `p` using a normal approximation for the distribution of `W*`. The default if `exact` is empty is to use the exact calculation if *N*, the total number of rows in `x` and `y`, is 25 or less, and to use the normal approximation if *N* > 25. Pass in `[]` for `alpha` and `tail` to use their default values while specifying a value for `exact`. Note that *N* is computed before any `NaN` values (representing missing data) are removed.

`[...] = ansaribradley(x,y,alpha,tail,exact,dim)` works along dimension `dim` of `x` and `y`.

The Ansari-Bradley test is a nonparametric alternative to the two-sample *F* test of equal variances. It does not require the assumption that `x` and `y` come from normal distributions. The dispersion of a distribution is generally measured by its variance or standard deviation, but the Ansari-Bradley test can be used with samples from distributions that do not have finite variances.

The theory behind the Ansari-Bradley test requires that the groups have equal medians. Under that assumption and if the distributions in each group are continuous and identical, the test does not depend on the distributions in each group. If the groups do not have the same medians, the results may be misleading. Ansari and Bradley recommend subtracting the median in that case, but the distribution of

the resulting test, under the null hypothesis, is no longer independent of the common distribution of `x` and `y`. If you want to perform the tests with medians subtracted, you should subtract the medians from `x` and `y` before calling `ansaribradley`.

Examples

Is the dispersion significantly different for two model years?

```
load carsmall
[h,p,stats] = ansaribradley(MPG(Model_Year==82),MPG(Model_Year==76))
h =
     0
p =
    0.8426
stats =
        W: 526.9000
    Wstar: 0.1986
```

See Also

`vartest` | `vartestn` | `ttest2`

Purpose

Interactive analysis of covariance

Syntax

```
aoctool(x,y,group)
aoctool(x,y,group,alpha)
aoctool(x,y,group,alpha,xname,yname,gname)
aoctool(x,y,group,alpha,xname,yname,gname,displayopt)
aoctool(x,y,group,alpha,xname,yname,gname,displayopt,model)
h = aoctool(...)
[h,atab,ctab] = aoctool(...)
[h,atab,ctab,stats] = aoctool(...)
```

Description

`aoctool(x,y,group)` fits a separate line to the column vectors, `x` and `y`, for each group defined by the values in the array `group`. `group` may be a categorical variable, vector, character array, or cell array of strings. (See "Grouped Data" on page 2-34.) These types of models are known as one-way analysis of covariance (ANOCOVA) models. The output consists of three figures:

- An interactive graph of the data and prediction curves
- An ANOVA table
- A table of parameter estimates

You can use the figures to change models and to test different parts of the model. More information about interactive use of the `aoctool` function appears in "Analysis of Covariance Tool" on page 8-27.

`aoctool(x,y,group,alpha)` determines the confidence levels of the prediction intervals. The confidence level is `100(1-alpha)`%. The default value of `alpha` is 0.05.

`aoctool(x,y,group,alpha,xname,yname,gname)` specifies the name to use for the `x`, `y`, and `g` variables in the graph and tables. If you enter simple variable names for the `x`, `y`, and `g` arguments, the aoctool function uses those names. If you enter an expression for one of these arguments, you can specify a name to use in place of that expression by supplying these arguments. For example, if you enter `m(:,2)` as the `x` argument, you might choose to enter `'Col 2'` as the `xname` argument.

`aoctool(x,y,group,alpha,xname,yname,gname,displayopt)` enables the graph and table displays when *`displayopt`* is `'on'` (default) and suppresses those displays when *`displayopt`* is `'off'`.

`aoctool(x,y,group,alpha,xname,yname,gname,displayopt,model)` specifies the initial model to fit. The value of *`model`* can be any of the following:

- `'same mean'` — Fit a single mean, ignoring grouping
- `'separate means'` — Fit a separate mean to each group
- `'same line'` — Fit a single line, ignoring grouping
- `'parallel lines'` — Fit a separate line to each group, but constrain the lines to be parallel
- `'separate lines'` — Fit a separate line to each group, with no constraints

`h = aoctool(...)` returns a vector of handles to the line objects in the plot.

`[h,atab,ctab] = aoctool(...)` returns cell arrays containing the entries in ANOVA table (`atab`) and the table of coefficient estimates (`ctab`). (You can copy a text version of either table to the clipboard by using the `Copy Text` item on the **Edit** menu.)

`[h,atab,ctab,stats] = aoctool(...)` returns a `stats` structure that you can use to perform a follow-up multiple comparison test. The ANOVA table output includes tests of the hypotheses that the slopes or intercepts are all the same, against a general alternative that they are not all the same. Sometimes it is preferable to perform a test to determine which pairs of values are significantly different, and which are not. You can use the `multcompare` function to perform such tests by supplying the `stats` structure as input. You can test either the slopes, the intercepts, or population marginal means (the heights of the curves at the mean `x` value).

Examples

This example illustrates how to fit different models non-interactively. After loading the smaller car data set and fitting a separate-slopes model, you can examine the coefficient estimates.

```
load carsmall
[h,a,c,s] = aoctool(Weight,MPG,Model_Year,0.05,...
                    '','','','off','separate lines');
c(:,1:2)
ans =
  'Term'       'Estimate'
  'Intercept'  [45.97983716833132]
  ' 70'        [-8.58050531454973]
  ' 76'        [-3.89017396094922]
  ' 82'        [12.47067927549897]
  'Slope'      [-0.00780212907455]
  ' 70'        [ 0.00195840368824]
  ' 76'        [ 0.00113831038418]
  ' 82'        [-0.00309671407243]
```

Roughly speaking, the lines relating `MPG` to `Weight` have an intercept close to 45.98 and a slope close to -0.0078. Each group's coefficients are offset from these values somewhat. For instance, the intercept for the cars made in 1970 is 45.98-8.58 = 37.40.

Next, try a fit using parallel lines. (The ANOVA table shows that the parallel-lines fit is significantly worse than the separate-lines fit.)

```
[h,a,c,s] = aoctool(Weight,MPG,Model_Year,0.05,...
                    '','','','off','parallel lines');

c(:,1:2)

ans =

  'Term'       'Estimate'
  'Intercept'  [43.38984085130596]
  ' 70'        [-3.27948192983761]
  ' 76'        [-1.35036234809006]
```

```
' 82'        [ 4.62984427792768]
'Slope'      [-0.00664751826198]
```

Again, there are different intercepts for each group, but this time the slopes are constrained to be the same.

See Also

`anova1` | `multcompare` | `polytool`

How To

- "Grouped Data" on page 2-34

Purpose

Append new trees to ensemble

Syntax

```
B = append(B,other)
```

Description

`B = append(B,other)` appends the trees from the `other` ensemble to those in `B`. This method checks for consistency of the `X` and `Y` properties of the two ensembles, as well as consistency of their compact objects and out-of-bag indices, before appending the trees. The output ensemble `B` takes training parameters such as `FBoot`, `Prior`, `Cost`, and `other` from the `B` input. There is no attempt to check if these training parameters are consistent between the two objects.

See Also

`CompactTreeBagger.combine`

ProbDistKernel.BandWidth property

Purpose

Read-only value specifying bandwidth of kernel smoothing function for ProbDistKernel object

Description

`BandWidth` is a read-only property of the `ProbDistKernel` class. `BandWidth` is a value specifying the width of the kernel smoothing function used to compute a nonparametric estimate of the probability distribution when creating a ProbDistKernel object.

Values

For a distribution specified to cover only the positive numbers or only a finite interval, the data are transformed before the kernel density is applied, and the bandwidth is on the scale of the transformed data.

Use this information to view and compare the width of the kernel smoothing function used to create distributions.

See Also

`ksdensity`

Purpose

Bartlett's test

Syntax

```
ndim = barttest(X,alpha)
[ndim,prob,chisquare] = barttest(X,alpha)
```

Description

`ndim = barttest(X,alpha)` returns the number of dimensions necessary to explain the nonrandom variation in the data matrix `X`, using the significance probability `alpha`. The dimension is determined by a series of hypothesis tests. The test for `ndim=1` tests the hypothesis that the variances of the data values along each principal component are equal, the test for `ndim=2` tests the hypothesis that the variances along the second through last components are equal, and so on.

`[ndim,prob,chisquare] = barttest(X,alpha)` returns the number of dimensions, the significance values for the hypothesis tests, and the χ^2 values associated with the tests.

Examples

```
X = mvnrnd([0 0],[1 0.99; 0.99 1],20);
X(:,3:4) = mvnrnd([0 0],[1 0.99; 0.99 1],20);
X(:,5:6) = mvnrnd([0 0],[1 0.99; 0.99 1],20);
[ndim, prob] = barttest(X,0.05)
ndim =
   3
prob =
     0
     0
     0
  0.5081
  0.6618
```

See Also

princomp | pcacov | pcares

bbdesign

Purpose

Box-Behnken design

Syntax

```
dBB = bbdesign(n)
[dBB,blocks] = bbdesign(n)
[...] = bbdesign(n,param,val)
```

Description

`dBB = bbdesign(n)` generates a Box-Behnken design for `n` factors. `n` must be an integer `3` or larger. The output matrix `dBB` is *m*-by-`n`, where *m* is the number of runs in the design. Each row represents one run, with settings for all factors represented in the columns. Factor values are normalized so that the cube points take values between `-1` and `1`.

`[dBB,blocks] = bbdesign(n)` requests a blocked design. The output `blocks` is an *m*-by-1 vector of block numbers for each run. Blocks indicate runs that are to be measured under similar conditions to minimize the effect of inter-block differences on the parameter estimates.

`[...] = bbdesign(n,param,val)` specifies one or more optional parameter/value pairs for the design. The following table lists valid parameter/value pairs.

Parameter	Description	Values
`'center'`	Number of center points.	Integer. The default depends on `n`.
`'blocksize'`	Maximum number of points per block.	Integer. The default is `Inf`.

Examples

The following creates a 3-factor Box-Behnken design:

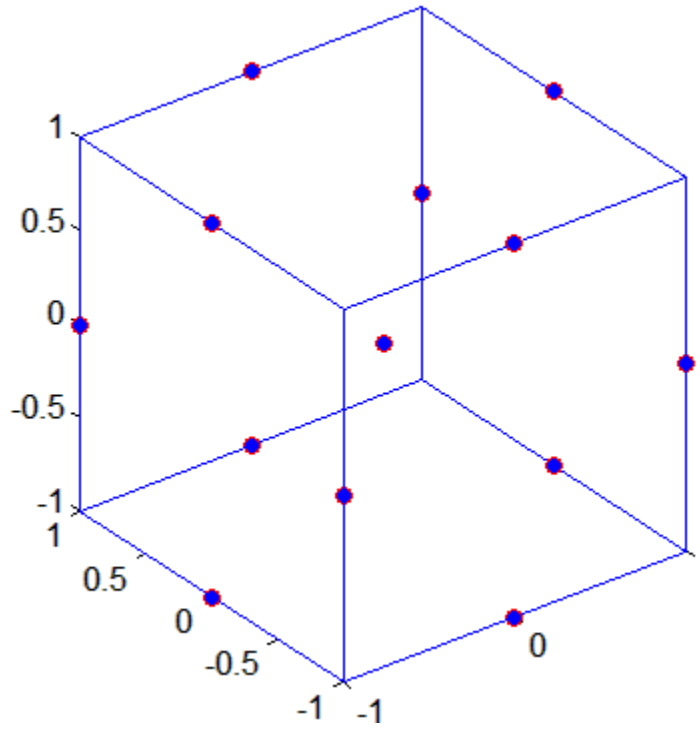
```
dBB = bbdesign(3)
dBB =
    -1    -1     0
    -1     1     0
     1    -1     0
```

```
 1     1     0
-1     0    -1
-1     0     1
 1     0    -1
 1     0     1
 0    -1    -1
 0    -1     1
 0     1    -1
 0     1     1
 0     0     0
 0     0     0
 0     0     0
```

The center point is run 3 times to allow for a more uniform estimate of the prediction variance over the entire design space.

Visualize the design as follows:

```
plot3(dBB(:,1),dBB(:,2),dBB(:,3),'ro',...
         'MarkerFaceColor','b')
X = [1 -1 -1 -1 1 -1 -1 -1 1 1 -1 -1; ...
     1 1 1 -1 1 1 1 -1 1 1 -1 -1];
Y = [-1 -1 1 -1 -1 -1 1 -1 1 -1 1 -1; ...
     1 -1 1 1 1 -1 1 1 1 -1 1 -1];
Z = [1 1 1 1 -1 -1 -1 -1 -1 -1 -1 -1; ...
     1 1 1 1 -1 -1 -1 -1 1 1 1 1];
line(X,Y,Z,'Color','b')
axis square equal
```



See Also

`ccdesign`

Purpose

Beta cumulative distribution function

Syntax

```
p = betacdf(X,A,B)
```

Description

`p = betacdf(X,A,B)` returns the beta cdf at each of the values in `X` using the corresponding parameters in `A` and `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `A` and `B` must all be positive, and the values in `X` must lie on the interval [0,1].

The beta cdf for a given value `x` and given pair of parameters `a` and `b` is

$$p = F(x \mid a,b) = \frac{1}{B(a,b)} \int_0^x t^{a-1}(1-t)^{b-1} dt$$

where $B(\cdot)$ is the Beta function.

Examples

```
x = 0.1:0.2:0.9;
a = 2;
b = 2;
p = betacdf(x,a,b)
p =
    0.0280   0.2160   0.5000   0.7840   0.9720

a = [1 2 3];
p = betacdf(0.5,a,a)
p =
    0.5000   0.5000   0.5000
```

See Also

`cdf` | `betapdf` | `betainv` | `betastat` | `betalike` | `betarnd` | `betafit`

How To

- "Beta Distribution" on page B-4

betafit

Purpose

Beta parameter estimates

Syntax

```
phat = betafit(data)
[phat,pci] = betafit(data,alpha)
```

Description

`phat = betafit(data)` computes the maximum likelihood estimates of the beta distribution parameters a and b from the data in the vector `data` and returns a column vector containing the a and b estimates, where the beta cdf is given by

$$F(x \mid a,b) = \frac{1}{B(a,b)} \int_0^x t^{a-1}(1-t)^{b-1} dt$$

and $B(\cdot)$ is the Beta function. The elements of `data` must lie in the open interval (0, 1), where the beta distribution is defined. However, it is sometimes also necessary to fit a beta distribution to data that include exact zeros or ones. For such data, the beta likelihood function is unbounded, and standard maximum likelihood estimation is not possible. In that case, `betafit` maximizes a modified likelihood that incorporates the zeros or ones by treating them as if they were values that have been left-censored at `sqrt(realmin)` or right-censored at 1-`eps`/2, respectively.

`[phat,pci] = betafit(data,alpha)` returns confidence intervals on the a and b parameters in the 2-by-2 matrix `pci`. The first column of the matrix contains the lower and upper confidence bounds for parameter a, and the second column contains the confidence bounds for parameter b. The optional input argument `alpha` is a value in the range [0, 1] specifying the width of the confidence intervals. By default, `alpha` is `0.05`, which corresponds to 95% confidence intervals. The confidence intervals are based on a normal approximation for the distribution of the logs of the parameter estimates.

Examples

This example generates 100 beta distributed observations. The true a and b parameters are 4 and 3, respectively. Compare these to the

values returned in `p` by the beta fit. Note that the columns of `ci` both bracket the true parameters.

```
data = betarnd(4,3,100,1);
[p,ci] = betafit(data,0.01)
p =
    5.5328    3.8097
ci =
    3.6538    2.6197
    8.3781    5.5402
```

References

[1] Hahn, Gerald J., and S. S. Shapiro. *Statistical Models in Engineering*. Hoboken, NJ: John Wiley & Sons, Inc., 1994, p. 95.

See Also

`mle` | `betapdf` | `betainv` | `betastat` | `betalike` | `betarnd` | `betacdf`

How To

• "Beta Distribution" on page B-4

betainv

Purpose

Beta inverse cumulative distribution function

Syntax

```
X = betainv(P,A,B)
```

Description

`X = betainv(P,A,B)` computes the inverse of the beta cdf with parameters specified by `A` and `B` for the corresponding probabilities in `P`. `P`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that are all the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `A` and `B` must all be positive, and the values in `P` must lie on the interval [0, 1].

The inverse beta cdf for a given probability p and a given pair of parameters a and b is

$$x = F^{-1}(p \mid a,b) = \{x : F(x \mid a,b) = p\}$$

where

$$p = F(x \mid a,b) = \frac{1}{B(a,b)} \int_0^x t^{a-1}(1-t)^{b-1} dt$$

and $B(\cdot)$ is the Beta function. Each element of output `X` is the value whose cumulative probability under the beta cdf defined by the corresponding parameters in `A` and `B` is specified by the corresponding value in `P`.

Algorithms

The `betainv` function uses Newton's method with modifications to constrain steps to the allowable range for x, i.e., [0 1].

Examples

```
p = [0.01 0.5 0.99];
x = betainv(p,10,5)
x =
  0.3726  0.6742  0.8981
```

According to this result, for a beta cdf with $a = 10$ and $b = 5$, a value less than or equal to 0.3726 occurs with probability 0.01. Similarly,

values less than or equal to 0.6742 and 0.8981 occur with respective probabilities 0.5 and 0.99.

See Also

`icdf` | `betapdf` | `betafit` | `betainv` | `betastat` | `betalike` | `betarnd` | `betacdf`

How To

- "Beta Distribution" on page B-4

betalike

Purpose

Beta negative log-likelihood

Syntax

```
nlogL = betalike(params,data)
[nlogL,AVAR] = betalike(params,data)
```

Description

`nlogL = betalike(params,data)` returns the negative of the beta log-likelihood function for the beta parameters a and b specified in vector `params` and the observations specified in the column vector `data`.

The elements of `data` must lie in the open interval (0, 1), where the beta distribution is defined. However, it is sometimes also necessary to fit a beta distribution to data that include exact zeros or ones. For such data, the beta likelihood function is unbounded, and standard maximum likelihood estimation is not possible. In that case, `betalike` computes a modified likelihood that incorporates the zeros or ones by treating them as if they were values that have been left-censored at `sqrt(realmin)` or right-censored at 1-`eps`/2, respectively.

`[nlogL,AVAR] = betalike(params,data)` also returns `AVAR`, which is the asymptotic variance-covariance matrix of the parameter estimates if the values in `params` are the maximum likelihood estimates. `AVAR` is the inverse of Fisher's information matrix. The diagonal elements of `AVAR` are the asymptotic variances of their respective parameters.

`betalike` is a utility function for maximum likelihood estimation of the beta distribution. The likelihood assumes that all the elements in the data sample are mutually independent. Since `betalike` returns the negative beta log-likelihood function, minimizing `betalike` using `fminsearch` is the same as maximizing the likelihood.

Examples

This example continues the `betafit` example, which calculates estimates of the beta parameters for some randomly generated beta distributed data.

```
r = betarnd(4,3,100,1);
[nlogl,AVAR] = betalike(betafit(r),r)
nlogl =
```

```
    -27.5996


AVAR =

    0.2783    0.1316
    0.1316    0.0867
```

See Also

betapdf | betafit | betainv | betastat | betarnd | betacdf

How To

- “Beta Distribution” on page B-4

betapdf

Purpose

Beta probability density function

Syntax

```
Y = betapdf(X,A,B)
```

Description

`Y = betapdf(X,A,B)` computes the beta pdf at each of the values in `X` using the corresponding parameters in `A` and `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions of the other inputs. The parameters in `A` and `B` must all be positive, and the values in `X` must lie on the interval `[0, 1]`.

The beta probability density function for a given value x and given pair of parameters a and b is

$$y = f(x \mid a,b) = \frac{1}{B(a,b)} x^{a-1}(1-x)^{b-1} I_{(0,1)}(x)$$

where $B(\cdot)$ is the Beta function. The indicator function $I_{(0,1)}(x)$ ensures that only values of x in the range (0 1) have nonzero probability. The uniform distribution on (0 1) is a degenerate case of the beta pdf where $a = 1$ and $b = 1$.

A *likelihood function* is the pdf viewed as a function of the parameters. Maximum likelihood estimators (MLEs) are the values of the parameters that maximize the likelihood function for a fixed value of x.

Examples

```
a = [0.5 1; 2 4]
a =
  0.5000  1.0000
  2.0000  4.0000
y = betapdf(0.5,a,a)
y =
  0.6366  1.0000
  1.5000  2.1875
```

See Also

`pdf` | `betafit` | `betainv` | `betastat` | `betalike` | `betarnd` | `betacdf`

How To

- "Beta Distribution" on page B-4

betarnd

Purpose

Beta random numbers

Syntax

```
R = betarnd(A,B)
R = betarnd(A,B,m,n,...)
R = betarnd(A,B,[m,n,...])
```

Description

`R = betarnd(A,B)` generates random numbers from the beta distribution with parameters specified by `A` and `B`. `A` and `B` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `A` or `B` is expanded to a constant array with the same dimensions as the other input.

`R = betarnd(A,B,m,n,...)` or `R = betarnd(A,B,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the beta distribution with parameters `A` and `B`. `A` and `B` can each be scalars or arrays of the same size as `R`.

Examples

```
a = [1 1;2 2];
b = [1 2;1 2];

r = betarnd(a,b)
r =
  0.6987  0.6139
  0.9102  0.8067

r = betarnd(10,10,[1 5])
r =
  0.5974  0.4777  0.5538  0.5465  0.6327

r = betarnd(4,2,2,3)
r =
  0.3943  0.6101  0.5768
  0.5990  0.2760  0.5474
```

See Also

`random` | `betapdf` | `betafit` | `betainv` | `betastat` | `betalike` | `betacdf`

How To

- "Beta Distribution" on page B-4

betastat

Purpose

Beta mean and variance

Syntax

```
[M,V] = betastat(A,B)
```

Description

`[M,V] = betastat(A,B)`, with `A>0` and `B>0`, returns the mean of and variance for the beta distribution with parameters specified by `A` and `B`. `A` and `B` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `M` and `V`. A scalar input for `A` or `B` is expanded to a constant array with the same dimensions as the other input.

The mean of the beta distribution with parameters a and b is $a / (a + b)$ and the variance is

$$\frac{ab}{(a+b+1)(a+b)^2}$$

Examples

If parameters a and b are equal, the mean is 1/2.

```
a = 1:6;
[m,v] = betastat(a,a)
m =
  0.5000  0.5000  0.5000  0.5000  0.5000  0.5000
v =
  0.0833  0.0500  0.0357  0.0278  0.0227  0.0192
```

See Also

`betapdf` | `betafit` | `betainv` | `betalike` | `betarnd` | `betacdf`

How To

- "Beta Distribution" on page B-4

Purpose

Bayes Information Criterion

Description

The Bayes Information Criterion: `2*NlogL+m*log(n)`, where `n` is the number of observations and `m` is the number of estimated parameters.

binocdf

Purpose

Binomial cumulative distribution function

Syntax

```
Y = binocdf(X,N,P)
```

Description

`Y = binocdf(X,N,P)` computes a binomial cdf at each of the values in `X` using the corresponding number of trials in `N` and probability of success for each trial in `P`. `X`, `N`, and `P` can be vectors, matrices, or multidimensional arrays that are all the same size. A scalar input is expanded to a constant array with the same dimensions of the other inputs. The values in `N` must all be positive integers, the values in `X` must lie on the interval `[0,N]`, and the values in `P` must lie on the interval [0, 1].

The binomial cdf for a given value x and a given pair of parameters n and p is

$$y = F(x \mid n, p) = \sum_{i=0}^{x} \binom{n}{i} p^i (1-p)^{(n-i)} I_{(0,1,\ldots,n)}(i).$$

The result, y, is the probability of observing up to x successes in n independent trials, where the probability of success in any given trial is p. The indicator function $I_{(0,1,\ldots,n)}(i)$ ensures that x only adopts values of $0,1,\ldots,n$.

Examples

If a baseball team plays 162 games in a season and has a 50-50 chance of winning any game, then the probability of that team winning more than 100 games in a season is:

```
1 - binocdf(100,162,0.5)
```

The result is `0.001` (i.e., `1-0.999`). If a team wins 100 or more games in a season, this result suggests that it is likely that the team's true probability of winning any game is greater than 0.5.

See Also

`cdf` | `binopdf` | `binoinv` | `binostat` | `binofit` | `binornd`

How To

- "Binomial Distribution" on page B-7

binofit

Purpose

Binomial parameter estimates

Syntax

```
phat = binofit(x,n)
[phat,pci] = binofit(x,n)
[phat,pci] = binofit(x,n,alpha)
```

Description

`phat = binofit(x,n)` returns a maximum likelihood estimate of the probability of success in a given binomial trial based on the number of successes, `x`, observed in `n` independent trials. If `x = (x(1), x(2), ... x(k))` is a vector, `binofit` returns a vector of the same size as `x` whose ith entry is the parameter estimate for `x(i)`. All `k` estimates are independent of each other. If `n = (n(1), n(2), ..., n(k))` is a vector of the same size as `x`, the binomial fit, `binofit`, returns a vector whose ith entry is the parameter estimate based on the number of successes `x(i)` in `n(i)` independent trials. A scalar value for `x` or `n` is expanded to the same size as the other input.

`[phat,pci] = binofit(x,n)` returns the probability estimate, `phat`, and the 95% confidence intervals, `pci`. `binofit` uses the Clopper-Pearson method to calculate confidence intervals.

`[phat,pci] = binofit(x,n,alpha)` returns the `100(1 - alpha)`% confidence intervals. For example, `alpha = 0.01` yields 99% confidence intervals.

Note `binofit` behaves differently than other Statistics Toolbox functions that compute parameter estimates, in that it returns independent estimates for each entry of `x`. By comparison, `expfit` returns a single parameter estimate based on all the entries of `x`.

Unlike most other distribution fitting functions, the `binofit` function treats its input `x` vector as a collection of measurements from separate samples. If you want to treat `x` as a single sample and compute a single parameter estimate for it, you can use `binofit(sum(x),sum(n))` when `n` is a vector, and `binofit(sum(X),N*length(X))` when `n` is a scalar.

Examples

This example generates a binomial sample of 100 elements, where the probability of success in a given trial is 0.6, and then estimates this probability from the outcomes in the sample.

```
r = binornd(100,0.6);
[phat,pci] = binofit(r,100)
phat =
  0.5800
pci =
  0.4771  0.6780
```

The 95% confidence interval, `pci`, contains the true value, 0.6.

References

[1] Johnson, N. L., S. Kotz, and A. W. Kemp. *Univariate Discrete Distributions*. Hoboken, NJ: Wiley-Interscience, 1993.

See Also

`mle` | `binopdf` | `binocdf` | `binoinv` | `binostat` | `binornd`

How To

- "Binomial Distribution" on page B-7

binoinv

Purpose

Binomial inverse cumulative distribution function

Syntax

```
X = binoinv(Y,N,P)
```

Description

`X = binoinv(Y,N,P)` returns the smallest integer `X` such that the binomial cdf evaluated at `X` is equal to or exceeds `Y`. You can think of `Y` as the probability of observing `X` successes in `N` independent trials where `P` is the probability of success in each trial. Each `X` is a positive integer less than or equal to `N`.

`Y`, `N`, and `P` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `N` must be positive integers, and the values in both `P` and `Y` must lie on the interval [0 1].

Examples

If a baseball team has a 50-50 chance of winning any game, what is a reasonable range of games this team might win over a season of 162 games?

```
binoinv([0.05 0.95],162,0.5)
ans =
    71    91
```

This result means that in 90% of baseball seasons, a .500 team should win between 71 and 91 games.

See Also

`icdf` | `binopdf` | `binocdf` | `binofit` | `binostat` | `binornd`

How To

- “Binomial Distribution” on page B-7

Purpose

Binomial probability density function

Syntax

```
Y = binopdf(X,N,P)
```

Description

`Y = binopdf(X,N,P)` computes the binomial pdf at each of the values in `X` using the corresponding number of trials in `N` and probability of success for each trial in `P`. `Y`, `N`, and `P` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions of the other inputs.

The parameters in `N` must be positive integers, and the values in `P` must lie on the interval [0, 1].

The binomial probability density function for a given value x and given pair of parameters n and p is

$$y = f(x \mid n, p) = \binom{n}{x} p^x q^{(n-x)} I_{(0,1,\ldots,n)}(x)$$

where $q = 1 - p$. The result, y, is the probability of observing x successes in n independent trials, where the probability of success in any *given* trial is p. The indicator function $I_{(0,1,\ldots,n)}(x)$ ensures that x only adopts values of 0, 1, ..., n.

Examples

A Quality Assurance inspector tests 200 circuit boards a day. If 2% of the boards have defects, what is the probability that the inspector will find no defective boards on any given day?

```
binopdf(0,200,0.02)
ans =
  0.0176
```

What is the most likely number of defective boards the inspector will find?

```
defects=0:200;
y = binopdf(defects,200,.02);
```

```
[x,i]=max(y);
defects(i)
ans =
  4
```

See Also

pdf | binoinv | binocdf | binofit | binostat | binornd

How To

- “Binomial Distribution” on page B-7

Purpose

Binomial random numbers

Syntax

```
R = binornd(N,P)
R = binornd(N,P,m,n,...)
R = binornd(N,P,[m,n,...])
```

Description

`R = binornd(N,P)` generates random numbers from the binomial distribution with parameters specified by the number of trials, `N`, and probability of success for each trial, `P`. `N` and `P` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `N` or `P` is expanded to a constant array with the same dimensions as the other input.

`R = binornd(N,P,m,n,...)` or `R = binornd(N,P,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the binomial distribution with parameters `N` and `P`. `N` and `P` can each be scalars or arrays of the same size as `R`.

Algorithms

The `binornd` function uses the direct method using the definition of the binomial distribution as a sum of Bernoulli random variables.

Examples

```
n = 10:10:60;

r1 = binornd(n,1./n)
r1 =
   2   1   0   1   1   2

r2 = binornd(n,1./n,[1 6])
r2 =
   0   1   2   1   3   1

r3 = binornd(n,1./n,1,6)
r3 =
   0   1   1   1   0   3
```

See Also

`random` | `binoinv` | `binocdf` | `binofit` | `binostat` | `binopdf`

How To

- "Binomial Distribution" on page B-7

Purpose

Binomial mean and variance

Syntax

```
[M,V] = binostat(N,P)
```

Description

`[M,V] = binostat(N,P)` returns the mean of and variance for the binomial distribution with parameters specified by the number of trials, `N`, and probability of success for each trial, `P`. `N` and `P` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `M` and `V`. A scalar input for `N` or `P` is expanded to a constant array with the same dimensions as the other input.

The mean of the binomial distribution with parameters n and p is np. The variance is npq, where $q = 1–p$.

Examples

```
n = logspace(1,5,5)
n =
     10     100    1000    10000   100000

[m,v] = binostat(n,1./n)
m =
   1   1   1   1   1
v =
  0.9000  0.9900  0.9990  0.9999  1.0000

[m,v] = binostat(n,1/2)
m =
      5     50     500    5000    50000
v =
  1.0e+04 *
  0.0003  0.0025  0.0250  0.2500  2.5000
```

See Also

`binoinv` | `binocdf` | `binofit` | `binornd` | `binopdf`

How To

- "Binomial Distribution" on page B-7

biplot

Purpose

Biplot

Syntax

```
biplot(coefs)
h = biplot(coefs,'Name',Value)
```

Description

`biplot(coefs)` creates a biplot of the coefficients in the matrix `coefs`. The biplot is 2-D if `coefs` has two columns or 3-D if it has three columns. `coefs` usually contains principal component coefficients created with `princomp`, `pcacov`, or factor loadings estimated with `factoran`. The axes in the biplot represent the principal components or latent factors (columns of `coefs`), and the observed variables (rows of `coefs`) are represented as vectors.

A biplot allows you to visualize the magnitude and sign of each variable's contribution to the first two or three principal components, and how each observation is represented in terms of those components.

`biplot` imposes a sign convention, forcing the element with largest magnitude in each column of coefs to be positive. This flips some of the vectors in coefs to the opposite direction, but often makes the plot easier to read. Interpretation of the plot is unaffected, because changing the sign of a coefficient vector does not change its meaning.

`h = biplot(coefs,'Name',Value)` specifies one or more name/value input pairs and returns a column vector of handles to the graphics objects created by `biplot`. The `h` contains, in order, handles corresponding to variables (line handles, followed by marker handles, followed by text handles), to observations (if present, marker handles followed by text handles), and to the axis lines.

Input Arguments

Name-Value Pair Arguments

`Scores`

Plots both `coefs` and the `scores` in the matrix `scores` in the biplot. `scores` usually contains principal component scores created with `princomp` or factor scores estimated with `factoran`.

Each observation (row of scores) is represented as a point in the biplot.

`VarLabels`

Labels each vector (variable) with the text in the character array or cell array `varlabels`.

`ObsLabels`

Uses the text in the character array or cell array `obslabels` as observation names when displaying data cursors.

`Positive`

- `'true'` — restricts the biplot to the positive quadrant (in 2-D) or octant (in 3-D).
- `'false'` — makes the biplot over the range `+/- max(coefs(:))` for all coordinates.

Default: `false`

`PropertyName`

Specifies optional property name/value pairs for all `line` graphics objects created by `biplot`.

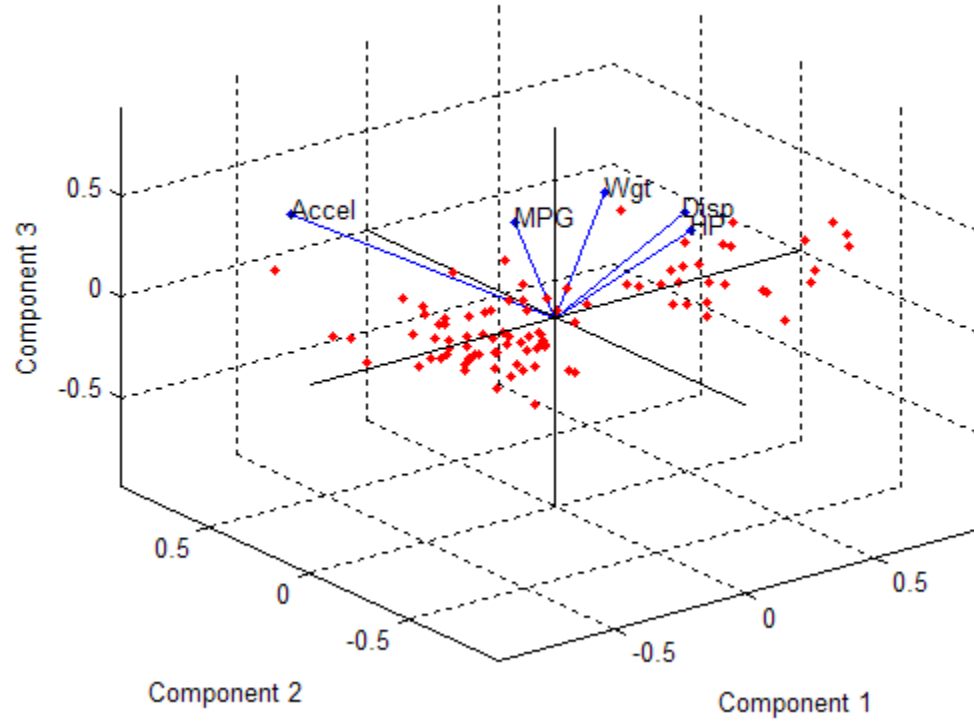
Examples

Perform a principal component analysis of the data in `carsmall.mat`:

```
load carsmall
x = [Acceleration Displacement Horsepower MPG Weight];
x = x(all(~isnan(x),2),:);

[coefs,score] = princomp(zscore(x));
```

View the data and the original variables in the space of the first three principal components:

```
vbls = {'Accel','Disp','HP','MPG','Wgt'};
biplot(coefs(:,1:3),'scores',score(:,1:3),...
                    'varlabels',vbls);
```



See Also

`factoran` | `nnmf` | `princomp` | `pcacov` | `rotatefactors`

Purpose

Bootstrap confidence interval

Syntax

```
ci = bootci(nboot,bootfun,...)
ci = bootci(nboot,{bootfun,...},'alpha',alpha)
ci = bootci(nboot,{bootfun,...},...,'type',type)
ci = bootci(nboot,{bootfun,...},...,'type','student',
   'nbootstd',nbootstd)
ci = bootci(nboot,{bootfun,...},...,'type','student','stderr',
   stderr)
ci = bootci(nboot,{bootfun,...},...,'Weights',weights)
ci = bootci(nboot,{bootfun,...},...,'Options',options)
[ci,bootstat] = bootci(...)
```

Description

`ci = bootci(nboot,bootfun,...)` computes the 95% bootstrap confidence interval of the statistic computed by the function `bootfun`. `nboot` is a positive integer indicating the number of bootstrap samples used in the computation. `bootfun` is a function handle specified with `@`, and must return a scalar. The third and later input arguments to `bootci` are data (scalars, column vectors, or matrices) that are used to create inputs to `bootfun`. `bootci` creates each bootstrap sample by sampling with replacement from the rows of the non-scalar data arguments (these must have the same number of rows). Scalar data are passed to `bootfun` unchanged.

If `bootfun` returns a scalar, `ci` is a vector containing the lower and upper bounds of the confidence interval. If `bootfun` returns a vector of length *m*, `ci` is an array of size 2-by-*m*, where `ci(1,:)` are lower bounds and `ci(2,:)` are upper bounds. If `bootfun` returns an array of size *m*-by-*n*-by-*p*-by-..., `ci` is an array of size 2-by-*m*-by-*n*-by-*p*-by-..., where `ci(1,:,:,:,...)` is an array of lower bounds and `ci(2,:,:,:,...)` is an array of upper bounds.

`ci = bootci(nboot,{bootfun,...},'alpha',alpha)` computes the `100*(1-alpha)` bootstrap confidence interval of the statistic defined by the function `bootfun`. `bootfun` and the data that `bootci` passes to it are contained in a single cell array. `alpha` is a scalar between `0` and `1`. The default value of `alpha` is `0.05`.

`ci = bootci(nboot,{bootfun,...},...,'type',type)` computes the bootstrap confidence interval of the statistic defined by the function `bootfun`. *`type`* is the confidence interval type, chosen from among the following strings:

- `'norm'` or `'normal'` — Normal approximated interval with bootstrapped bias and standard error.
- `'per'` or `'percentile'` — Basic percentile method.
- `'cper'` or `'corrected percentile'` — Bias corrected percentile method.
- `'bca'` — Bias corrected and accelerated percentile method. This is the default.
- `'stud'` or `'student'` — Studentized confidence interval.

`ci = bootci(nboot,{bootfun,...},...,'type','student','nbootstd',nbootstd)` computes the studentized bootstrap confidence interval of the statistic defined by the function `bootfun`. The standard error of the bootstrap statistics is estimated using bootstrap, with `nbootstd` bootstrap data samples. `nbootstd` is a positive integer value. The default value of `nbootstd` is `100`.

`ci = bootci(nboot,{bootfun,...},...,'type','student','stderr',stderr)` computes the studentized bootstrap confidence interval of statistics defined by the function `bootfun`. The standard error of the bootstrap statistics is evaluated by the function `stderr`. `stderr` is a function handle. `stderr` takes the same arguments as `bootfun` and returns the standard error of the statistic computed by `bootfun`.

`ci = bootci(nboot,{bootfun,...},...,'Weights',weights)` specifies observation weights. `weights` must be a vector of non-negative numbers with at least one positive element. The number of elements in `weights` must be equal to the number of rows in non-scalar input arguments to `bootfun`. To obtain one bootstrap replicate,

`bootstrp` samples *N* out of *N* with replacement using these weights as multinomial sampling probabilities.

`ci = bootci(nboot,{bootfun,...},...,'Options',options)` specifies options that govern the computation of bootstrap iterations. One option requests that `bootci` perform bootstrap iterations using multiple processors, if the Parallel Computing Toolbox is available. Two options specify the random number streams to be used in bootstrap resampling. This argument is a struct that you can create with a call to `statset`. You can retrieve values of the individual fields with a call to `statget`. Applicable `statset` parameters are:

- `'UseParallel'` — If `'always'` and if a `matlabpool` of the Parallel Computing Toolbox is open, compute bootstrap iterations in parallel. If the Parallel Computing Toolbox is not installed, or a `matlabpool` is not open, computation occurs in serial mode. Default is `'never'`, or serial computation.
- `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. Default is `'never'`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
- `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `bootci` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case
  - You have an open MATLAB pool
  - `UseParallel` is `'always'`
  - `UseSubstreams` is `'never'`

  In that case, use a cell array the same size as the MATLAB pool.

For more information on using parallel computing, see Chapter 17, “Parallel Statistics”.

`[ci,bootstat] = bootci(...)` also returns the bootstrapped statistic computed for each of the `nboot` bootstrap replicate samples. Each row of `bootstat` contains the results of applying `bootfun` to one bootstrap

sample. If `bootfun` returns a matrix or array, then this output is converted to a row vector for storage in `bootstat`.

Examples

Compute the confidence interval for the capability index in statistical process control:

```
y = normrnd(1,1,30,1);                % Simulated process data
LSL = -3; USL = 3;                    % Process specifications
capable = @(x)(USL-LSL)./(6* std(x)); % Process capability
ci = bootci(2000,capable,y)           % BCa confidence interval
ci =
    0.8122
    1.2657

sci = bootci(2000,{capable,y},'type','student') % Studentized ci
sci =
    0.7739
    1.2707
```

See Also

`bootstrp` | `jackknife` | `statget` | `statset` | `randsample` | `parfor`

Purpose

Bootstrap sampling

Syntax

```
bootstat = bootstrp(nboot,bootfun,d1,...)
[bootstat,bootsam] = bootstrp(...)
bootstat = bootstrp(...,'Name',Value)
```

Description

`bootstat = bootstrp(nboot,bootfun,d1,...)` draws `nboot` bootstrap data samples, computes statistics on each sample using `bootfun`, and returns the results in the matrix `bootstat`. `nboot` must be a positive integer. `bootfun` is a function handle specified with `@`. Each row of `bootstat` contains the results of applying `bootfun` to one bootstrap sample. If `bootfun` returns a matrix or array, then this output is converted to a row vector for storage in `bootstat`.

The third and later input arguments (`d1,...`) are data (scalars, column vectors, or matrices) used to create inputs to `bootfun`. `bootstrp` creates each bootstrap sample by sampling with replacement from the rows of the non-scalar data arguments (these must have the same number of rows). `bootfun` accepts scalar data unchanged.

`[bootstat,bootsam] = bootstrp(...)` returns an `n`-by-`nboot` matrix of bootstrap indices, `bootsam`. Each column in `bootsam` contains indices of the values that were drawn from the original data sets to constitute the corresponding bootstrap sample. For example, if `d1,...` each contain 16 values, and `nboot = 4`, then `bootsam` is a 16-by-4 matrix. The first column contains the indices of the 16 values drawn from `d1,...`, for the first of the four bootstrap samples, the second column contains the indices for the second of the four bootstrap samples, and so on. (The bootstrap indices are the same for all input data sets.) To get the output samples `bootsam` without applying a function, set `bootfun` to empty (`[]`).

`bootstat = bootstrp(...,'Name',Value)` uses additional arguments specified by one or more `Name,Value` pair arguments. The name-value pairs must appear after the data arguments. The available name-value pairs:

- `'Weights'` — Observation weights. The `weights` value must be a vector of nonnegative numbers with at least one positive element. The number of elements in `weights` must be equal to the number of rows in non-scalar input arguments to `bootstrp`. To obtain one bootstrap replicate, `bootstrp` samples *N* out of *N* with replacement using these weights as multinomial sampling probabilities.
- `'Options'` — The value is a structure that contains options specifying whether to compute bootstrap iterations in parallel, and specifying how to use random numbers during the bootstrap sampling. Create the options structure with `statset`. Applicable `statset` parameters are:
  - `'UseParallel'` — If `'always'` and if a `matlabpool` of the Parallel Computing Toolbox is open, compute bootstrap iterations in parallel. If the Parallel Computing Toolbox is not installed, or a `matlabpool` is not open, computation occurs in serial mode. Default is `'never'`, meaning serial computation.
  - `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. Default is `'never'`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
  - `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `bootstrp` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case
    - You have an open MATLAB pool
    - `UseParallel` is `'always'`
    - `UseSubstreams` is `'never'`

    In that case, use a cell array the same size as the MATLAB pool.

  For more information on using parallel computing, see Chapter 17, "Parallel Statistics".

Examples

Bootstrapping a Correlation Coefficient Standard Error

Load a data set containing the LSAT scores and law-school GPA for 15 students. These 15 data points are resampled to create 1000 different data sets, and the correlation between the two variables is computed for each data set.

```
load lawdata
[bootstat,bootsam] = bootstrp(1000,@corr,lsat,gpa);
```

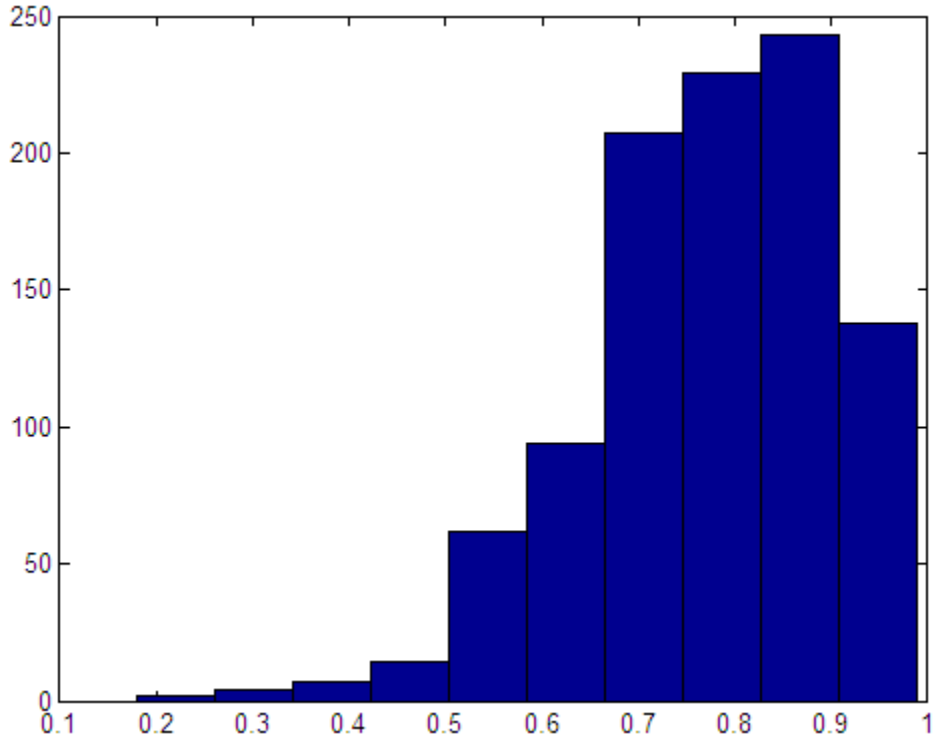
Display the first 5 bootstrapped correlation coefficients.

```
bootstat(1:5,:)
ans =
    0.6600
    0.7969
    0.5807
    0.8766
    0.9197
```

Display the indices of the data selected for the first 5 bootstrap samples.

```
bootsam(:,1:5)
ans =
     9     8    15    11    15
    14     7     6     7    14
     4     6    10     3    11
     3    10    11     9     2
    15     4    13     4    14
     9     4     5     2    10
     8     5     4     3    13
     1     9     1    15    11
    10     8     6    12     3
     1     4     5     2     8
     1     1    10     6     2
     3    10    15    10     8
    14     6    10     3     8
    13    12     1     2     4
    12     6     4     9     8
```

```
hist(bootstat)
```



The histogram shows the variation of the correlation coefficient across all the bootstrap samples. The sample minimum is positive, indicating that the relationship between LSAT score and GPA is not accidental.

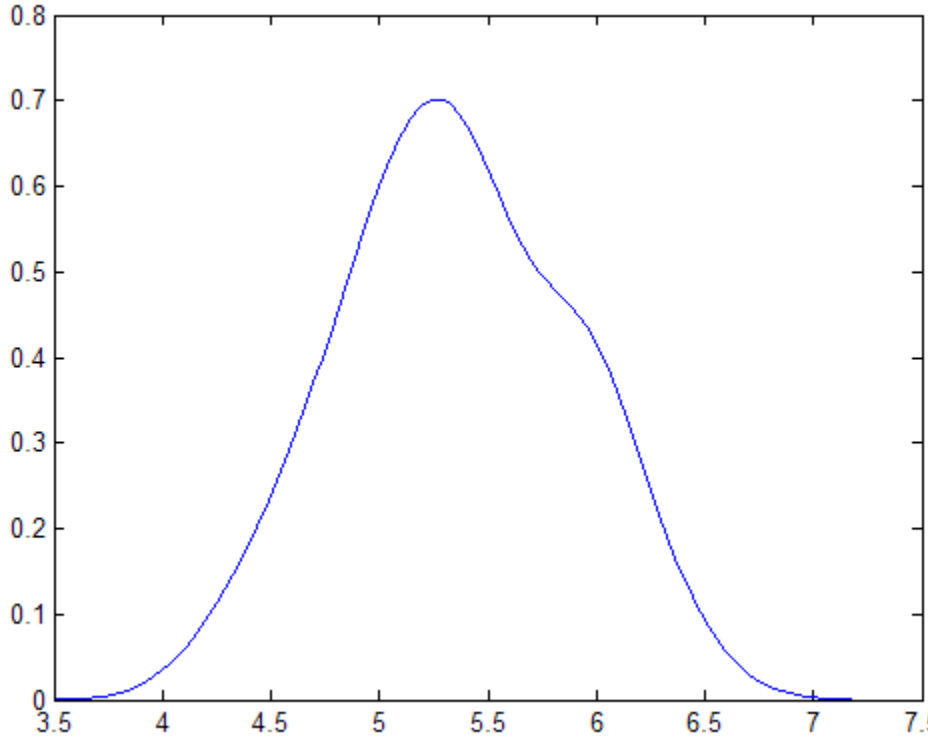
Finally, compute a bootstrap standard of error for the estimated correlation coefficient.

```
se = std(bootstat)
se =
    0.1327
```

Estimating the Density of Bootstrapped Statistic

Compute a sample of 100 bootstrapped means of random samples taken from the vector Y, and plot an estimate of the density of these bootstrapped means:

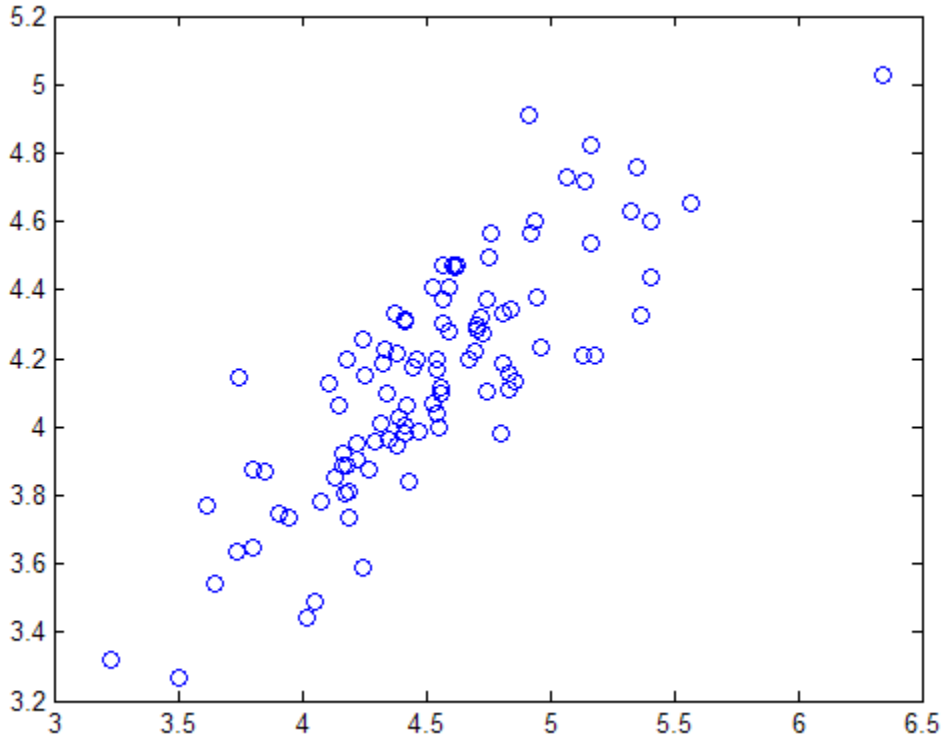
```
y = exprnd(5,100,1);
m = bootstrp(100,@mean,y);
[fi,xi] = ksdensity(m);
plot(xi,fi);
```



Bootstrapping More Than One Statistic

Compute a sample of 100 bootstrapped means and standard deviations of random samples taken from the vector Y, and plot the bootstrap estimate pairs:

```
y = exprnd(5,100,1);
stats = bootstrp(100,@(x)[mean(x) std(x)],y);
plot(stats(:,1),stats(:,2),'o')
```



Bootstrapping a Regression Model

Estimate the standard errors for a coefficient vector in a linear regression by bootstrapping residuals:

```
load hald
x = [ones(size(heat)),ingredients];
y = heat;
b = regress(y,x);
yfit = x*b;
resid = y - yfit;
se = std(bootstrp(...
         1000,@(bootr)regress(yfit+bootr,x),resid));
```

See Also

hist | bootci | ksdensity | parfor | random | randsample | RandStream | statget | statset

boxplot

Purpose

Box plot

Syntax

```
boxplot(X)
boxplot(X,G)
boxplot(axes,X,...)
boxplot(...,'Name',value)
```

Description

`boxplot(X)` produces a box plot of the data in `X`. If `X` is a matrix, there is one box per column; if `X` is a vector, there is just one box. On each box, the central mark is the median, the edges of the box are the 25th and 75th percentiles, the whiskers extend to the most extreme data points not considered outliers, and outliers are plotted individually.

`boxplot(X,G)` specifies one or more grouping variables `G`, producing a separate box for each set of `X` values sharing the same `G` value or values (see "Grouped Data" on page 2-34). Grouping variables must have one row per element of `X`, or one row per column of `X`. Specify a single grouping variable in `G` using a vector, a character array, a cell array of strings, or a vector categorical array; specify multiple grouping variables in `G` using a cell array of these variable types, such as `{G1 G2 G3}`, or by using a matrix. If multiple grouping variables are used, they must all be the same length. Groups that contain a `NaN` value or an empty string in a grouping variable are omitted, and are not counted in the number of groups considered by other parameters.

By default, character and string grouping variables are sorted in the order they initially appear in the data, categorical grouping variables are sorted by the order of their levels, and numeric grouping variables are sorted in numeric order. To control the order of groups, do one of the following:

- Use categorical variables in `G` and specify the order of their levels.
- Use the `'grouporder'` parameter described below.
- Pre-sort your data.

`boxplot(axes,X,...)` creates the plot in the axes with handle `axes`.

`boxplot(...,'Name',value)` specifies one or more optional parameter name/value pairs, as described in the following table. Specify *`Name`* in single quotes.

Name	Value
`plotstyle`	• `'traditional'` — Traditional box style. This is the default. • `'compact'` — Box style designed for plots with many groups. This style changes the defaults for some other parameters, as described in the following table.
`boxstyle`	• `'outline'` — Draws an unfilled box with dashed whiskers. This is the default. • `'filled'` — Draws a narrow filled box with lines for whiskers.
`colorgroup`	One or more grouping variables, of the same type as permitted for `G`, specifying that the box color should change when the specified variables change. The default is `[]` for no box color change.
`colors`	Colors for boxes, specified as a single color (such as `'r'` or `[1 0 0]`) or multiple colors (such as `'rgbm'` or a three-column matrix of RGB values). The sequence is replicated or truncated as required, so for example `'rb'` gives boxes that alternate in color. The default when no `'colorgroup'` is specified is to use the same color scheme for all boxes. The default when `'colorgroup'` is specified is a modified `hsv colormap`.

Name	Value
`datalim`	A two-element vector containing lower and upper limits, used by `'extrememode'` to determine which points are extreme. The default is `[-Inf Inf]`.
`extrememode`	• `'clip'` — Moves data outside the `datalim` limits to the limit. This is the default. • `'compress'` — Evenly distributes data outside the `datalim` limits in a region just outside the limit, retaining the relative order of the points. A dotted line marks the limit if any points are outside it, and two gray lines mark the compression region if any points are compressed. Values at +/–`Inf` can be clipped or compressed, but `NaN` values still do not appear on the plot. Box notches are drawn to scale and may extend beyond the bounds if the median is inside the limit; they are not drawn if the median is outside the limits.
`factordirection`	• `'data'` — Arranges factors with the first value next to the origin. This is the default. • `'list'` — Arranges factors left-to-right if on the *x* axis or top-to-bottom if on the *y* axis. • `'auto'` — Uses `'data'` for numeric grouping variables and `'list'` for strings.

Name	Value
`fullfactors`	• `'off'` — One group for each unique row of `G`. This is the default. • `'on'` — Create a group for each possible combination of group variable values, including combinations that do not appear in the data.
`factorseparator`	Specifies which factors should have their values separated by a grid line. The value may be `'auto'` or a vector of grouping variable numbers. For example, `[1 2]` adds a separator line when the first or second grouping variable changes value. `'auto'` is `[]` for one grouping variable and `[1]` for two or more grouping variables. The default is `[]`.
`factorgap`	Specifies an extra gap to leave between boxes when the corresponding grouping factor changes value, expressed as a percentage of the width of the plot. For example, with `[3 1]`, the gap is 3% of the width of the plot between groups with different values of the first grouping variable, and 1% between groups with the same value of the first grouping variable but different values for the second. `'auto'` specifies that `boxplot` should choose a gap automatically. The default is `[]`.
`grouporder`	Order of groups for plotting, specified as a cell array of strings. With multiple grouping variables, separate values within each string with a comma. Using categorical arrays as grouping variables is an easier way to control the order of the boxes. The default is `[]`, which does not reorder the boxes.

Name	Value
`jitter`	Maximum distance *d* to displace outliers along the factor axis by a uniform random amount, in order to make duplicate points visible. A *d* of `1` makes the jitter regions just touch between the closest adjacent groups. The default is `0`.
`labels`	A character array, cell array of strings, or numeric vector of box labels. There may be one label per group or one label per `X` value. Multiple label variables may be specified via a numeric matrix or a cell array containing any of these types. **Tip** To remove labels from a plot, use the following command: `set(gca,'XTickLabel',{' '})`
`labelorientation`	• `'inline'` — Rotates the labels to be vertical. This is the default when `plotstyle` is `'compact'`. • `'horizontal'` — Leaves the labels horizontal. This is the default when `plotstyle` has the default value of `'traditional'`. When the labels are on the *y* axis, both settings leave the labels horizontal.

Name	Value
`labelverbosity`	• `'all'` — Displays every label. This is the default. • `'minor'` — Displays a label for a factor only when that factor has a different value from the previous group. • `'majorminor'` — Displays a label for a factor when that factor or any factor major to it has a different value from the previous group.
`medianstyle`	• `'line'` — Draws a line for the median. This is the default. • `'target'` — Draws a black dot inside a white circle for the median.
`notch`	• `'on'` — Draws comparison intervals using notches when `plotstyle` is `'traditional'`, or triangular markers when `plotstyle` is `'compact'`. • `'marker'` — Draws comparison intervals using triangular markers. • `'off'` — Omits notches. This is the default. Two medians are significantly different at the 5% significance level if their intervals do not overlap. Interval endpoints are the extremes of the notches or the centers of the triangular markers. When the sample size is small, notches may extend beyond the end of the box.
`orientation`	• `'vertical'` — Plots `X` on the *y* axis. This is the default. • `'horizontal'` — Plots `X` on the *x* axis.

Name	Value
`outliersize`	Size of the marker used for outliers, in points. The default is `6` (6/72 inch).
`positions`	Box positions specified as a numeric vector with one entry per group or `X` value. The default is `1:numGroups`, where `numGroups` is the number of groups.
`symbol`	Symbol and color to use for outliers, using the same values as the `LineSpec` parameter in `plot`. The default is `'r+'`. If the symbol is omitted then the outliers are invisible; if the color is omitted then the outliers have the same color as their corresponding box.
`whisker`	Maximum whisker length w. The default is a w of `1.5`. Points are drawn as outliers if they are larger than $q_3 + w(q_3 - q_1)$ or smaller than $q_1 - w(q_3 - q_1)$, where q_1 and q_3 are the 25th and 75th percentiles, respectively. The default of `1.5` corresponds to approximately +/–2.7σ and 99.3 coverage if the data are normally distributed. The plotted whisker extends to the *adjacent value*, which is the most extreme data value that is not an outlier. Set `whisker` to `0` to give no whiskers and to make every point outside of q_1 and q_3 an outlier.
`widths`	A scalar or vector of box widths for when `boxstyle` is `'outline'`. The default is half of the minimum separation between boxes, which is `0.5` when the `positions` argument takes its default value. The list of values is replicated or truncated as necessary.

When the `plotstyle` parameter takes the value `'compact'`, the following default values for other parameters apply.

Parameter	Default when `plotstyle` is `'compact'`
`boxstyle`	`'filled'`
`factorseparator`	`'auto'`
`factorgap`	`'auto'`
`jitter`	`0.5`
`labelorientation`	`'inline'`
`labelverbosity`	`'majorminor'`
`medianstyle`	`'target'`
`outliersize`	`4`
`symbol`	`'o'`

You can see data values and group names using the data cursor in the figure window. The cursor shows the original values of any points affected by the `datalim` parameter. You can label the group to which an outlier belongs using the `gname` function.

To modify graphics properties of a box plot component, use `findobj` with the `Tag` property to find the component's handle. `Tag` values for box plot components depend on parameter settings, and are listed in the table below.

Parameter Settings	`Tag` Values
All settings	• `'Box'` • `'Outliers'`
When `plotstyle` is `'traditional'`	• `'Median'` • `'Upper Whisker'` • `'Lower Whisker'` • `'Upper Adjacent Value'` • `'Lower Adjacent Value'`

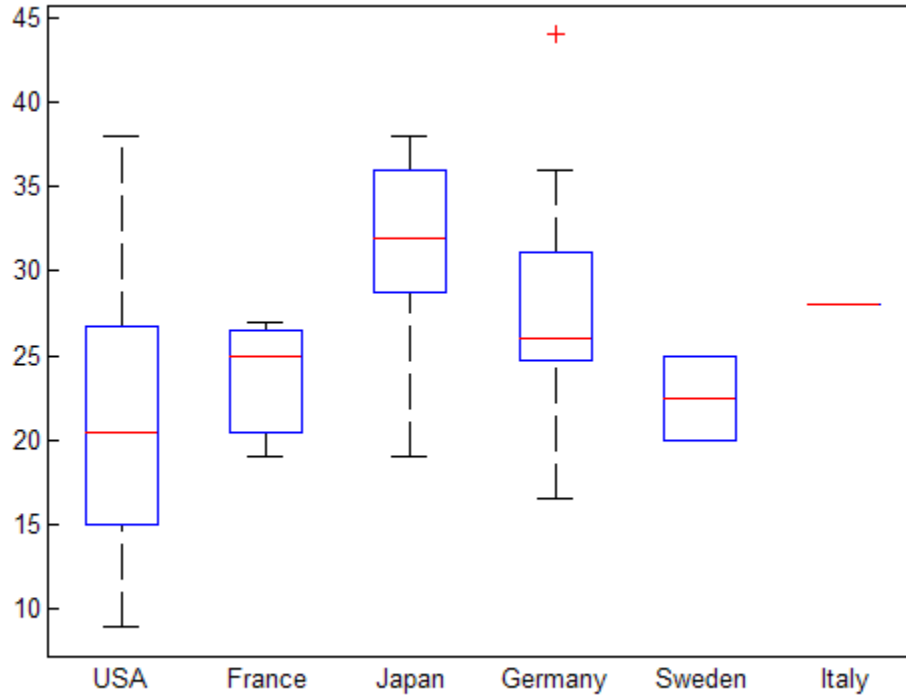
Parameter Settings	`Tag` Values
When `plotstyle` is `'compact'`	• `'Whisker'` • `'MedianOuter'` • `'MedianInner'`
When `notch` is `'marker'`	• `'NotchLo'` • `'NotchHi'`

Examples

Example 1

Create a box plot of car mileage, grouped by country:

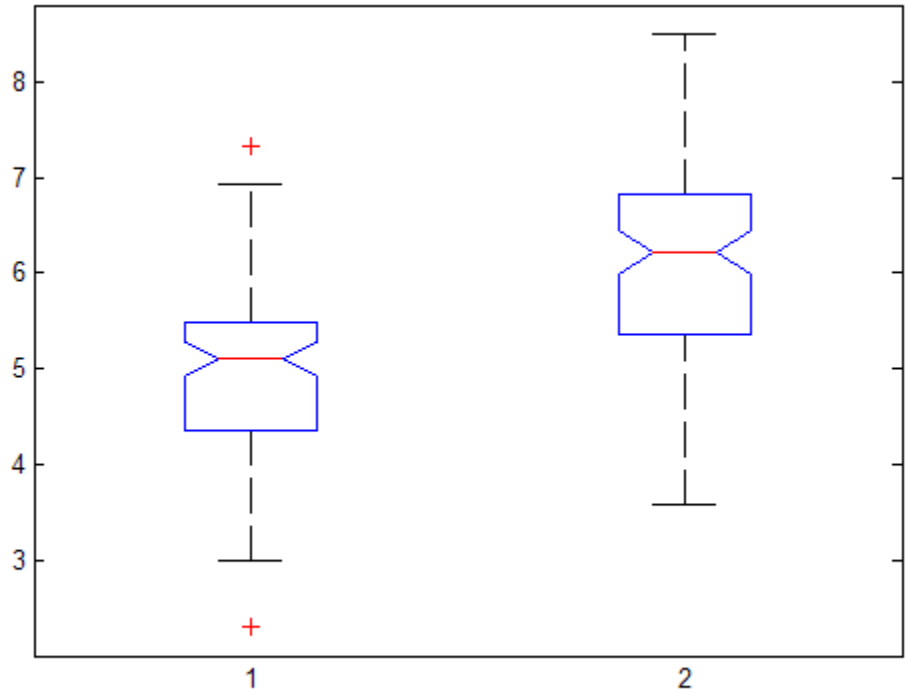
```
load carsmall
boxplot(MPG,Origin)
```



Example 2

Create notched box plots for two groups of sample data:

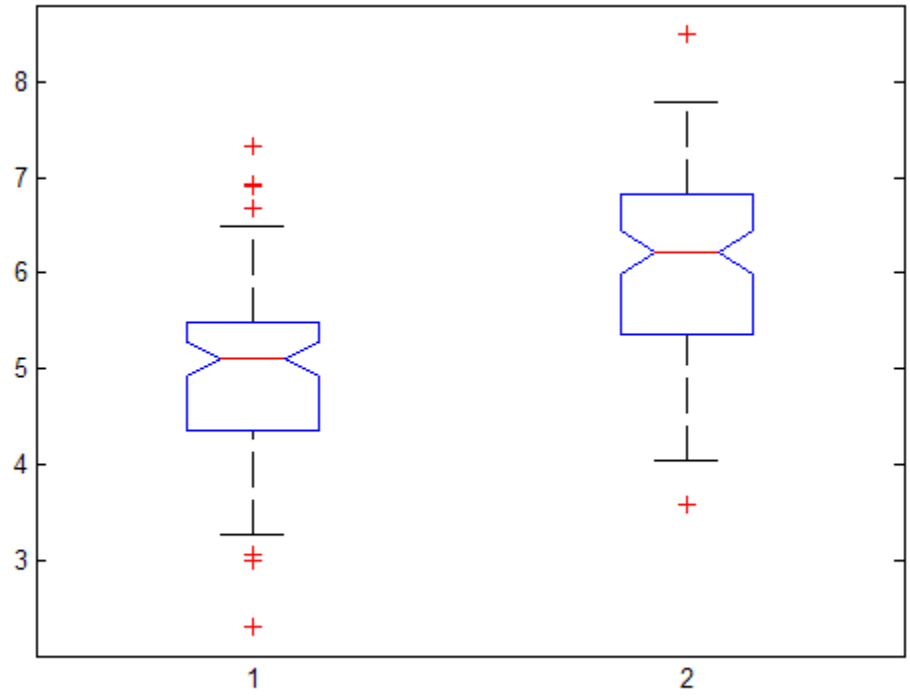
```
x1 = normrnd(5,1,100,1);
x2 = normrnd(6,1,100,1);
boxplot([x1,x2],'notch','on')
```



The difference between the medians of the two groups is approximately 1. Since the notches in the box plot do not overlap, you can conclude, with 95% confidence, that the true medians do differ.

The following figure shows the box plot for the same data with the length of the whiskers specified as 1.0 times the interquartile range. Points beyond the whiskers are displayed using +.

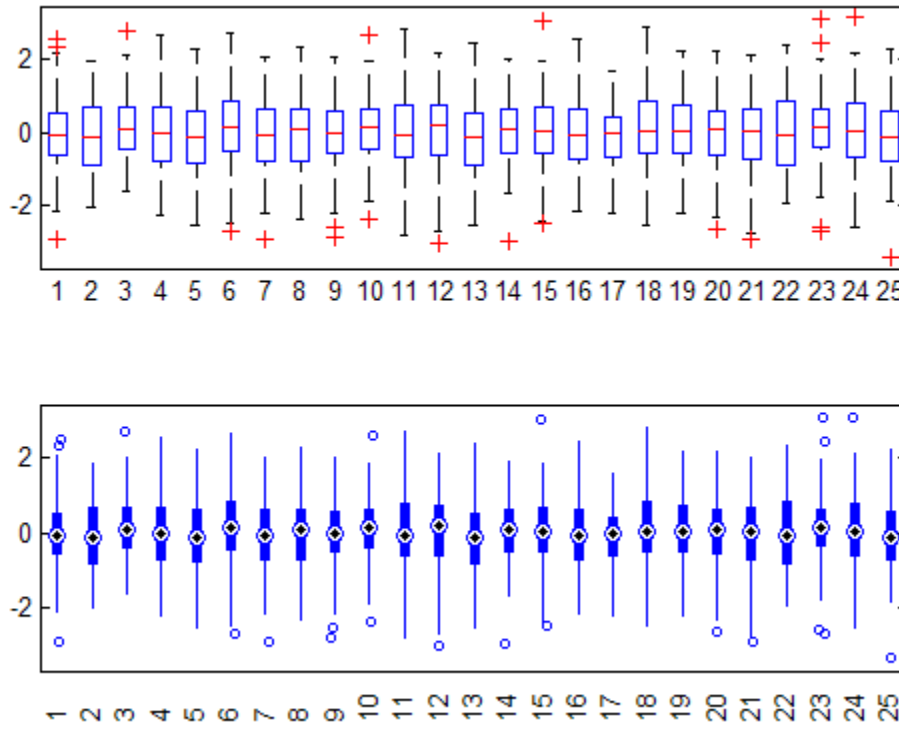
```
boxplot([x1,x2],'notch','on','whisker',1)
```



Example 3

A `plotstyle` of `'compact'` is useful for large numbers of groups:

```
X = randn(100,25);

subplot(2,1,1)
boxplot(X)

subplot(2,1,2)
boxplot(X,'plotstyle','compact')
```



References

[1] McGill, R., J. W. Tukey, and W. A. Larsen. "Variations of Boxplots." *The American Statistician*. Vol. 32, No. 1, 1978, pp. 12–16.

[2] Velleman, P.F., and D.C. Hoaglin. *Applications, Basics, and Computing of Exploratory Data Analysis*. Pacific Grove, CA: Duxbury Press, 1981.

[3] Nelson, L. S. "Evaluating Overlapping Confidence Intervals." *Journal of Quality Technology*. Vol. 21, 1989, pp. 140–141.

See Also

anova1 | axes_props | kruskalwallis | multcompare

How To

- “Grouped Data” on page 2-34

piecewisedistribution.boundary

Purpose

Piecewise distribution boundaries

Syntax

```
[p,q] = boundary(obj)
[p,q] = boundary(obj,i)
```

Description

`[p,q] = boundary(obj)` returns the boundary points between segments of the piecewise distribution object, `obj`. `p` is a vector of cumulative probabilities at each boundary. `q` is a vector of quantiles at each boundary.

`[p,q] = boundary(obj,i)` returns `p` and `q` for the *i*th boundary.

Examples

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);
[p,q] = boundary(obj)
p =
    0.1000
    0.9000
q =
   -1.7766
    1.8432
```

See Also

`paretotails` | `cdf` | `icdf` | `nsegments`

Purpose

D-optimal design from candidate set using row exchanges

Syntax

```
rlist = candexch(C,nrows)
rlist = candexch(C,nrows,Name,Value)
```

Description

`rlist = candexch(C,nrows)` uses a row-exchange algorithm to select a *D*-optimal design from the candidate set `C`.

`rlist = candexch(C,nrows,Name,Value)` generates a *D*-optimal design with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`C`

`N`-by-`P` matrix containing the values of `P` model terms at each of `N` points.

`nrows`

The desired number of rows in the design.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`display`

When `'on'`, displays iteration number. Disable the display by setting to `'off'`.

Default: `'on'`, except when the `UseParallel` option is `'always'`

`init`

`nrows`-by-`P` matrix giving an initial design.

Default: A random subset of the rows of `C`

`maxiter`

Maximum number of iterations, a positive integer.

Default: `10`

`options`

A structure that specifies whether to run in parallel, and specifies the random stream or streams. Create the `options` structure with `statset`. Option fields:

- `UseParallel` — Set to `'always'` to compute in parallel. Default is `'never'`.
- `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. Default is `'never'`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
- `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `candexch` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case
  - You have an open MATLAB pool
  - `UseParallel` is `'always'`
  - `UseSubstreams` is `'never'`

  In that case, use a cell array the same size as the MATLAB pool.

For more information on using parallel computing, see Chapter 17, “Parallel Statistics”.

Default: `[]`

`start`

An `nobs`-by-*p* matrix of factor settings, specifying a set of `nobs` fixed design points to include in the design. `candexch` finds

`nrows` additional rows to add to the `start` design. The parameter provides the same functionality as the `daugment` function, using a row-exchange algorithm rather than a coordinate-exchange algorithm.

Default: `[]`

`tries`

Number of times to try to generate a design from a new starting point. The algorithm uses random points for each try, except possibly the first.

Default: `1`

Output Arguments

`rlist`

Vector of length `nrows` listing the selected rows.

Examples

This example shows how to generate a *D*-optimal design when there is a restriction on the candidate set, so the `rowexch` function isn't appropriate.

```
F = (fullfact([5 5 5])-1)/4; % factor settings in unit cube
T = sum(F,2)<=1.51;          % find rows matching a restriction
F = F(T,:);                  % take only those rows
C = [ones(size(F,1),1) F F.^2];
                             % compute model terms including
                             % a constant and all squared terms
R = candexch(C,12);          % find a D-optimal 12-point subset
X = F(R,:);                  % get factor settings
```

Algorithms

`candexch` selects a starting design `X` at random, and uses a row-exchange algorithm to iteratively replace rows of `X` by rows of `C` in an attempt to improve the determinant of `X'*X`.

Alternatives

The `rowexch` function also generates *D*-optimal designs using a row-exchange algorithm, but it automatically generates a candidate

set that is appropriate for a specified model. The `daugment` function augments a set of fixed design points using a coordinate-exchange algorithm; the `'start'` parameter provides the same functionality using the row exchange algorithm.

See Also

`candgen` | `rowexch` | `cordexch` | `daugment` | `x2fx`

Tutorials

- "Specifying Candidate Sets" on page 15-21

How To

- "D-Optimal Designs" on page 15-15

Purpose

Candidate set generation

Syntax

```
dC = candgen(nfactors,'model')
[dC,C] = candgen(nfactors,'model')
[...] = candgen(nfactors,'model','Name',value)
```

Description

`dC = candgen(nfactors,'model')` generates a candidate set `dC` of treatments appropriate for estimating the parameters in the *`model`* with `nfactors` factors. `dC` has `nfactors` columns and one row for each candidate treatment. *`model`* is one of the following strings, specified inside single quotes:

- `linear` — Constant and linear terms. This is the default.
- `interaction` — Constant, linear, and interaction terms
- `quadratic` — Constant, linear, interaction, and squared terms
- `purequadratic` — Constant, linear, and squared terms

Alternatively, *`model`* can be a matrix specifying polynomial terms of arbitrary order. In this case, *`model`* should have one column for each factor and one row for each term in the model. The entries in any row of *`model`* are powers for the factors in the columns. For example, if a model has factors `X1`, `X2`, and `X3`, then a row `[0 1 2]` in *`model`* specifies the term `(X1.^0).*(X2.^1).*(X3.^2)`. A row of all zeros in *`model`* specifies a constant term, which can be omitted.

`[dC,C] = candgen(nfactors,'model')` also returns the design matrix `C` evaluated at the treatments in `dC`. The order of the columns of `C` for a full quadratic model with n terms is:

1. The constant term
2. The linear terms in order 1, 2, ..., n
3. The interaction terms in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n–1, n)
4. The squared terms in order 1, 2, ..., n

Other models use a subset of these terms, in the same order.

Pass `C` to `candexch` to generate a *D*-optimal design using a coordinate-exchange algorithm.

`[...] = candgen(nfactors,'model','Name',value)` specifies one or more optional name/value pairs for the design. Valid parameters and their values are listed in the following table. Specify `Name` inside single quotes.

Name	Value
`bounds`	Lower and upper bounds for each factor, specified as a 2-by-`nfactors` matrix. Alternatively, this value can be a cell array containing `nfactors` elements, each element specifying the vector of allowable values for the corresponding factor.
`categorical`	Indices of categorical predictors.
`levels`	Vector of number of levels for each factor.

Note The `rowexch` function automatically generates a candidate set using `candgen`, and then creates a *D*-optimal design from that candidate set using `candexch`. Call `candexch` separately to specify your own candidate set to the row-exchange algorithm.

Examples

The following example uses `rowexch` to generate a five-run design for a two-factor pure quadratic model using a candidate set that is produced internally:

```
dRE1 = rowexch(2,5,'purequadratic','tries',10)
dRE1 =
    -1     1
     0     0
     1    -1
     1     0
```

```
     1     1
```

The same thing can be done using `candgen` and `candexch` in sequence:

```
[dC,C] = candgen(2,'purequadratic') % Candidate set, C
dC =
    -1    -1
     0    -1
     1    -1
    -1     0
     0     0
     1     0
    -1     1
     0     1
     1     1
C =
     1    -1    -1     1     1
     1     0    -1     0     1
     1     1    -1     1     1
     1    -1     0     1     0
     1     0     0     0     0
     1     1     0     1     0
     1    -1     1     1     1
     1     0     1     0     1
     1     1     1     1     1
treatments = candexch(C,5,'tries',10) % Find D-opt subset
treatments =
     2
     1
     7
     3
     4
dRE2 = dC(treatments,:) % Display design
dRE2 =
     0    -1
    -1    -1
    -1     1
```

```
     1    -1
    -1     0
```

See Also

candexch | rowexch

Purpose

Canonical correlation

Syntax

```
[A,B] = canoncorr(X,Y)
[A,B,r] = canoncorr(X,Y)
[A,B,r,U,V] = canoncorr(X,Y)
[A,B,r,U,V,stats] = canoncorr(X,Y)
```

Description

`[A,B] = canoncorr(X,Y)` computes the sample canonical coefficients for the `n`-by-`d1` and `n`-by-`d2` data matrices `X` and `Y`. `X` and `Y` must have the same number of observations (rows) but can have different numbers of variables (columns). `A` and `B` are `d1`-by-`d` and `d2`-by-`d` matrices, where `d = min(rank(X),rank(Y))`. The `j`th columns of `A` and `B` contain the canonical coefficients, i.e., the linear combination of variables making up the `j`th canonical variable for `X` and `Y`, respectively. Columns of `A` and `B` are scaled to make the covariance matrices of the canonical variables the identity matrix (see `U` and `V` below). If `X` or `Y` is less than full rank, `canoncorr` gives a warning and returns zeros in the rows of `A` or `B` corresponding to dependent columns of `X` or `Y`.

`[A,B,r] = canoncorr(X,Y)` also returns a 1-by-`d` vector containing the sample canonical correlations. The `j`th element of `r` is the correlation between the *j*th columns of `U` and `V` (see below).

`[A,B,r,U,V] = canoncorr(X,Y)` also returns the canonical variables, scores. `U` and `V` are `n`-by-`d` matrices computed as

```
U = (X-repmat(mean(X),N,1))*A
V = (Y-repmat(mean(Y),N,1))*B
```

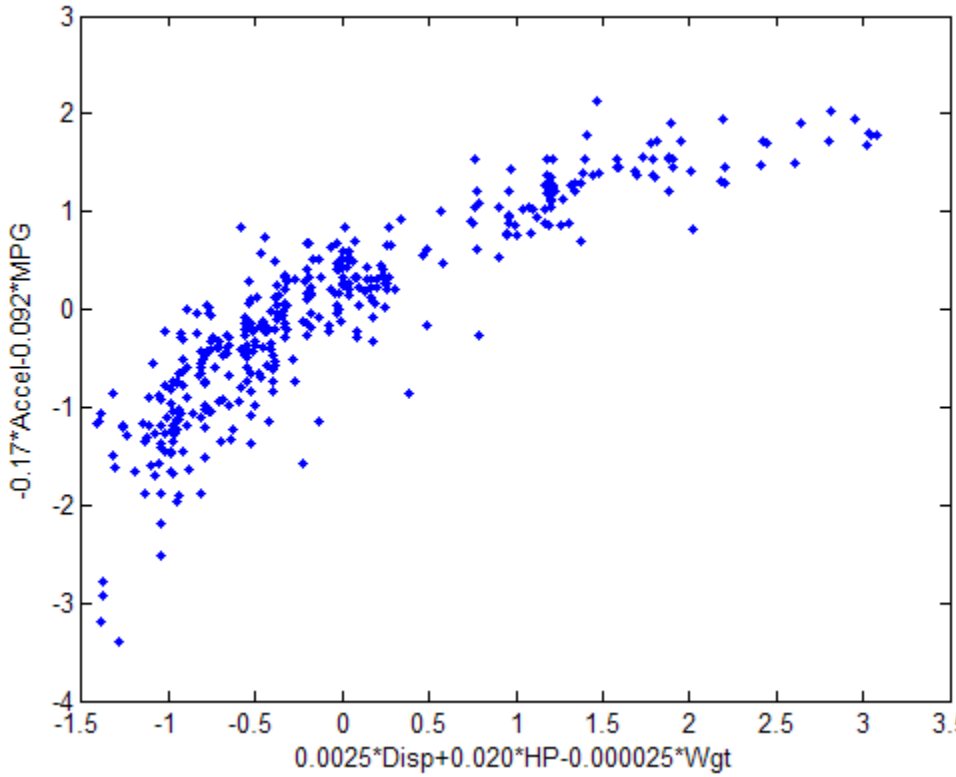
`[A,B,r,U,V,stats] = canoncorr(X,Y)` also returns a structure `stats` containing information relating to the sequence of `d` null

hypotheses $H_0^{(k)}$, that the (`k`+1)st through `d`th correlations are all zero, for `k = 0:(d-1)`. `stats` contains seven fields, each a `1`-by-`d` vector with elements corresponding to the values of `k`, as described in the following table:

Field	Description
`Wilks`	Wilks' lambda (likelihood ratio) statistic
`chisq`	Bartlett's approximate chi-squared statistic for $H_0^{(k)}$ with Lawley's modification
`pChisq`	Right-tail significance level for `chisq`
`F`	Rao's approximate F statistic for $H_0^{(k)}$
`pF`	Right-tail significance level for `F`
`df1`	Degrees of freedom for the chi-squared statistic, and the numerator degrees of freedom for the F statistic
`df2`	Denominator degrees of freedom for the F statistic

Examples

```
load carbig;
X = [Displacement Horsepower Weight Acceleration MPG];
nans = sum(isnan(X),2) > 0;
[A B r U V] = canoncorr(X(~nans,1:3),X(~nans,4:5));

plot(U(:,1),V(:,1),'.')
xlabel('0.0025*Disp+0.020*HP-0.000025*Wgt')
ylabel('-0.17*Accel-0.092*MPG')
```



References

[1] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

[2] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

See Also

`manova1` | `princomp`

Purpose

Process capability indices

Syntax

```
S = capability(data,specs)
```

Description

`S = capability(data,specs)` estimates capability indices for measurements in `data` given the specifications in `specs`. `data` can be either a vector or a matrix of measurements. If `data` is a matrix, indices are computed for the columns. `specs` can be either a two-element vector of the form `[L,U]` containing lower and upper specification limits, or (if `data` is a matrix) a two-row matrix with the same number of columns as `data`. If there is no lower bound, use `-Inf` as the first element of `specs`. If there is no upper bound, use `Inf` as the second element of `specs`.

The output `S` is a structure with the following fields:

- `mu` — Sample mean
- `sigma` — Sample standard deviation
- `P` — Estimated probability of being within limits
- `Pl` — Estimated probability of being below `L`
- `Pu` — Estimated probability of being above `U`
- `Cp` — `(U-L)/(6*sigma)`
- `Cpl` — `(mu-L)./(3.*sigma)`
- `Cpu` — `(U-mu)./(3.*sigma)`
- `Cpk` — `min(Cpl,Cpu)`

Indices are computed under the assumption that data values are independent samples from a normal population with constant mean and variance.

Indices divide a “specification width” (between specification limits) by a “process width” (between control limits). Higher ratios indicate a process with fewer measurements outside of specification.

Examples

Simulate a sample from a process with a mean of 3 and a standard deviation of 0.005:

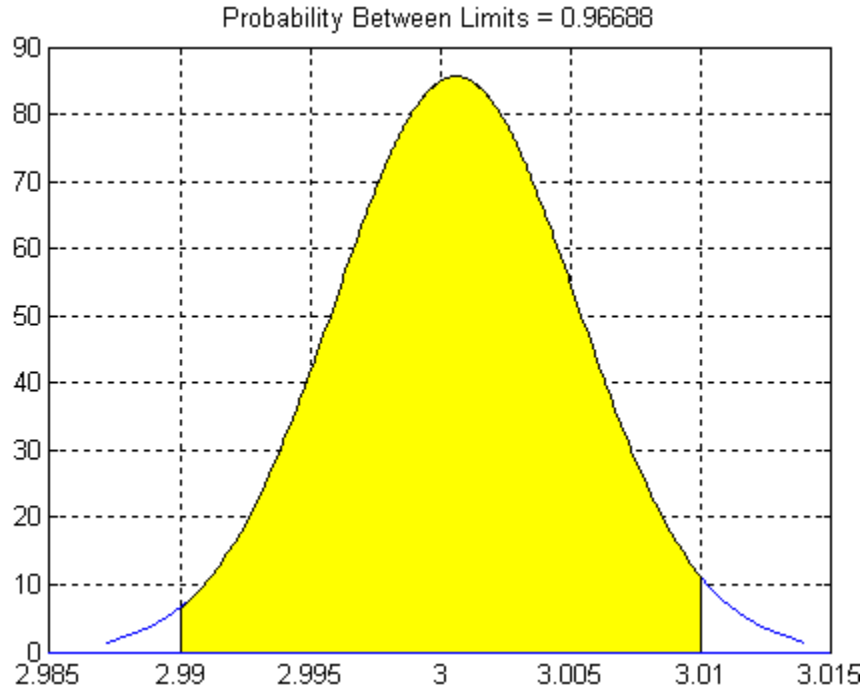
```
data = normrnd(3,0.005,100,1);
```

Compute capability indices if the process has an upper specification limit of 3.01 and a lower specification limit of 2.99:

```
S = capability(data,[2.99 3.01])
S =
       mu: 3.0006
    sigma: 0.0047
        P: 0.9669
       Pl: 0.0116
       Pu: 0.0215
       Cp: 0.7156
      Cpl: 0.7567
      Cpu: 0.6744
      Cpk: 0.6744
```

Visualize the specification and process widths:

```
capaplot(data,[2.99 3.01]);
grid on
```



References

[1] Montgomery, D. *Introduction to Statistical Quality Control*. Hoboken, NJ: John Wiley & Sons, 1991, pp. 369–374.

See Also

`capaplot` | `histfit`

Purpose

Process capability plot

Syntax

```
p = capaplot(data,specs)
[p,h] = capaplot(data,specs)
```

Description

`p = capaplot(data,specs)` estimates the mean of and variance for the observations in input vector `data`, and plots the pdf of the resulting T distribution. The observations in `data` are assumed to be normally distributed. The output, `p`, is the probability that a new observation from the estimated distribution will fall within the range specified by the two-element vector `specs`. The portion of the distribution between the lower and upper bounds specified in `specs` is shaded in the plot.

`[p,h] = capaplot(data,specs)` additionally returns handles to the plot elements in `h`.

`capaplot` treats `NaN` values in `data` as missing, and ignores them.

Examples

Simulate a sample from a process with a mean of 3 and a standard deviation of 0.005:

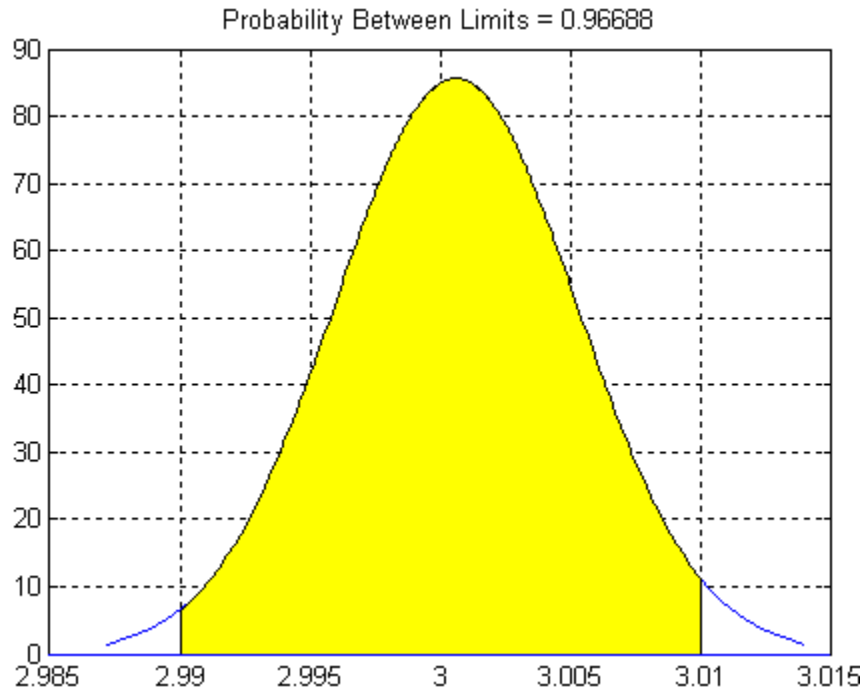
```
data = normrnd(3,0.005,100,1);
```

Compute capability indices if the process has an upper specification limit of 3.01 and a lower specification limit of 2.99:

```
S = capability(data,[2.99 3.01])
S =
       mu: 3.0006
    sigma: 0.0047
        P: 0.9669
       Pl: 0.0116
       Pu: 0.0215
       Cp: 0.7156
      Cpl: 0.7567
      Cpu: 0.6744
      Cpk: 0.6744
```

Visualize the specification and process widths:

```
capaplot(data,[2.99 3.01]);
grid on
```



See Also

`capability` | `histfit`

Purpose

Read case names from file

Syntax

```
names = caseread('filename')
names = caseread
```

Description

`names = caseread('filename')` reads the contents of *`filename`* and returns a string matrix of `names`. *`filename`* is the name of a file in the current folder, or the complete path name of any file elsewhere. `caseread` treats each line as a separate case.

`names = caseread` displays the **Select File to Open** dialog box for interactive selection of the input file.

Examples

Read the file `months.dat` created using the `casewrite` function.

```
type months.dat

January
February
March
April
May

names = caseread('months.dat')
names =
January
February
March
April
May
```

See Also

`casewrite` | `gname` | `tdfread` | `tblread`

casewrite

Purpose

Write case names to file

Syntax

```
casewrite(strmat,'filename')
casewrite(strmat)
```

Description

`casewrite(strmat,'filename')` writes the contents of string matrix `strmat` to *`filename`*. Each row of `strmat` represents one case name. *`filename`* is the name of a file in the current folder, or the complete path name of any file elsewhere. `casewrite` writes each name to a separate line in *`filename`*.

`casewrite(strmat)` displays the **Select File to Write** dialog box for interactive specification of the output file.

Examples

```
strmat = char('January','February',...
                'March','April','May')
strmat =
January
February
March
April
May

casewrite(strmat,'months.dat')
type months.dat

January
February
March
April
May
```

See Also

`gname` | `caseread` | `tblwrite` | `tdfread`

Purpose

Concatenate categorical arrays

Syntax

```
c = cat(dim,A,B,...)
```

Description

`c = cat(dim,A,B,...)` concatenates the categorical arrays `A,B,...` along dimension `dim`. All inputs must have the same size except along dimension `dim`. The set of categorical levels for `C` is the sorted union of the sets of levels of the inputs, as determined by their labels.

See Also

`cat` | `horzcat` | `vertcat`

categorical

Purpose

Arrays for categorical data

Description

`categorical` is an abstract class, and you cannot create instances of it directly. You must create `nominal` or `ordinal` arrays.

Categorical arrays store data with values in a discrete set of levels. Each level is meant to capture a single, defining characteristic of an observation. If you do not encode ordering in the levels, the data and the array are `nominal`. If you do encode an ordering, the data and the array are `ordinal`.

Construction

categorical	Create categorical array

Methods

addlevels	Add levels to categorical array
cat	Concatenate categorical arrays
cellstr	Convert categorical array to cell array of strings
char	Convert categorical array to character array
circshift	Shift categorical array circularly
ctranspose	Transpose categorical matrix
disp	Display categorical array
display	Display categorical array
double	Convert categorical array to double array
droplevels	Drop levels
end	Last index in indexing expression for categorical array

flipdim	Flip categorical array along specified dimension
fliplr	Flip categorical matrix in left/right direction
flipud	Flip categorical matrix in up/down direction
getlabels	Access categorical array labels
getlevels	Get categorical array levels
hist	Plot histogram of categorical data
horzcat	Horizontal concatenation for categorical arrays
int16	Convert categorical array to signed 16-bit integer array
int32	Convert categorical array to signed 32-bit integer array
int64	Convert categorical array to signed 64-bit integer array
int8	Convert categorical array to signed 8-bit integer array
intersect	Set intersection for categorical arrays
ipermute	Inverse permute dimensions of categorical array
isempty	True for empty categorical array
isequal	True if categorical arrays are equal
islevel	Test for levels
ismember	True for elements of categorical array in set

isscalar	True if categorical array is scalar
isundefined	Test for undefined elements
isvector	True if categorical array is vector
length	Length of categorical array
levelcounts	Element counts by level
ndims	Number of dimensions of categorical array
numel	Number of elements in categorical array
permute	Permute dimensions of categorical array
reorderlevels	Reorder levels
repmat	Replicate and tile categorical array
reshape	Resize categorical array
rot90	Rotate categorical matrix 90 degrees
setdiff	Set difference for categorical arrays
setlabels	Label levels
setxor	Set exclusive-or for categorical arrays
shiftdim	Shift dimensions of categorical array
single	Convert categorical array to single array
size	Size of categorical array

squeeze	Squeeze singleton dimensions from categorical array
subsasgn	Subscripted assignment for categorical array
subsindex	Subscript index for categorical array
subsref	Subscripted reference for categorical array
summary	Summary statistics for categorical array
times	Product of categorical arrays
transpose	Transpose categorical matrix
uint16	Convert categorical array to unsigned 16-bit integers
uint32	Convert categorical array to unsigned 32-bit integers
uint64	Convert categorical array to unsigned 64-bit integers
uint8	Convert categorical array to unsigned 8-bit integers
union	Set union for categorical arrays
unique	Unique values in categorical array
vertcat	Vertical concatenation for categorical arrays

Properties

labels	Text labels for levels
undeflabel	Text label for undefined levels

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

How To

- “Categorical Arrays” on page 2-13

Purpose

Create categorical array

Description

`categorical` is an abstract class, and you cannot create instances of it directly. You must create `nominal` or `ordinal` arrays.

See Also

`nominal` | `ordinal`

dataset.cat

Purpose

Concatenate dataset arrays

Syntax

```
ds = cat(dim, ds1, ds2, ...)
```

Description

`ds = cat(dim, ds1, ds2, ...)` concatenates the dataset arrays `ds1`, `ds2`, `...` along dimension `dim` by calling the `dataset/horzcat` or `dataset/vertcat` method. `dim` must be 1 or 2.

See Also

`horzcat` | `vertcat`

Purpose

Categorical splits used for branches in decision tree

Syntax

```
v=catsplit(t)
v=catsplit(t,j)
```

Description

`v=catsplit(t)` returns an `n`-by-2 cell array `v`. Each row in `v` gives left and right values for a categorical split. For each branch node `j` based on a categorical predictor variable `z`, the left child is chosen if `z` is in `v(j,1)` and the right child is chosen if `z` is in `v(j,2)`. The splits are in the same order as nodes of the tree. Nodes for these splits can be found by running `cuttype` and selecting `'categorical'` cuts from top to bottom.

`v=catsplit(t,j)` takes an array `j` of rows and returns the splits for the specified rows.

See Also

`classregtree`

gmdistribution.cdf

Purpose

Cumulative distribution function for Gaussian mixture distribution

Syntax

```
y = cdf(obj,X)
```

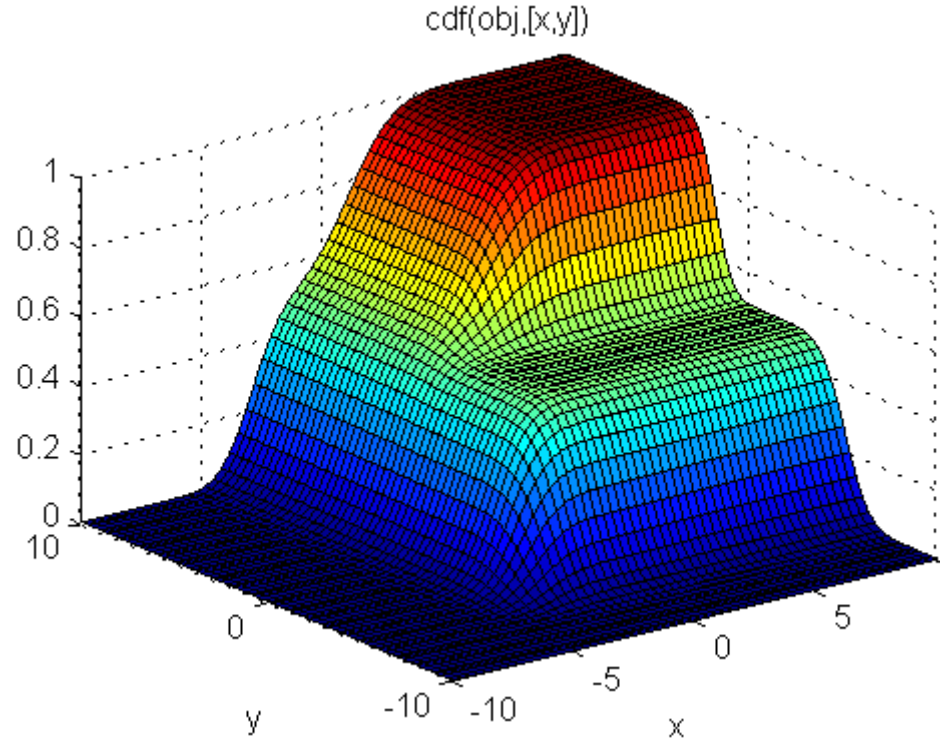
Description

`y = cdf(obj,X)` returns a vector `y` of length n containing the values of the cumulative distribution function (cdf) for the `gmdistribution` object `obj`, evaluated at the n-by-d data matrix `X`, where n is the number of observations and d is the dimension of the data. `obj` is an object created by `gmdistribution` or `fit`. `y(I)` is the cdf of observation `I`.

Examples

Create a `gmdistribution` object defining a two-component mixture of bivariate Gaussian distributions:

```
MU = [1 2;-3 -5];
SIGMA = cat(3,[2 0;0 .5],[1 0;0 1]);
p = ones(1,2)/2;
obj = gmdistribution(MU,SIGMA,p);

ezsurf(@(x,y)cdf(obj,[x y]),[-10 10],[-10 10])
```



See Also

`gmdistribution` | `fit` | `pdf` | `mvncdf`

Purpose

Central composite design

Syntax

```
dCC = ccdesign(n)
[dCC,blocks] = ccdesign(n)
[...] = ccdesign(n,'Name',value)
```

Description

`dCC = ccdesign(n)` generates a central composite design for `n` factors. `n` must be an integer `2` or larger. The output matrix `dCC` is *m*-by-`n`, where *m* is the number of runs in the design. Each row represents one run, with settings for all factors represented in the columns. Factor values are normalized so that the cube points take values between `-1` and `1`.

`[dCC,blocks] = ccdesign(n)` requests a blocked design. The output `blocks` is an *m*-by-1 vector of block numbers for each run. Blocks indicate runs that are to be measured under similar conditions to minimize the effect of inter-block differences on the parameter estimates.

`[...] = ccdesign(n,'Name',value)` specifies one or more optional name/value pairs for the design. Valid parameters and their values are listed in the following table. Specify *`Name`* in single quotes.

Parameter	Description	Values
`center`	Number of center points.	• Integer — Number of center points to include. • `'uniform'` — Select number of center points to give uniform precision. • `'orthogonal'` — Select number of center points to give an orthogonal design. This is the default.
`fraction`	Fraction of full-factorial cube, expressed	• `0` — Whole design. This is the default. • `1` — 1/2 fraction.

Parameter	Description	Values
	as an exponent of 1/2.	• `2` — 1/4 fraction.
`type`	Type of CCD.	• `'circumscribed'` — Circumscribed (CCC). This is the default. • `'inscribed'` — Inscribed (CCI). • `'faced'` — Faced (CCF).
`blocksize`	Maximum number of points per block.	Integer. The default is `Inf`.

Examples

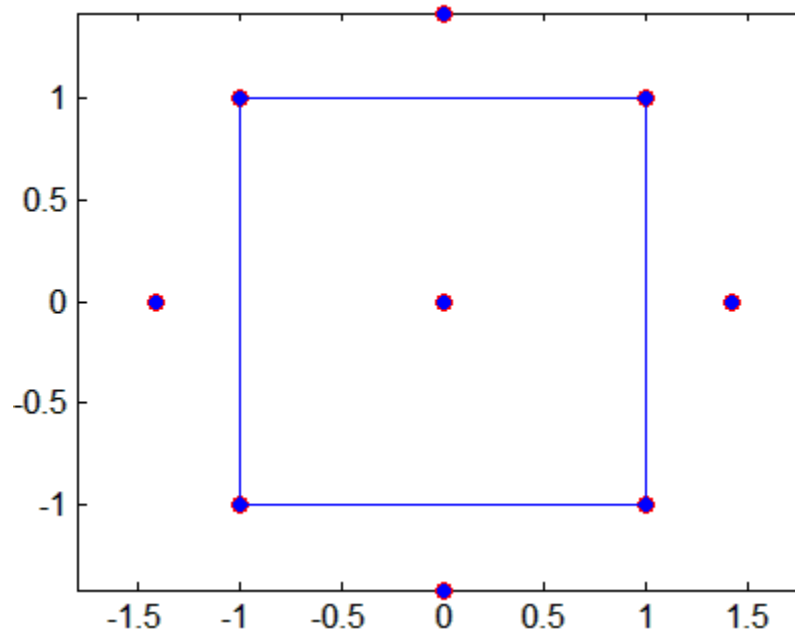
The following creates a 2-factor CCC:

```
dCC = ccdesign(2,'type','circumscribed')
dCC =
   -1.0000   -1.0000
   -1.0000    1.0000
    1.0000   -1.0000
    1.0000    1.0000
   -1.4142         0
    1.4142         0
         0   -1.4142
         0    1.4142
         0         0
         0         0
         0         0
         0         0
         0         0
         0         0
         0         0
         0         0
```

The center point is run 8 times to reduce the correlations among the coefficient estimates.

Visualize the design as follows:

```
plot(dCC(:,1),dCC(:,2),'ro','MarkerFaceColor','b')
X = [1 -1 -1 -1; 1 1 1 -1];
Y = [-1 -1 1 -1; 1 -1 1 1];
line(X,Y,'Color','b')
axis square equal
```



See Also

`bbdesign`

Purpose

Cumulative distribution functions

Syntax

```
Y = cdf('name',X,A)
Y = cdf('name',X,A,B)
Y = cdf('name',X,A,B,C)
```

Description

`Y = cdf('name',X,A)` computes the cumulative distribution function for the one-parameter family of distributions specified by `name`. `A` contains parameter values for the distribution. The cumulative distribution function is evaluated at the values in `X` and its values are returned in `Y`.

If `X` and `A` are arrays, they must be the same size. If `X` is a scalar, it is expanded to a constant matrix the same size as `A`. If `A` is a scalar, it is expanded to a constant matrix the same size as `X`.

`Y` is the common size of `X` and `A` after any necessary scalar expansion.

`Y = cdf('name',X,A,B)` computes the cumulative distribution function for two-parameter families of distributions, where parameter values are given in `A` and `B`.

If `X`, `A`, and `B` are arrays, they must be the same size. If `X` is a scalar, it is expanded to a constant matrix the same size as `A` and `B`. If either `A` or `B` are scalars, they are expanded to constant matrices the same size as `X`.

`Y` is the common size of `X`, `A`, and `B` after any necessary scalar expansion.

`Y = cdf('name',X,A,B,C)` computes the cumulative distribution function for three-parameter families of distributions, where parameter values are given in `A`, `B`, and `C`.

If `X`, `A`, `B`, and `C` are arrays, they must be the same size. If `X` is a scalar, it is expanded to a constant matrix the same size as `A`, `B`, and `C`. If any of `A`, `B` or `C` are scalars, they are expanded to constant matrices the same size as `X`.

`Y` is the common size of `X`, `A`, `B`, and `C` after any necessary scalar expansion.

Acceptable strings for `name` (specified in single quotes) are:

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
`beta` or `Beta`	"Beta Distribution" on page B-4	`a`	`b`	—
`bino` or `Binomial`	"Binomial Distribution" on page B-7	`n`: number of trials	`p`: probability of success for each trial	—
`chi2` or `Chisquare`	"Chi-Square Distribution" on page B-12	ν: degrees of freedom	—	—
`exp` or `Exponential`	"Exponential Distribution" on page B-16	μ: mean	—	—
`ev` or `Extreme Value`	"Extreme Value Distribution" on page B-19	μ: location parameter	σ: scale parameter	—
`f` or `F`	"F Distribution" on page B-25	$\nu 1$: numerator degrees of freedom	$\nu 2$: denominator degrees of freedom	—
`gam` or `Gamma`	"Gamma Distribution" on page B-27	`a`: shape parameter	`b`: scale parameter	—
`gev` or `Generalized Extreme Value`	"Generalized Extreme Value Distribution" on page B-32	`k`: shape parameter	σ: scale parameter	μ: location parameter
`gp` or `Generalized Pareto`	"Generalized Pareto Distribution" on page B-37	`k`: tail index (shape) parameter	σ: scale parameter	μ: threshold (location) parameter

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
`geo` or `Geometric`	"Geometric Distribution" on page B-41	`p`: probability parameter	—	—
`hyge` or `Hypergeometric`	"Hypergeometric Distribution" on page B-43	`M`: size of the population	`K`: number of items with the desired characteristic in the population	`n`: number of samples drawn
`logn` or `Lognormal`	"Lognormal Distribution" on page B-51	μ	σ	—
`nbin` or `Negative Binomial`	"Negative Binomial Distribution" on page B-72	`r`: number of successes	`p`: probability of success in a single trial	—
`ncf` or `Noncentral F`	"Noncentral F Distribution" on page B-78	$\nu 1$: numerator degrees of freedom	$\nu 2$: denominator degrees of freedom	δ: noncentrality parameter
`nct` or `Noncentral t`	"Noncentral t Distribution" on page B-80	ν: degrees of freedom	δ: noncentrality parameter	—
`ncx2` or `Noncentral Chi-square`	"Noncentral Chi-Square Distribution" on page B-76	ν: degrees of freedom	δ: noncentrality parameter	—
`norm` or `Normal`	"Normal Distribution" on page B-83	μ: mean	σ: standard deviation	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
poiss or Poisson	"Poisson Distribution" on page B-89	λ: mean	—	—
rayl or Rayleigh	"Rayleigh Distribution" on page B-91	b: scale parameter	—	—
t or T	"Student's t Distribution" on page B-95	ν: degrees of freedom	—	—
unif or Uniform	"Uniform Distribution (Continuous)" on page B-99	a: lower endpoint (minimum)	b: upper endpoint (maximum)	—
unid or Discrete Uniform	"Uniform Distribution (Discrete)" on page B-101	N: maximum observable value	—	—
wbl or Weibull	"Weibull Distribution" on page B-103	a: scale parameter	b: shape parameter	—

Examples

Compute the cdf of the normal distribution with mean 0 and standard deviation 1 at inputs –2, –1, 0, 1, 2:

```
p1 = cdf('Normal',-2:2,0,1)
p1 =
  0.0228  0.1587  0.5000  0.8413  0.9772
```

The order of the parameters is the same as for `normcdf`.

Compute the cdfs of Poisson distributions with rate parameters 0, 1, ..., 4 at inputs 1, 2, ..., 5, respectively:

```
p2 = cdf('Poisson',0:4,1:5)
p2 =
  0.3679   0.4060   0.4232   0.4335   0.4405
```

The order of the parameters is the same as for `poisscdf`.

See Also

`pdf` | `icdf`

piecewisedistribution.cdf

Purpose

Cumulative distribution function for piecewise distribution

Syntax

```
P = cdf(obj,X)
```

Description

`P = cdf(obj,X)` returns an array `P` of values of the cumulative distribution function for the piecewise distribution object `obj`, evaluated at the values in the array `X`.

Examples

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);
[p,q] = boundary(obj)
p =
    0.1000
    0.9000
q =
   -1.7766
    1.8432

cdf(obj,q)
ans =
    0.1000
    0.9000
```

See Also

`paretotails` | `pdf` | `icdf`

Purpose

Return cumulative distribution function (CDF) for ProbDist object

Syntax

```
Y = cdf(PD, X)
```

Description

`Y = cdf(PD, X)` returns `Y`, an array containing the cumulative distribution function (CDF) for the ProbDist object `PD`, evaluated at values in `X`.

Input Arguments

`PD`	An object of the class `ProbDistUnivParam` or `ProbDistUnivKernel`.
`X`	A numeric array of values where you want to evaluate the CDF.

Output Arguments

`Y`	An array containing the cumulative distribution function (CDF) for the ProbDist object `PD`.

See Also

`cdf`

cdfplot

Purpose

Empirical cumulative distribution function plot

Syntax

```
cdfplot(X)
h = cdfplot(X)
[h,stats] = cdfplot(X)
```

Description

`cdfplot(X)` displays a plot of the empirical cumulative distribution function (cdf) for the data in the vector `X`. The empirical cdf *F(x)* is defined as the proportion of `X` values less than or equal to *x*.

This plot, like those produced by `hist` and `normplot`, is useful for examining the distribution of a sample of data. You can overlay a theoretical cdf on the same plot to compare the empirical distribution of the sample to the theoretical distribution.

The `kstest`, `kstest2`, and `lillietest` functions compute test statistics that are derived from the empirical cdf. You may find the empirical cdf plot produced by `cdfplot` useful in helping you to understand the output from those functions.

`h = cdfplot(X)` returns a handle to the cdf curve.

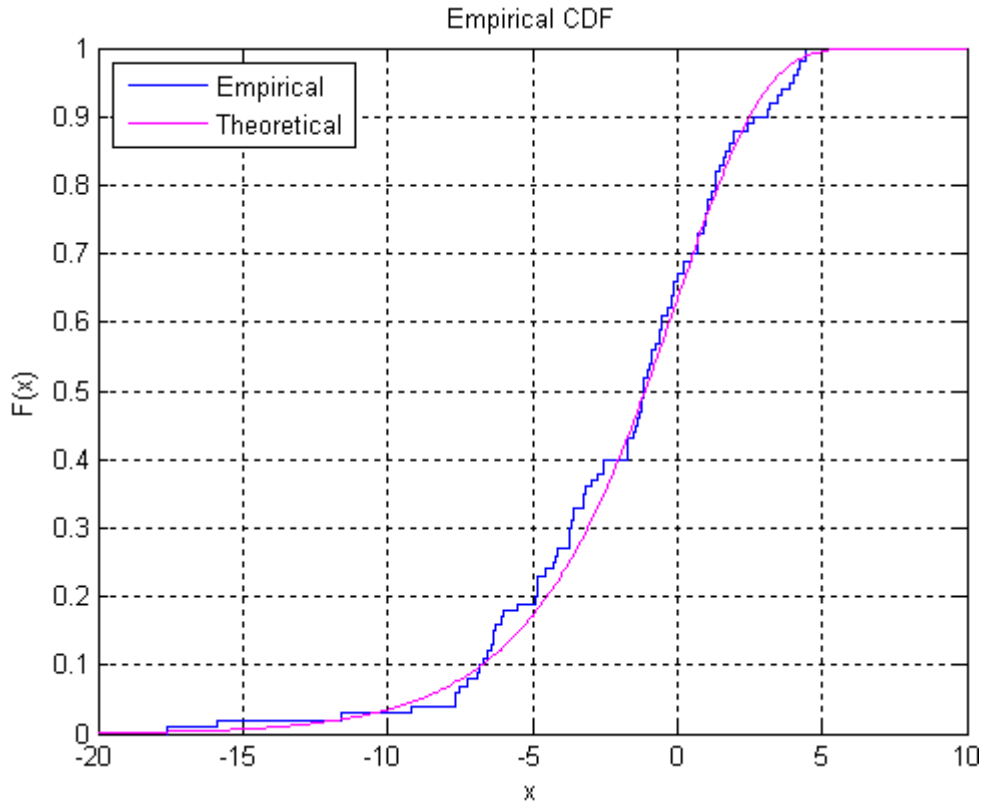
`[h,stats] = cdfplot(X)` also returns a `stats` structure with the following fields.

Field	Description
`stats.min`	Minimum value
`stats.max`	Maximum value
`stats.mean`	Sample mean
`stats.median`	Sample median (50th percentile)
`stats.std`	Sample standard deviation

Examples

The following example compares the empirical cdf for a sample from an extreme value distribution with a plot of the cdf for the sampling distribution. In practice, the sampling distribution would be unknown, and would be chosen to match the empirical cdf.

```
y = evrnd(0,3,100,1);
cdfplot(y)
hold on
x = -20:0.1:10;
f = evcdf(x,0,3);
plot(x,f,'m')
legend('Empirical','Theoretical','Location','NW')
```



See Also

ecdf

categorical.cellstr

Purpose

Convert categorical array to cell array of strings

Syntax

```
B = cellstr(A)
```

Description

`B = cellstr(A)` converts the categorical array `A` to a cell array of strings. Each element of `B` contains the categorical level label for the corresponding element of `A`.

See Also

`char` | `getlabels`

Purpose

Create cell array of strings from dataset array

Syntax

```
B = cellstr(A)
B = cellstr(A,VARS)
```

Description

`B = cellstr(A)` returns the contents of the dataset `A`, converted to a cell array of strings. The variables in the dataset must support the conversion and must have compatible sizes.

`B = cellstr(A,VARS)` returns the contents of the dataset variables specified by `VARS`. `VARS` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

See Also

`dataset.double` | `dataset.replacedata`

categorical.char

Purpose

Convert categorical array to character array

Syntax

```
B = char(A)
```

Description

`B = char(A)` converts the categorical array `A` to a 2-D character matrix. `char` does not preserve the shape of `A`. `B` contains `numel(A)` rows, and each row of `B` contains the categorical level label for the corresponding element of `A(:)`.

See Also

`cellstr` | `getlabels`

Purpose

Chi-square cumulative distribution function

Syntax

```
P = chi2cdf(X,V)
```

Description

`P = chi2cdf(X,V)` computes the chi-square cdf at each of the values in `X` using the corresponding degrees of freedom in `V`. `X` and `V` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input.

The degrees of freedom parameters in `V` must be positive integers, and the values in `X` must lie on the interval `[0 Inf]`.

The χ^2 cdf for a given value x and degrees-of-freedom ν is

$$p = F(x \mid \nu) = \int_0^x \frac{t^{(\nu-2)/2} e^{-t/2}}{2^{\nu/2}\Gamma(\nu/2)}\,dt$$

where $\Gamma(\cdot)$ is the Gamma function.

The chi-square density function with ν degrees-of-freedom is the same as the gamma density function with parameters $\nu/2$ and 2.

Examples

```
probability = chi2cdf(5,1:5)
probability =
  0.9747  0.9179  0.8282  0.7127  0.5841

probability = chi2cdf(1:5,1:5)
probability =
  0.6827  0.6321  0.6084  0.5940  0.5841
```

See Also

`cdf` | `chi2pdf` | `chi2inv` | `chi2stat` | `chi2rnd`

How To

- “Chi-Square Distribution” on page B-12

chi2gof

Purpose

Chi-square goodness-of-fit test

Syntax

```
h = chi2gof(x)
[h,p] = chi2gof(...)
[h,p,stats] = chi2gof(...)
[...] = chi2gof(X,'Name',value)
```

Description

`h = chi2gof(x)` performs a chi-square goodness-of-fit test of the default null hypothesis that the data in vector `x` are a random sample from a normal distribution with mean and variance estimated from `x`, against the alternative that the data are not normally distributed with the estimated mean and variance. The result `h` is `1` if the null hypothesis can be rejected at the 5% significance level. The result `h` is `0` if the null hypothesis cannot be rejected at the 5% significance level.

The null distribution can be changed from a normal distribution to an arbitrary discrete or continuous distribution. See the syntax for specifying optional argument name/value pairs below.

The test is performed by grouping the data into bins, calculating the observed and expected counts for those bins, and computing the chi-square test statistic

$$\chi^2 = \sum_{i=1}^{N} (O_i - E_i)^2 / E_i$$

where O_i are the observed counts and E_i are the expected counts. The statistic has an approximate chi-square distribution when the counts are sufficiently large. Bins in either tail with an expected count less than 5 are pooled with neighboring bins until the count in each extreme bin is at least 5. If bins remain in the interior with counts less than 5, `chi2gof` displays a warning. In this case, you should use fewer bins, or provide bin centers or edges, to increase the expected counts in all bins. (See the syntax for specifying optional argument name/value pairs below.) `chi2gof` sets the number of bins, `nbins`, to 10 by default, and compares the test statistic to a chi-square distribution with `nbins – 3` degrees of freedom to take into account the two estimated parameters.

`[h,p] = chi2gof(...)` also returns the *p* value of the test, `p`. The *p* value is the probability, under assumption of the null hypothesis, of observing the given statistic or one more extreme.

`[h,p,stats] = chi2gof(...)` also returns a structure `stats` with the following fields:

- `chi2stat` — The chi-square statistic
- `df` — Degrees of freedom
- `edges` — Vector of bin edges after pooling
- `O` — Observed count in each bin
- `E` — Expected count in each bin

`[...] = chi2gof(X,'Name',value)` specifies one or more optional argument name/value pairs chosen from the following lists. Argument names are case insensitive and partial matches are allowed. Specify *Name* in single quotes.

The following name/value pairs control the initial binning of the data before pooling. You should not specify more than one of these options.

- `nbins` — The number of bins to use. Default is 10.
- `ctrs` — A vector of bin centers
- `edges` — A vector of bin edges

The following name/value pairs determine the null distribution for the test. Do not specify both `cdf` and `expected`.

- `cdf` — A fully specified cumulative distribution function. This can be a function name, a function handle, or a ProbDist object of the `ProbDistUnivParam` class or `ProbDistUnivKernel` class. When `'cdf'` is a function name or handle, the distribution function must take `x` as its only argument. Alternately, you can provide a cell array whose first element is a function name or handle, and whose later

elements are parameter values, one per cell. The function must take `x` as its first argument, and other parameters as later arguments.

- `expected` — A vector with one element per bin specifying the expected counts for each bin.
- `nparams` — The number of estimated parameters; used to adjust the degrees of freedom to be `nbins – 1 – nparams`, where `nbins` is the number of bins.

If your `cdf` or `expected` input depends on estimated parameters, you should use `nparams` to ensure that the degrees of freedom for the test is correct. If `cdf`is a cell array, the default value of `nparams` is the number of parameters in the array; otherwise the default is 0.

The following name/value pairs control other aspects of the test.

- `emin` — The minimum allowed expected value for a bin; any bin in either tail having an expected value less than this amount is pooled with a neighboring bin. Use the value 0 to prevent pooling. The default is 5.
- `frequency` — A vector the same length as `x` containing the frequency of the corresponding `x`values
- `alpha` — Significance level for the test. The default is 0.05.

Examples

Example 1

Equivalent ways to test against an unspecified normal distribution with estimated parameters:

```
x = normrnd(50,5,100,1);

[h,p] = chi2gof(x)
h =
     0
p =
    0.7532
```

```
[h,p] = chi2gof(x,'cdf',@(z)normcdf(z,mean(x),std(x)),'nparams',2)
h =
     0
p =
    0.7532

[h,p] = chi2gof(x,'cdf',{@normcdf,mean(x),std(x)})
h =
     0
p =
    0.7532
```

Example 2

Test against the standard normal:

```
x = randn(100,1);

[h,p] = chi2gof(x,'cdf',@normcdf)
h =
     0
p =
    0.9443
```

Example 3

Test against the standard uniform:

```
x = rand(100,1);

n = length(x);
edges = linspace(0,1,11);
expectedCounts = n * diff(edges);
[h,p,st] = chi2gof(x,'edges',edges,...
                     'expected',expectedCounts)
h =
     0
p =
    0.3191
```

```
st =
    chi2stat: 10.4000
          df: 9
       edges: [1x11 double]
           O: [6 11 4 12 15 8 14 9 11 10]
           E: [1x10 double]
```

Example 4

Test against the Poisson distribution by specifying observed and expected counts:

```
bins = 0:5;
obsCounts = [6 16 10 12 4 2];
n = sum(obsCounts);
lambdaHat = sum(bins.*obsCounts)/n;
expCounts = n*poisspdf(bins,lambdaHat);

[h,p,st] = chi2gof(bins,'ctrs',bins,...
                        'frequency',obsCounts, ...
                        'expected',expCounts,...
                        'nparams',1)
h =
     0
p =
    0.4654
st =
    chi2stat: 2.5550
          df: 3
       edges: [1x6 double]
           O: [6 16 10 12 6]
           E: [7.0429 13.8041 13.5280 8.8383 6.0284]
```

See Also

`crosstab` | `lillietest` | `kstest` | `chi2cdf` | `chi2pdf` | `chi2inv` | `chi2stat` | `chi2rnd`

How To

- “Chi-Square Distribution” on page B-12

Purpose

Chi-square inverse cumulative distribution function

Syntax

```
X = chi2inv(P,V)
```

Description

`X = chi2inv(P,V)` computes the inverse of the chi-square cdf with degrees of freedom specified by `V` for the corresponding probabilities in `P`. `P` and `V` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

The degrees of freedom parameters in `V` must be positive integers, and the values in `P` must lie in the interval [0 1].

The inverse chi-square cdf for a given probability p and v degrees of freedom is

$$x = F^{-1}(p \mid \nu) = \{x : F(x \mid \nu) = p\}$$

where

$$p = F(x \mid \nu) = \int_0^x \frac{t^{(\nu-2)/2} e^{-t/2}}{2^{\nu/2}\Gamma(\nu/2)} dt$$

and $\Gamma(\cdot)$ is the Gamma function. Each element of output `X` is the value whose cumulative probability under the chi-square cdf defined by the corresponding degrees of freedom parameter in `V` is specified by the corresponding value in `P`.

Examples

Find a value that exceeds 95% of the samples from a chi-square distribution with 10 degrees of freedom.

```
x = chi2inv(0.95,10)
x =
  18.3070
```

You would observe values greater than 18.3 only 5% of the time by chance.

See Also `icdf` | `chi2cdf` | `chi2pdf` | `chi2stat` | `chi2rnd`

How To

- "Chi-Square Distribution" on page B-12

Purpose

Chi-square probability density function

Syntax

```
Y = chi2pdf(X,V)
```

Description

`Y = chi2pdf(X,V)` computes the chi-square pdf at each of the values in `X` using the corresponding degrees of freedom in `V`. `X` and `V` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of the output `Y`. A scalar input is expanded to a constant array with the same dimensions as the other input.

The degrees of freedom parameters in `V` must be positive integers, and the values in `X` must lie on the interval `[0 Inf]`.

The chi-square pdf for a given value x and ν degrees of freedom is

$$y = f(x \mid \nu) = \frac{x^{(\nu-2)/2} e^{-x/2}}{2^{\nu/2}\Gamma(\nu/2)}$$

where $\Gamma(\cdot)$ is the Gamma function.

If x is standard normal, then x^2 is distributed chi-square with one degree of freedom. If x_1, x_2, ..., x_n are n independent standard normal observations, then the sum of the squares of the x's is distributed chi-square with n degrees of freedom (and is equivalent to the gamma density function with parameters $\nu/2$ and 2).

Examples

```
nu = 1:6;
x = nu;
y = chi2pdf(x,nu)
y =
  0.2420   0.1839   0.1542   0.1353   0.1220   0.1120
```

The mean of the chi-square distribution is the value of the degrees of freedom parameter, `nu`. The above example shows that the probability density of the mean falls as `nu` increases.

See Also

`pdf` | `chi2cdf` | `chi2inv` | `chi2stat` | `chi2rnd`

How To

- "Chi-Square Distribution" on page B-12

Purpose

Chi-square random numbers

Syntax

```
R = chi2rnd(V)
R = chi2rnd(V,m,n,...)
R = chi2rnd(V,[m,n,...])
```

Description

`R = chi2rnd(V)` generates random numbers from the chi-square distribution with degrees of freedom parameters specified by `V`. `V` can be a vector, a matrix, or a multidimensional array. `R` is the same size as `V`.

`R = chi2rnd(V,m,n,...)` or `R = chi2rnd(V,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the chi-square distribution with degrees of freedom parameter `V`. `V` can be a scalar or an array of the same size as `R`.

Examples

Note that the first and third commands are the same, but are different from the second command.

```
r = chi2rnd(1:6)
r =
    0.0037  3.0377  7.8142  0.9021  3.2019  9.0729

r = chi2rnd(6,[1 6])
r =
    6.5249  2.6226  12.2497  3.0388  6.3133  5.0388

r = chi2rnd(1:6,1,6)
r =
  0.7638  6.0955  0.8273  3.2506  1.5469  10.9197
```

See Also

`random` | `chi2cdf` | `chi2pdf` | `chi2inv` | `chi2stat`

How To

- "Chi-Square Distribution" on page B-12

chi2stat

Purpose

Chi-square mean and variance

Syntax

```
[M,V] = chi2stat(NU)
```

Description

`[M,V] = chi2stat(NU)` returns the mean of and variance for the chi-square distribution with degrees of freedom parameters specified by `NU`.

The mean of the chi-square distribution is v, the degrees of freedom parameter, and the variance is 2v.

Examples

```
nu = 1:10;
nu = nu'*nu;
[m,v] = chi2stat(nu)
m =
 1   2   3   4   5   6   7   8   9  10
 2   4   6   8  10  12  14  16  18  20
 3   6   9  12  15  18  21  24  27  30
 4   8  12  16  20  24  28  32  36  40
 5  10  15  20  25  30  35  40  45  50
 6  12  18  24  30  36  42  48  54  60
 7  14  21  28  35  42  49  56  63  70
 8  16  24  32  40  48  56  64  72  80
 9  18  27  36  45  54  63  72  81  90
10  20  30  40  50  60  70  80  90 100

v =
 2   4   6   8  10  12  14  16  18  20
 4   8  12  16  20  24  28  32  36  40
 6  12  18  24  30  36  42  48  54  60
 8  16  24  32  40  48  56  64  72  80
10  20  30  40  50  60  70  80  90 100
12  24  36  48  60  72  84  96 108 120
14  28  42  56  70  84  98 112 126 140
16  32  48  64  80  96 112 128 144 160
18  36  54  72  90 108 126 144 162 180
20  40  60  80 100 120 140 160 180 200
```

See Also

`chi2cdf` | `chi2pdf` | `chi2inv` | `chi2rnd`

How To

- “Chi-Square Distribution” on page B-12

classregtree.children

Purpose

Child nodes

Syntax

```
C = children(t)
C = children(t,nodes)
```

Description

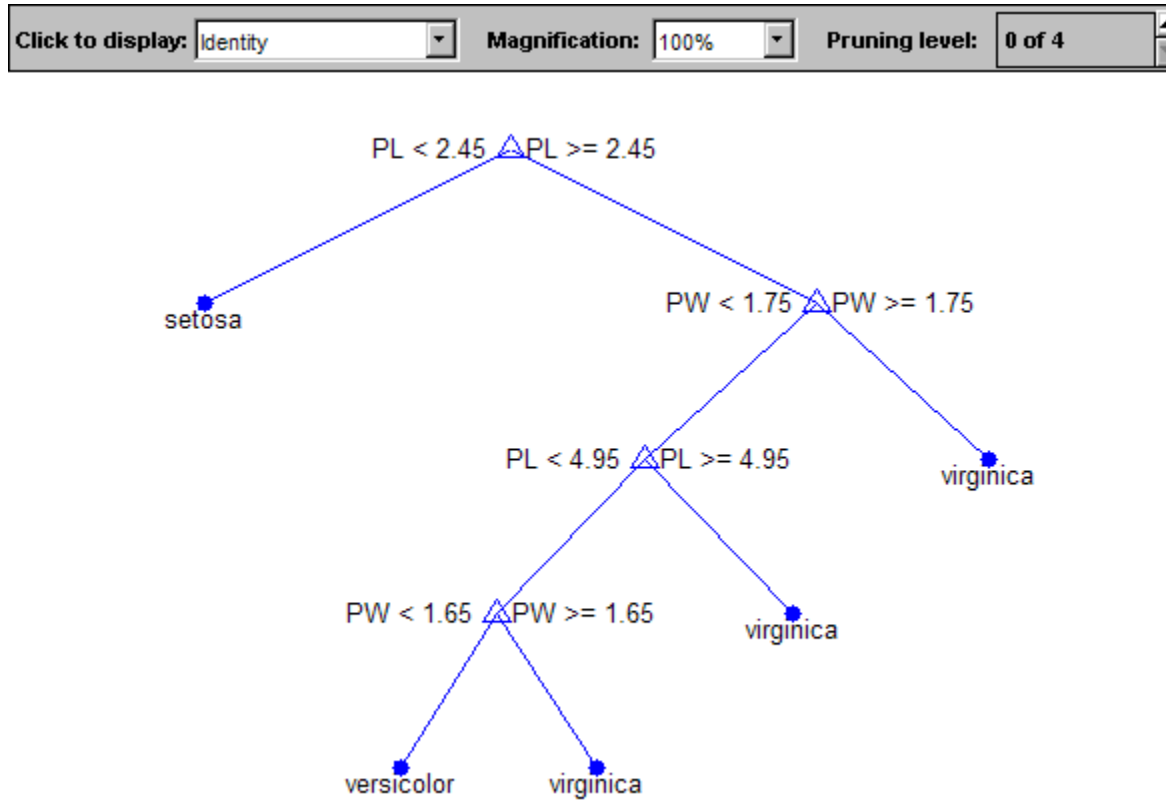
`C = children(t)` returns an n-by-2 array `C` containing the numbers of the child nodes for each node in the tree `t`, where n is the number of nodes. Leaf nodes have child node `0`.

`C = children(t,nodes)` takes a vector `nodes` of node numbers and returns the children for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
C = children(t)
C =
     2     3
     0     0
     4     5
     6     7
     0     0
     8     9
     0     0
     0     0
```

```
     0     0
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes` | `parent`

Purpose

Cholesky-like covariance decomposition

Syntax

```
T = cholcov(SIGMA)
[T,num] = cholcov(SIGMA)
[T,num] = cholcov(SIGMA,0)
```

Description

`T = cholcov(SIGMA)` computes `T` such that `SIGMA = T'*T`. `SIGMA` must be square, symmetric, and positive semi-definite. If `SIGMA` is positive definite, then `T` is the square, upper triangular Cholesky factor. If `SIGMA` is not positive definite, `T` is computed from an eigenvalue decomposition of `SIGMA`. `T` is not necessarily triangular or square in this case. Any eigenvectors whose corresponding eigenvalue is close to zero (within a small tolerance) are omitted. If any remaining eigenvalues are negative, `T` is empty.

`[T,num] = cholcov(SIGMA)` returns the number `num` of negative eigenvalues of `SIGMA`, and `T` is empty if `num` is positive. If `num` is zero, `SIGMA` is positive semi-definite. If `SIGMA` is not square and symmetric, `num` is `NaN` and `T` is empty.

`[T,num] = cholcov(SIGMA,0)` returns `num` equal to zero if `SIGMA` is positive definite, and `T` is the Cholesky factor. If `SIGMA` is not positive definite, `num` is a positive integer and `T` is empty. `[...] = cholcov(SIGMA,1)` is equivalent to `[...] = cholcov(SIGMA)`.

Examples

The following 4-by-4 covariance matrix is rank-deficient:

```
C1 = [2 1 1 2;1 2 1 2;1 1 2 2;2 2 2 3]
C1 =
     2     1     1     2
     1     2     1     2
     1     1     2     2
     2     2     2     3
rank(C1)
ans =
     3
```

Use `cholcov` to factor `C1`:

```
T = cholcov(C1)
T =
   -0.2113    0.7887   -0.5774         0
    0.7887   -0.2113   -0.5774         0
    1.1547    1.1547    1.1547    1.7321

C2 = T'*T
C2 =
    2.0000   1.0000   1.0000   2.0000
    1.0000   2.0000   1.0000   2.0000
    1.0000   1.0000   2.0000   2.0000
    2.0000   2.0000   2.0000   3.0000
```

Use `T` to generate random data with the specified covariance:

```
C3 = cov(randn(1e6,3)*T)
C3 =
    1.9973    0.9982    0.9995    1.9975
    0.9982    1.9962    0.9969    1.9956
    0.9995    0.9969    1.9980    1.9972
    1.9975    1.9956    1.9972    2.9951
```

See Also

`chol` | `cov`

Purpose

Shift categorical array circularly

Syntax

```
B = circshift(A,shiftsize)
```

Description

`B = circshift(A,shiftsize)` circularly shifts the values in the categorical array `A` by `shiftsize` elements. `shiftsize` is a vector of integer scalars where the `n`-th element specifies the shift amount for the `n`-th dimension of array `A`. If an element in `shiftsize` is positive, the values of `A` are shifted down (or to the right). If it is negative, the values of `A` are shifted up (or to the left).

See Also

`permute` | `shiftdim`

NaiveBayes.CIsNonEmpty property

Purpose

Flag for non-empty classes

Description

The `CIsNonEmpty` property is a logical vector of length `NClasses` specifying which classes are not empty. When the grouping variable is categorical, it may contain categorical levels that don't appear in the elements of the grouping variable. Those levels are empty and `NaiveBayes` ignores them for the purposes of training the classifier.

Purpose

Class counts

Syntax

```
P = classcount(t)
P = classcount(t,nodes)
```

Description

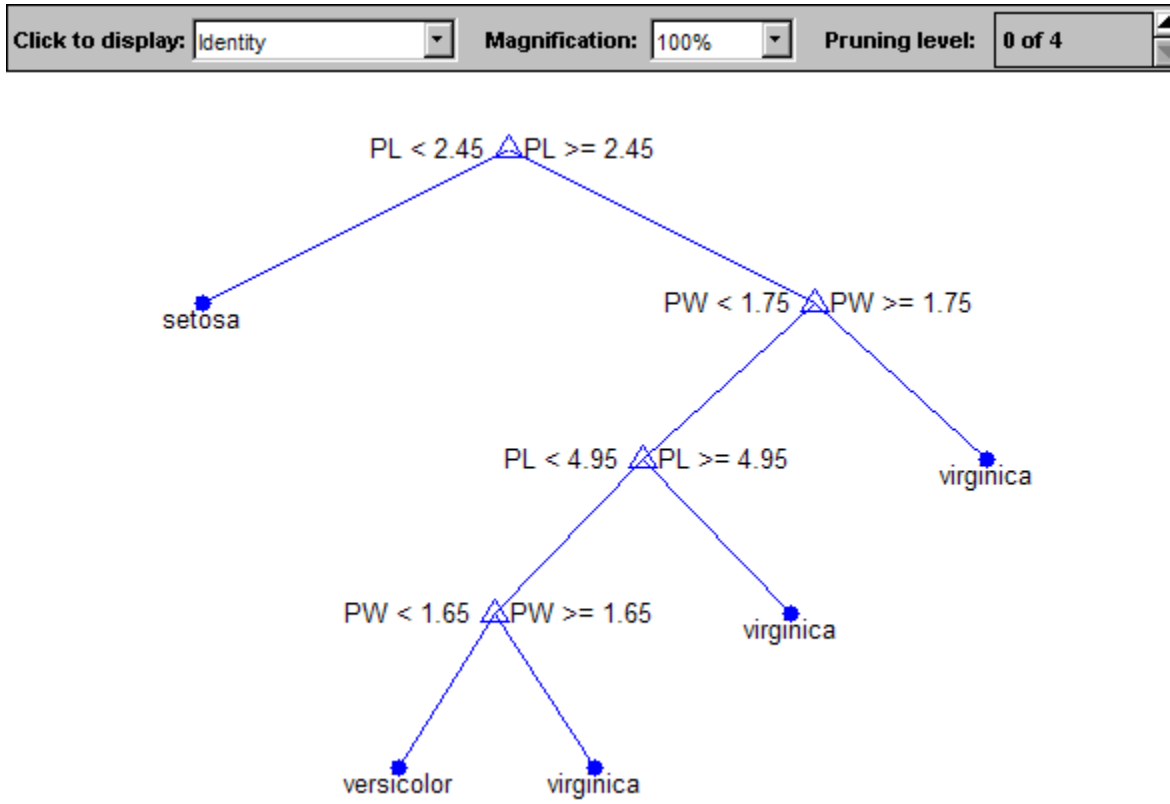
`P = classcount(t)` returns an n-by-m array `P` of class counts for the nodes in the classification tree `t`, where n is the number of nodes and m is the number of classes. For any node number `i`, the class counts `P(i,:)` are counts of observations (from the data used in fitting the tree) from each class satisfying the conditions for node `i`.

`P = classcount(t,nodes)` takes a vector `nodes` of node numbers and returns the class counts for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
P = classcount(t)
P =
    50    50    50
    50     0     0
     0    50    50
     0    49     5
     0     1    45
     0    47     1
     0     2     4
     0    47     0
```

```
     0     0     1
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes`

ClassificationBaggedEnsemble

Purpose

Classification ensemble grown by resampling

Description

`ClassificationBaggedEnsemble` combines a set of trained weak learner models and data on which these learners were trained. It can predict ensemble response for new data by aggregating predictions from its weak learners.

Construction

`ens = fitensemble(X,Y,'bag',nlearn,learners,'type','classification')` creates a bagged classification ensemble. For syntax details, see the `fitensemble` reference page.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CombineWeights`

String describing how `ens` combines weak learner weights, either `'WeightedSum'` or `'WeightedAverage'`.

`FitInfo`

Numeric array of fit information. The `FitInfoDescription` property describes the content of this array.

`FitInfoDescription`

String describing the meaning of the `FitInfo` array.

`FResample`

Numeric scalar between `0` and `1`. `FResample` is the fraction of training data `fitensemble` resampled at random for every weak learner when constructing the ensemble.

`Method`

String describing the method that creates `ens`.

`ModelParams`

Parameters used in training `ens`.

`NTrained`

Number of trained weak learners in `ens`, a scalar.

`PredictorNames`

Cell array of names for the predictor variables, in the order in which they appear in `X`.

`ReasonForTermination`

String describing the reason `fitensemble` stopped adding weak learners to the ensemble.

`Replace`

Logical value indicating if the ensemble was trained with replacement (`true`) or without replacement (`false`).

`ResponseName`

String with the name of the response variable `Y`.

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `ClassificationTree.fit`.

Add or change a `ScoreTransform` function by dot addressing:

```
ens.ScoreTransform = 'function'
```

or

```
ens.ScoreTransform = @function
```

`Trained`

Trained learners, a cell array of compact classification models.

`TrainedWeights`

Numeric vector of trained weights for the weak learners in `ens`. `TrainedWeights` has `T` elements, where `T` is the number of weak learners in `learners`.

`UseObsForLearner`

Logical matrix of size `N`-by-`NTrained`, where `N` is the number of observations in the training data and `NTrained` is the number of trained weak learners. `UseObsForLearner(I,J)` is `true` if observation `I` was used for training learner `J`, and is `false` otherwise.

`W`

Scaled `weights`, a vector with length `n`, the number of rows in `X`. The sum of the elements of `W` is `1`.

`X`

Matrix of predictor values that trained the ensemble. Each column of `X` represents one variable, and each row represents one observation.

`Y`

Numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding row of `X`.

Methods

oobEdge	Out-of-bag classification edge
oobLoss	Out-of-bag classification error
oobMargin	Out-of-bag classification margins
oobPredict	Predict out-of-bag response of ensemble

Inherited Methods

compact	Compact classification ensemble
crossval	Cross validate ensemble
resubEdge	Classification edge by resubstitution
resubLoss	Classification error by resubstitution
resubMargin	Classification margins by resubstitution
resubPredict	Predict ensemble response by resubstitution
resume	Resume training ensemble
edge	Classification edge
loss	Classification error
margin	Classification margins
predict	Predict classification
predictorImportance	Estimates of predictor importance

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Construct a bagged ensemble for the `ionosphere` data, and examine its resubstitution loss:

```
load ionosphere
rng(0,'twister') % for reproducibility
ens = fitensemble(X,Y,'bag',100,'Tree',...
    'type','classification');
L = resubLoss(ens)
```

```
L =
     0
```

The ensemble does a perfect job classifying its training data.

See Also

`ClassificationEnsemble` | `fitensemble`

How To

- “Ensemble Methods” on page 13-51

Superclasses

CompactClassificationDiscriminant

Purpose

Discriminant analysis classification

Description

A `ClassificationDiscriminant` object encapsulates a discriminant analysis classifier, which is a Gaussian mixture model for data generation. A `ClassificationDiscriminant` object can predict responses for new data using the `predict` method. The object contains the data used for training, so can compute resubstitution predictions.

Construction

`obj = ClassificationDiscriminant.fit(X,Y)` creates a discriminant classification object based on the input variables (also known as predictors, features, or attributes) `X` and output (response) `Y`. For syntax details, see `ClassificationDiscriminant.fit`.

`obj = ClassificationDiscriminant.fit(X,Y,Name,Value)` creates a classifier with additional options specified by one or more `Name,Value` pair arguments. If you use one of the following five options, `obj` is of class `ClassificationPartitionedModel`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Otherwise, `obj` is of class `ClassificationDiscriminant`.

Input Arguments

`X`

Matrix of numeric predictor values. Each column of `X` represents one variable, and each row represents one observation.

`NaN` values in `X` are considered missing values. Observations with missing values for `X` are not used in the fit.

`Y`

Numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding row of `X`. `NaN` values in `Y` are considered missing values. Observations with missing values for `Y` are not used in the fit.

Properties

`BetweenSigma`

`p`-by-`p` matrix, the between-class covariance, where `p` is the number of predictors.

`CategoricalPredictors`

List of categorical predictors, always empty (`[]`) for discriminant analysis.

`ClassNames`

List of the elements in the training data `Y` with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument `Y`.

`Coeffs`

`k`-by-`k` structure of coefficient matrices, where `k` is the number of classes. `Coeffs(i,j)` contains coefficients of the linear or quadratic boundaries between classes `i` and `j`. Fields in `Coeffs(i,j)`:

- `DiscrimType`
- `Class1` — `ClassNames(i)`
- `Class2` — `ClassNames(j)`
- `Const` — A scalar
- `Linear` — A vector with `p` components, where `p` is the number of columns in `X`
- `Quadratic` — `p`-by-`p` matrix, exists for quadratic `DiscrimType`

The equation of the boundary between class `i` and class `j` is

```
Const + Linear * x + x' * Quadratic * x = 0,
```

where `x` is a column vector of length `p`.

If `ClassificationDiscriminant.fit` had the `FillCoeffs` name-value pair set to `'off'` when constructing the classifier, `Coeffs` is empty (`[]`).

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. `Cost` is `K`-by-`K`, where `K` is the number of classes.

Change a `Cost` matrix using dot addressing:

```
obj.Cost = costMatrix
```

`DiscrimType`

String specifying the discriminant type. One of:

- `'linear'`
- `'quadratic'`
- `'diagLinear'`
- `'diagQuadratic'`
- `'pseudoLinear'`
- `'pseudoQuadratic'`

`LogDetSigma`

Logarithm of the determinant of the within-class covariance matrix. The type of `LogDetSigma` depends on the discriminant type:

- Scalar for linear discriminant analysis
- Vector of length `K` for quadratic discriminant analysis, where `K` is the number of classes

`ModelParams`

Parameters used in training `obj`.

`Mu`

Matrix of class means of size `K`-by-`p`, where `K` is the number of classes, and `p` is the number of predictors. Each row of `Mu` represents the mean of the multivariate normal distribution of the corresponding class. The class indices are in the `ClassNames` attribute.

`NObservations`

Number of observations in the training data, a numeric scalar. `NObservations` can be less than the number of rows of input data `X` when there are missing values in `X` or response `Y`.

`PredictorNames`

Cell array of names for the predictor variables, in the order in which they appear in the training data `X`.

`Prior`

Prior probabilities for each class. `Prior` is a numeric vector whose entries relate to the corresponding `ClassNames` property.

Add or change a `Prior` vector using dot addressing:

```
obj.Prior = priorVector
```

`ResponseName`

String describing the response variable `Y`.

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `ClassificationDiscriminant.fit`.

Add or change a `ScoreTransform` function by dot addressing:

```
cobj.ScoreTransform = 'function'
```

or

```
cobj.ScoreTransform = @function
```

`Sigma`

Within-class covariance matrix or matrices. The dimensions depend on `DiscrimType`:

- `'linear'` (default) — Matrix of size `p`-by-`p`, where `p` is the number of predictors
- `'quadratic'` — Array of size `p`-by-`p`-by-`K`, where `K` is the number of classes
- `'diagLinear'` — Row vector of length `p`
- `'diagQuadratic'` — Array of size `1`-by-`p`-by-`K`
- `'pseudoLinear'` — Matrix of size `p`-by-`p`
- `'pseudoQuadratic'` — Array of size `p`-by-`p`-by-`K`

`W`

Scaled `weights`, a vector with length `n`, the number of rows in `X`.

`X`

Matrix of predictor values. Each column of `X` represents one predictor (variable), and each row represents one observation.

`Xcentered`

`X` data with class means subtracted. If `Y(i)` is of class `j`,

```
Xcentered(i,:) = X(i,:) – Mu(j,:),
```

where `Mu` is the class mean property.

`Y`

Numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding row of `X`.

Methods

compact	Compact discriminant analysis classifier
crossval	Cross-validated discriminant analysis classifier
fit	Fit discriminant analysis classifier
make	Construct discriminant analysis classifier from parameters
resubEdge	Classification edge by resubstitution
resubLoss	Classification error by resubstitution
resubMargin	Classification margins by resubstitution
resubPredict	Predict resubstitution response of classifier

Inherited Methods

edge	Classification edge
loss	Classification error
mahal	Mahalanobis distance to class means
margin	Classification margins
predict	Predict classification

Definitions

Discriminant Classification

The model for discriminant analysis is:

- Each class (`Y`) generates data (`X`) using a multivariate normal distribution. That is, the model assumes `X` has a Gaussian mixture distribution (`gmdistribution`).
  - For linear discriminant analysis, the model has the same covariance matrix for each class, only the means vary.
  - For quadratic discriminant analysis, both means and covariances of each class vary.

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \underset{y=1,\ldots,K}{\arg\min} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

For details, see “How the predict Method Classifies” on page 12-6.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Create a discriminant analysis classifier for the Fisher iris data:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species)

obj =
ClassificationDiscriminant:
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
         ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
     NObservations: 150
       DiscrimType: 'linear'
                Mu: [3x4 double]
            Coeffs: [3x3 struct]
```

See Also

`CompactClassificationDiscriminant` | `ClassificationDiscriminant.fit`

How To

- “Discriminant Analysis” on page 12-3

Superclasses

CompactClassificationEnsemble

Purpose

Ensemble classifier

Description

`ClassificationEnsemble` combines a set of trained weak learner models and data on which these learners were trained. It can predict ensemble response for new data by aggregating predictions from its weak learners. It also stores data used for training and can compute resubstitution predictions. It can resume training if desired.

Construction

`ens = fitensemble(X,Y,method,nlearn,learners)` returns an ensemble model that can predict responses to data. The ensemble consists of models listed in `learners`. For more information on the syntax, see the `fitensemble` function reference page.

`ens = fitensemble(X,Y,method,nlearn,learners,Name,Value)` returns an ensemble model with additional options specified by one or more `Name,Value` pair arguments. For more information on the syntax, see the `fitensemble` function reference page.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`ClassNames`

List of the elements in `Y` with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument `Y`.

`CombineWeights`

String describing how `ens` combines weak learner weights, either `'WeightedSum'` or `'WeightedAverage'`.

`Cost`

Square matrix where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`.

`FitInfo`

Numeric array of fit information. The `FitInfoDescription` property describes the content of this array.

`FitInfoDescription`

String describing the meaning of the `FitInfo` array.

`LearnerNames`

Cell array of strings with names of weak learners in the ensemble. The name of each learner appears just once. For example, if you have an ensemble of 100 trees, `LearnerNames` is `{'Tree'}`.

`Method`

String describing the method that creates `ens`.

`ModelParams`

Parameters used in training `ens`.

`NObservations`

Numeric scalar containing the number of observations in the training data.

`NTrained`

Number of trained weak learners in `ens`, a scalar.

`PredictorNames`

Cell array of names for the predictor variables, in the order in which they appear in `X`.

`Prior`

Prior probabilities for each class. `Prior` is a numeric vector whose entries relate to the corresponding `ClassNames` property.

`ReasonForTermination`

String describing the reason `fitensemble` stopped adding weak learners to the ensemble.

`ResponseName`

String with the name of the response variable `Y`.

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `ClassificationTree.fit`.

Add or change a `ScoreTransform` function by dot addressing:

```
ens.ScoreTransform = 'function'
```

or

```
ens.ScoreTransform = @function
```

`Trained`

Trained learners, a cell array of compact classification models.

`TrainedWeights`

Numeric vector of trained weights for the weak learners in `ens`. `TrainedWeights` has `T` elements, where `T` is the number of weak learners in `learners`.

`W`

Scaled `weights`, a vector with length `n`, the number of rows in `X`. The sum of the elements of `W` is `1`.

`X`

Matrix of predictor values that trained the ensemble. Each column of `X` represents one variable, and each row represents one observation.

`Y`

Numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding row of `X`.

Methods

compact	Compact classification ensemble
crossval	Cross validate ensemble
resubEdge	Classification edge by resubstitution
resubLoss	Classification error by resubstitution
resubMargin	Classification margins by resubstitution
resubPredict	Predict ensemble response by resubstitution
resume	Resume training ensemble

Inherited Methods

edge	Classification edge
loss	Classification error
margin	Classification margins
predict	Predict classification
predictorImportance	Estimates of predictor importance

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Construct a boosted classification ensemble for the `ionosphere` data, using the `AdaBoostM1` method:

```
load ionosphere
ens = fitensemble(X,Y,'AdaBoostM1',100,'Tree')

ens =
classreg.learning.classif.ClassificationEnsemble:
           PredictorNames: {1x34 cell}
    CategoricalPredictors: []
             ResponseName: 'Response'
                ClassNames: {'b'  'g'}
           ScoreTransform: 'none'
            NObservations: 351
                 NTrained: 100
                   Method: 'AdaBoostM1'
             LearnerNames: {'Tree'}
     ReasonForTermination: [1x77 char]
                  FitInfo: [100x1 double]
       FitInfoDescription: [2x83 char]
```

Predict the classification of the mean of `X`:

```
ypredict = predict(ens,mean(X))

ypredict =
    'g'
```

See Also

`ClassificationTree` | `fitensemble` | `RegressionEnsemble` | `CompactClassificationEnsemble`

How To

- Chapter 13, “Nonparametric Supervised Learning”

ClassificationPartitionedEnsemble

Purpose

Cross-validated classification ensemble

Description

`ClassificationPartitionedEnsemble` is a set of classification ensembles trained on cross-validated folds. Estimate the quality of classification by cross validation using one or more "kfold" methods: `kfoldPredict`, `kfoldLoss`, `kfoldMargin`, `kfoldEdge`, and `kfoldfun`.

Every "kfold" method uses models trained on in-fold observations to predict response for out-of-fold observations. For example, suppose you cross validate using five folds. In this case, every training fold contains roughly 4/5 of the data and every test fold contains roughly 1/5 of the data. The first model stored in `Trained{1}` was trained on `X` and `Y` with the first 1/5 excluded, the second model stored in `Trained{2}` was trained on `X` and `Y` with the second 1/5 excluded, and so on. When you call `kfoldPredict`, it computes predictions for the first 1/5 of the data using the first model, for the second 1/5 of data using the second model, and so on. In short, response for every observation is computed by `kfoldPredict` using the model trained without this observation.

Construction

`cvens = crossval(ens)` creates a cross-validated ensemble from `ens`, a classification ensemble. For syntax details, see the `crossval` method reference page.

`cvens = fitensemble(X,Y,method,nlearn,learners,name,value)` creates a cross-validated ensemble when `name` is one of `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. For syntax details, see the `fitensemble` function reference page.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`ClassNames`

List of the elements in `Y` with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables (nominal

or ordinal), logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument `Y`.

`Combiner`

Cell array of combiners across all folds.

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`.

`CrossValidatedModel`

Name of the cross-validated model, a string.

`Kfold`

Number of folds used in a cross-validated ensemble, a positive integer.

`ModelParams`

Object holding parameters of `cvens`.

`NObservations`

Number of data points used in training the ensemble, a positive integer.

`NTrainedPerFold`

Number of data points used in training each fold of the ensemble, a positive integer.

`Partition`

Partition of class `cvpartition` used in creating the cross-validated ensemble.

`PredictorNames`

Cell array of names for the predictor variables, in the order in which they appear in `X`.

`Prior`

Prior probabilities for each class. `Prior` is a numeric vector whose entries relate to the corresponding `ClassNames` property.

`ResponseName`

Name of the response variable `Y`, a string.

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `ClassificationTree.fit`.

Add or change a `ScoreTransform` function by dot addressing:

```
ens.ScoreTransform = 'function'
```

or

```
ens.ScoreTransform = @function
```

`Trainable`

Cell array of ensembles trained on cross-validation folds. Every ensemble is full, meaning it contains its training data and weights.

`Trained`

Cell array of compact ensembles trained on cross-validation folds.

`W`

Scaled `weights`, a vector with length `n`, the number of rows in `X`.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

kfoldEdge	Classification edge for observations not used for training
kfoldLoss	Classification loss for observations not used for training
resume	Resume training learners on cross-validation folds

Inherited Methods

kfoldEdge	Classification edge for observations not used for training
kfoldfun	Cross validate function
kfoldLoss	Classification loss for observations not used for training
kfoldMargin	Classification margins for observations not used for training
kfoldPredict	Predict response for observations not used for training

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Evaluate the k-fold cross-validation error for a classification ensemble that models the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
cvens = crossval(ens);
L = kfoldLoss(cvens)
```

```
L =
    0.0533
```

See Also

`RegressionPartitionedEnsemble` | `ClassificationPartitionedModel` | `ClassificationEnsemble`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Cross-validated classification model

Description

`ClassificationPartitionedModel` is a set of classification models trained on cross-validated folds. Estimate the quality of classification by cross validation using one or more "kfold" methods: `kfoldPredict`, `kfoldLoss`, `kfoldMargin`, `kfoldEdge`, and `kfoldfun`.

Every "kfold" method uses models trained on in-fold observations to predict response for out-of-fold observations. For example, suppose you cross validate using five folds. In this case, every training fold contains roughly 4/5 of the data and every test fold contains roughly 1/5 of the data. The first model stored in `Trained{1}` was trained on `X` and `Y` with the first 1/5 excluded, the second model stored in `Trained{2}` was trained on `X` and `Y` with the second 1/5 excluded, and so on. When you call `kfoldPredict`, it computes predictions for the first 1/5 of the data using the first model, for the second 1/5 of data using the second model, and so on. In short, response for every observation is computed by `kfoldPredict` using the model trained without this observation.

Construction

`cvmodel = crossval(obj)` creates a cross-validated classification model from a classification model.

`cvmodel = ClassificationTree.fit(X,Y,name,value)` or `cvmodel = ClassificationDiscriminant.fit(X,Y,name,value)` creates a cross-validated model when `name` is one of `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. For syntax details, see the `ClassificationTree.fit` or `ClassificationDiscriminant.fit` function reference pages.

Input Arguments

`obj`

A classification model. `obj` can be a classification tree constructed using `ClassificationTree.fit`, or a discriminant analysis classifier constructed using `ClassificationDiscriminant.fit`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`ClassNames`

List of the elements in `Y` with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument `Y`.

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`.

If `cvmodel` is a cross-validated `ClassificationDiscriminant` model, you can change a `Cost` matrix by dot addressing:

```
cvmodel.Cost = costMatrix
```

`CrossValidatedModel`

Name of the cross-validated model, a string.

`Kfold`

Number of folds used in cross-validated model, a positive integer.

`ModelParams`

Object holding parameters of `cvmodel`.

`Partition`

The partition of class `cvpartition` used in creating the cross-validated model.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`Prior`

Prior probabilities for each class. `Prior` is a numeric vector whose entries relate to the corresponding `ClassNames` property.

If `cvmodel` is a cross-validated `ClassificationDiscriminant` model, you can change a `Prior` vector by dot addressing:

```
cvmodel.Prior = priorVector
```

`ResponseName`

Name of the response variable `Y`, a string.

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function.

String	Formula
`'symmetric'`	$2x - 1$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'symmetricismax'`	Set score for the class with the largest score to `1`, and scores for all other classes to `-1`.
`'none'`	x
`'logit'`	$1/(1 + e^{-x})$
`'doublelogit'`	$1/(1 + e^{-2x})$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$

You can include your own function handle for transforming scores. Your function should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Add or change a `ScoreTransform` function by dot addressing:

```
cvmodel.ScoreTransform = 'function'
or
cvmodel.ScoreTransform = @function
```

`Trained`

The trained learners, a cell array of compact classification models.

`W`

The scaled `weights`, a vector with length `n`, the number of rows in `X`.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

kfoldEdge	Classification edge for observations not used for training
kfoldfun	Cross validate function
kfoldLoss	Classification loss for observations not used for training

kfoldMargin	Classification margins for observations not used for training
kfoldPredict	Predict response for observations not used for training

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Evaluate the k-fold cross-validation error for a classification tree model of the Fisher iris data:

```
load fisheriris
tree = ClassificationTree.fit(meas,species);
cvtree = crossval(tree);
L = kfoldLoss(cvtree)

L =
    0.0600
```

See Also

`ClassificationPartitionedEnsemble` | `RegressionPartitionedModel`

How To

- Chapter 13, “Nonparametric Supervised Learning”
- “Example: Cross Validating a Discriminant Analysis Classifier” on page 12-18

ClassificationTree

Superclasses

CompactClassificationTree

Purpose

Binary decision tree for classification

Description

A decision tree with binary splits for classification. An object of class `ClassificationTree` can predict responses for new data with the `predict` method. The object contains the data used for training, so can compute resubstitution predictions.

Construction

`tree = ClassificationTree.fit(X,Y)` returns a classification tree based on the input variables (also known as predictors, features, or attributes) `X` and output (response) `Y`. `tree` is a binary tree, where each branching node is split based on the values of a column of `X`.

`tree = ClassificationTree.fit(X,Y,Name,Value)` fits a tree with additional options specified by one or more `Name,Value` pair arguments. If you use one of the following five options, `tree` is of class `ClassificationPartitionedModel`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Otherwise, `tree` is of class `ClassificationTree`.

Input Arguments

`X`

A matrix of numeric predictor values. Each column of `X` represents one variable, and each row represents one observation.

`NaN` values in `X` are taken to be missing values. Observations with all missing values for `X` are not used in the fit. Observations with some missing values for `X` are used to find splits on variables for which these observations have valid values.

`Y`

A numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding

row of X. For numeric Y, consider using RegressionTree.fit instead of ClassificationTree.fit.

NaN values in Y are taken to be missing values. Observations with missing values for Y are not used in the fit.

Name-Value Pair Arguments

Optional comma-separated pairs of Name,Value arguments, where Name is the argument name and Value is the corresponding value. Name must appear inside single quotes (''). You can specify several name-value pair arguments in any order as Name1,Value1, ,NameN,ValueN.

`CategoricalPredictors`

List of categorical predictors. Pass CategoricalPredictors as one of:

- A numeric vector with indices from 1 to p, where p is the number of columns of X.
- A logical vector of length p, where a true entry means that the corresponding column of X is a categorical variable.
- 'all', meaning all predictors are categorical.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in PredictorNames values.
- A character matrix, where each row of the matrix is a name of a predictor variable. The names must match entries in PredictorNames values. Pad the names with extra blanks so each row of the character matrix has the same length.

Default: []

`ClassNames`

Array of class names. Use the data type that exists in Y.

Use `ClassNames` to order the classes or to select a subset of classes for training.

Default: The class names that exist in `Y`

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. Alternatively, `Cost` can be a structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same type as `Y`, and `S.ClassificationCosts` containing the cost matrix.

Default: `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`

`crossval`

If `'on'`, grows a cross-validated decision tree with 10 folds. You can use `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'` parameters to override this cross-validation setting. You can only use one of these four parameters (`'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`) at a time when creating a cross-validated tree.

Alternatively, cross validate `tree` later using the `crossval` method.

Default: `'off'`

`cvpartition`

Partition created with `cvpartition` to use in a cross-validated tree. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar

from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`kfold`

Number of folds to use in a cross-validated tree, a positive integer. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: `10`

`leaveout`

Use leave-one-out cross validation by setting to `'on'`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`MergeLeaves`

When `'on'`, `ClassificationTree.fit` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, `ClassificationTree.fit` does not merge leaves.

Default: `'on'`

`MinLeaf`

Each leaf has at least `MinLeaf` observations per tree leaf. If you supply both `MinParent` and `MinLeaf`, `ClassificationTree.fit` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: `1`

`MinParent`

Each branch node in the tree has at least `MinParent` observations. If you supply both `MinParent` and `MinLeaf`, `ClassificationTree.fit` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: `10`

`NVarToSample`

Number of predictors to select at random for each split. Can be a positive integer or `'all'`, which means use all available predictors.

Default: `'all'`

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

Default: `{'x1','x2',...}`

`prior`

Prior probabilities for each class. Specify as one of:

- A string:
  - `'empirical'` determines class probabilities from class frequencies in `Y`. If you pass observation weights, they are used to compute the class probabilities.
  - `'uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class)
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as `Y`

- `S.ClassProbs` containing a vector of corresponding probabilities

If you set values for both `weights` and `prior`, the weights are renormalized to add up to the value of the prior probability in the respective class.

Default: `'empirical'`

`Prune`

When `'on'`, `ClassificationTree.fit` grows the classification tree, and computes the optimal sequence of pruned subtrees. When `'off'` `ClassificationTree.fit` grows the classification tree without pruning.

Default: `'on'`

`PruneCriterion`

String with the pruning criterion, either `'error'` or `'impurity'`.

Default: `'error'`

`ResponseName`

Name of the response variable `Y`, a string.

Default: `'Response'`

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function.

String	Formula
`'symmetric'`	$2x - 1$
`'invlogit'`	$\log(x / (1-x))$

String	Formula
`'ismax'`	Set score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'symmetricismax'`	Set score for the class with the largest score to `1`, and scores for all other classes to `-1`.
`'none'`	x
`'logit'`	$1/(1 + e^{-x})$
`'doublelogit'`	$1/(1 + e^{-2x})$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$

You can include your own function handle for transforming scores. Your function should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Default: `'none'`

`SplitCriterion`

Criterion for choosing a split. One of `'gdi'` (Gini's diversity index), `'twoing'` for the twoing rule, or `'deviance'` for maximum deviance reduction (also known as cross entropy).

Default: `'gdi'`

`Surrogate`

When `'on'`, `ClassificationTree.fit` finds surrogate splits at each branch node. This setting improves the accuracy of predictions for data with missing values. The setting also enables

you to compute measures of predictive association between predictors. This setting can use much time and memory.

Default: `'off'`

`weights`

Vector of observation weights. The length of `weights` is the number of rows in `X`. `ClassificationTree.fit` normalizes the weights in each class to add up to the value of the prior probability of the class.

Default: `ones(size(X,1),1)`

Properties

`CategoricalPredictors`

List of categorical predictors, a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CatSplit`

An *n*-by-2 cell array, where *n* is the number of nodes in `tree`. Each row in `CatSplit` gives left and right values for a categorical split. For each branch node `j` based on a categorical predictor variable `z`, the left child is chosen if `z` is in `CatSplit(j,1)` and the right child is chosen if `z` is in `CatSplit(j,2)`. The splits are in the same order as nodes of the tree. Find the nodes for these splits by selecting `'categorical'` cuts from top to bottom in the `CutType` property.

`Children`

An *n*-by-2 array containing the numbers of the child nodes for each node in `tree`, where *n* is the number of nodes. Leaf nodes have child node `0`.

`ClassCount`

An *n*-by-*k* array of class counts for the nodes in `tree`, where *n* is the number of nodes and *k* is the number of classes. For any node number `i`, the class counts `ClassCount(i,:)` are counts of

observations (from the data used in fitting the tree) from each class satisfying the conditions for node `i`.

`ClassNames`

List of the elements in `Y` with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument `Y`.

`ClassProb`

An *n*-by-*k* array of class probabilities for the nodes in `tree`, where *n* is the number of nodes and *k* is the number of classes. For any node number `i`, the class probabilities `ClassProb(i,:)` are the estimated probabilities for each class for a point satisfying the conditions for node `i`.

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`.

`CutCategories`

An *n*-by-2 cell array of the categories used at branches in `tree`, where *n* is the number of nodes. For each branch node `i` based on a categorical predictor variable `x`, the left child is chosen if `x` is among the categories listed in `CutCategories{i,1}`, and the right child is chosen if `x` is among those listed in `CutCategories{i,2}`. Both columns of `CutCategories` are empty for branch nodes based on continuous predictors and for leaf nodes.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutPoint`

An *n*-element vector of the values used as cut points in `tree`, where *n* is the number of nodes. For each branch node `i` based on a continuous predictor variable `x`, the left child is chosen if `x<CutPoint(i)` and the right child is chosen if `x>=CutPoint(i)`.

`CutPoint` is `NaN` for branch nodes based on categorical predictors and for leaf nodes.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutType`

An *n*-element cell array indicating the type of cut at each node in `tree`, where *n* is the number of nodes. For each node `i`, `CutType{i}` is:

- `'continuous'` — If the cut is defined in the form `x < v` for a variable `x` and cut point `v`.
- `'categorical'` — If the cut is defined by whether a variable `x` takes a value in a set of categories.
- `''` — If `i` is a leaf node.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutVar`

An *n*-element cell array of the names of the variables used for branching in each node in `tree`, where *n* is the number of nodes. These variables are sometimes known as *cut variables*. For leaf nodes, `CutVar` contains an empty string.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`IsBranch`

An *n*-element logical vector that is `true` for each branch node and `false` for each leaf node of `tree`.

`ModelParams`

Parameters used in training `tree`.

`NObservations`

Number of observations in the training data, a numeric scalar. `NObservations` can be less than the number of rows of input data `X` when there are missing values in `X` or response `Y`.

`NodeClass`

An *n*-element cell array with the names of the most probable classes in each node of `tree`, where *n* is the number of nodes in the tree. Every element of this array is a string equal to one of the class names in `ClassNames`.

`NodeErr`

An *n*-element vector of the errors of the nodes in `tree`, where *n* is the number of nodes. `NodeErr(i)` is the misclassification probability for node `i`.

`NodeProb`

An *n*-element vector of the probabilities of the nodes in `tree`, where *n* is the number of nodes. The probability of a node is computed as the proportion of observations from the original data that satisfy the conditions for the node. This proportion is adjusted for any prior probabilities assigned to each class.

`NodeSize`

An *n*-element vector of the sizes of the nodes in `tree`, where *n* is the number of nodes. The size of a node is defined as the number of observations from the data used to create the tree that satisfy the conditions for the node.

`NumNodes`

The number of nodes in `tree`.

`Parent`

An *n*-element vector containing the number of the parent node for each node in `tree`, where *n* is the number of nodes. The parent of the root node is `0`.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`Prior`

Prior probabilities for each class. `Prior` is a numeric vector whose entries relate to the corresponding `ClassNames` property.

`PruneList`

An n-element numeric vector with the pruning levels in each node of `tree`, where n is the number of nodes.

`ResponseName`

String describing the response variable `Y`.

`Risk`

An n-element vector of the risk of the nodes in `tree`, where n is the number of nodes.

- If `tree` was grown with `SplitCriterion` set to either `'gdi'` (default) or `'deviance'`, then the risk at node `i` is the impurity of node `i` times the node probability. See "Definitions" on page 20-210.
- Otherwise,

  `Risk(i) = NodeErr(i) * NodeProb(i).`

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`.

Add or change a `ScoreTransform` function by dot addressing:

```
tree.ScoreTransform = 'function'
or
tree.ScoreTransform = @function
```

`SurrCutCategories`

An n-element cell array of the categories used for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutCategories{k}` is a cell array. The length of `SurrCutCategories{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutCategories{k}` is either an empty string for a continuous surrogate predictor, or is a two-element cell array with categories for a categorical surrogate predictor. The first element of this two-element cell array lists categories assigned to the left child by this surrogate split, and the second element of this two-element cell array lists categories assigned to the right child by this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutCategories` contains an empty cell.

`SurrCutFlip`

An n-element cell array of the numeric cut assignments used for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutFlip{k}` is a numeric vector. The length of `SurrCutFlip{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutFlip{k}` is either zero for a categorical surrogate predictor, or a numeric cut assignment for a continuous surrogate predictor. The numeric cut assignment can be either –1 or +1. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and the cut assignment for this surrogate split is +1, or if $Z\geq C$ and the cut assignment for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and the cut assignment for this surrogate split is +1, or if $Z<C$ and the cut assignment for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutFlip` contains an empty array.

`SurrCutPoint`

An n-element cell array of the numeric values used for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutPoint{k}` is a numeric vector. The length of `SurrCutPoint{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutPoint{k}` is either `NaN` for a categorical surrogate predictor, or a numeric cut for a continuous surrogate predictor. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and `SurrCutFlip` for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and `SurrCutFlip` for this surrogate split is +1, or if $Z<C$ and `SurrCutFlip` for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables returned by `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutPoint` contains an empty cell.

`SurrCutType`

An n-element cell array indicating types of surrogate splits at each node in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutType{k}` is a cell array with the types of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutType` contains an empty cell. A surrogate split type can be either `'continuous'` if the cut is defined in the form `Z<V` for a variable `Z` and cut point `V` or `'categorical'` if the cut is defined by whether `Z` takes a value in a set of categories.

`SurrCutVar`

An *n*-element cell array of the names of the variables used for surrogate splits in each node in `tree`, where *n* is the number of nodes in `tree`. Every element of `SurrCutVar` is a cell array with the names of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutVar` contains an empty cell.

`SurrVarAssoc`

An *n*-element cell array of the predictive measures of association for surrogate splits in `tree`, where *n* is the number of nodes in `tree`. For each node `k`, `SurrVarAssoc{k}` is a numeric vector. The length of `SurrVarAssoc{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrVarAssoc{k}` gives the predictive measure of association between the optimal split and this surrogate split. The order of the surrogate split variables at each node is the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrVarAssoc` contains an empty cell.

`W`

The scaled `weights`, a vector with length `n`, the number of rows in `X`.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding row of `X`.

Methods

compact	Compact tree
crossval	Cross-validated decision tree
cvloss	Classification error by cross validation
fit	Fit classification tree
prune	Produce sequence of subtrees by pruning
resubEdge	Classification edge by resubstitution
resubLoss	Classification error by resubstitution
resubMargin	Classification margins by resubstitution
resubPredict	Predict resubstitution response of tree
template	Create classification template

Inherited Methods

edge	Classification edge
loss	Classification error
margin	Classification margins
meanSurrVarAssoc	Mean predictive measure of association for surrogate splits in decision tree
predict	Predict classification
predictorImportance	Estimates of predictor importance
view	View tree

Definitions

Impurity and Node Error

`ClassificationTree` splits nodes based on either *impurity* or *node error*. Impurity means one of several things, depending on your choice of the `SplitCriterion` name-value pair:

- Gini's Diversity Index (`gdi`) — The Gini index of a node is

  $$1 - \sum_i p^2(i),$$

  where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index `0`; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.

- Deviance (`'deviance'`) — With $p(i)$ defined as for the Gini index, the deviance of a node is

  $$-\sum_i p(i) \log p(i).$$

  A pure node has deviance `0`; otherwise, the deviance is positive.

- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

  $$P(L)P(R)\left(\sum_i |L(i) - R(i)|\right)^2,$$

  where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.

- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with largest number of training samples at a node, the node error is

  $1 - p(j)$.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Construct a classification tree for the data in `ionosphere.mat`:

```
load ionosphere
tc = ClassificationTree.fit(X,Y)

tc =

ClassificationTree:
           PredictorNames: {1x34 cell}
    CategoricalPredictors: []
             ResponseName: 'Response'
               ClassNames: {'b'  'g'}
                     Cost: [2x2 double]
                    Prior: [0.3590 0.6410]
           ScoreTransform: 'none'
                        X: [351x34 double]
                        Y: {351x1 cell}
                        W: [351x1 double]
             ModelParams: [1x1 classreg.learning.modelparams.TreeParams]
```

See Also

`RegressionTree` | `ClassificationEnsemble` | `ClassificationTree.fit` | `CompactClassificationTree` | `predict`

How To

- “Classification Trees and Regression Trees” on page 13-27

classify

Purpose

Discriminant analysis

Syntax

```
class = classify(sample,training,group)
class = classify(sample,training,group,'type')
class = classify(sample,training,group,'type',prior)
[class,err] = classify(...)
[class,err,POSTERIOR] = classify(...)
[class,err,POSTERIOR,logp] = classify(...)
[class,err,POSTERIOR,logp,coeff] = classify(...)
```

Description

`class = classify(sample,training,group)` classifies each row of the data in `sample` into one of the groups in `training`. (See "Grouped Data" on page 2-34.) `sample` and `training` must be matrices with the same number of columns. `group` is a grouping variable for `training`. Its unique values define groups; each element defines the group to which the corresponding row of `training` belongs. `group` can be a categorical variable, a numeric vector, a string array, or a cell array of strings. `training` and `group` must have the same number of rows. `classify` treats `NaN`s or empty strings in `group` as missing values, and ignores the corresponding rows of `training`. The output `class` indicates the group to which each row of `sample` has been assigned, and is of the same type as `group`.

`class = classify(sample,training,group,'type')` allows you to specify the type of discriminant function. Specify *`type`* inside single quotes. *`type`* is one of:

- `linear` — Fits a multivariate normal density to each group, with a pooled estimate of covariance. This is the default.
- `diaglinear` — Similar to `linear`, but with a diagonal covariance matrix estimate (naive Bayes classifiers).
- `quadratic` — Fits multivariate normal densities with covariance estimates stratified by group.
- `diagquadratic` — Similar to `quadratic`, but with a diagonal covariance matrix estimate (naive Bayes classifiers).

- `mahalanobis` — Uses Mahalanobis distances with stratified covariance estimates.

`class = classify(sample,training,group,'type',prior)` allows you to specify prior probabilities for the groups. *`prior`* is one of:

- A numeric vector the same length as the number of unique values in `group` (or the number of levels defined for `group`, if `group` is categorical). If `group` is numeric or categorical, the order of *`prior`* must correspond to the ordered values in `group`, or, if `group` contains strings, to the order of first occurrence of the values in `group`.
- A 1-by-1 structure with fields:
  - `prob` — A numeric vector.
  - `group` — Of the same type as `group`, containing unique values indicating the groups to which the elements of `prob` correspond.

  As a structure, *`prior`* can contain groups that do not appear in `group`. This can be useful if `training` is a subset a larger training set. `classify` ignores any groups that appear in the structure but not in the `group` array.
- The string `'empirical'`, indicating that group prior probabilities should be estimated from the group relative frequencies in `training`.

`prior` defaults to a numeric vector of equal probabilities, i.e., a uniform distribution. *`prior`* is not used for discrimination by Mahalanobis distance, except for error rate calculation.

`[class,err] = classify(...)` also returns an estimate `err` of the misclassification error rate based on the `training` data. `classify` returns the apparent error rate, i.e., the percentage of observations in `training` that are misclassified, weighted by the prior probabilities for the groups.

`[class,err,POSTERIOR] = classify(...)` also returns a matrix `POSTERIOR` of estimates of the posterior probabilities that the *j*th training group was the source of the *i*th sample observation, i.e.,

Pr(*group j*|*obs i*). `POSTERIOR` is not computed for Mahalanobis discrimination.

`[class,err,POSTERIOR,logp] = classify(...)` also returns a vector `logp` containing estimates of the logarithms of the unconditional predictive probability density of the sample observations, $p(obs\ i) = \sum p(obs\ i|group\ j)Pr(group\ j)$ over all groups. `logp` is not computed for Mahalanobis discrimination.

`[class,err,POSTERIOR,logp,coeff] = classify(...)` also returns a structure array `coeff` containing coefficients of the boundary curves between pairs of groups. Each element `coeff(I,J)` contains information for comparing group `I` to group `J` in the following fields:

- `type` — Type of discriminant function, from the *`type`* input.
- `name1` — Name of the first group.
- `name2` — Name of the second group.
- `const` — Constant term of the boundary equation (K)
- `linear` — Linear coefficients of the boundary equation (L)
- `quadratic` — Quadratic coefficient matrix of the boundary equation (Q)

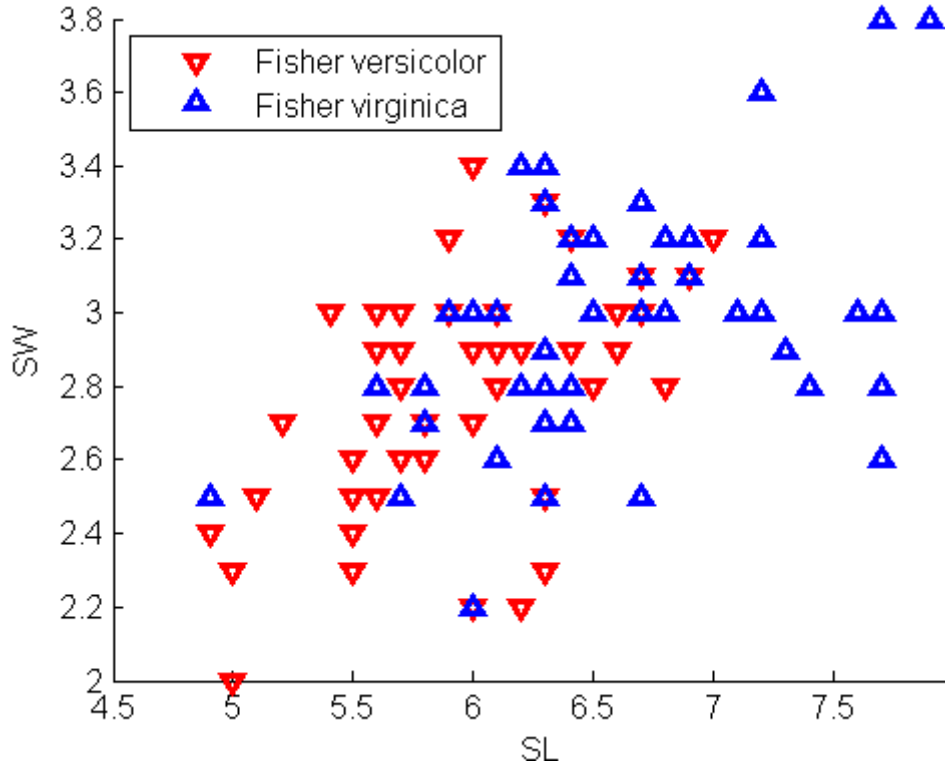
For the `linear` and `diaglinear` types, the `quadratic` field is absent, and a row `x` from the `sample` array is classified into group `I` rather than group `J` if `0 < K+x*L`. For the other types, `x` is classified into group `I` if `0 < K+x*L+x*Q*x'`.

Examples

For training data, use Fisher's sepal measurements for iris versicolor and virginica:

```
load fisheriris
SL = meas(51:end,1);
SW = meas(51:end,2);
group = species(51:end);
h1 = gscatter(SL,SW,group,'rb','v^',[],'off');
```

```
set(h1,'LineWidth',2)
legend('Fisher versicolor','Fisher virginica',...
       'Location','NW')
```

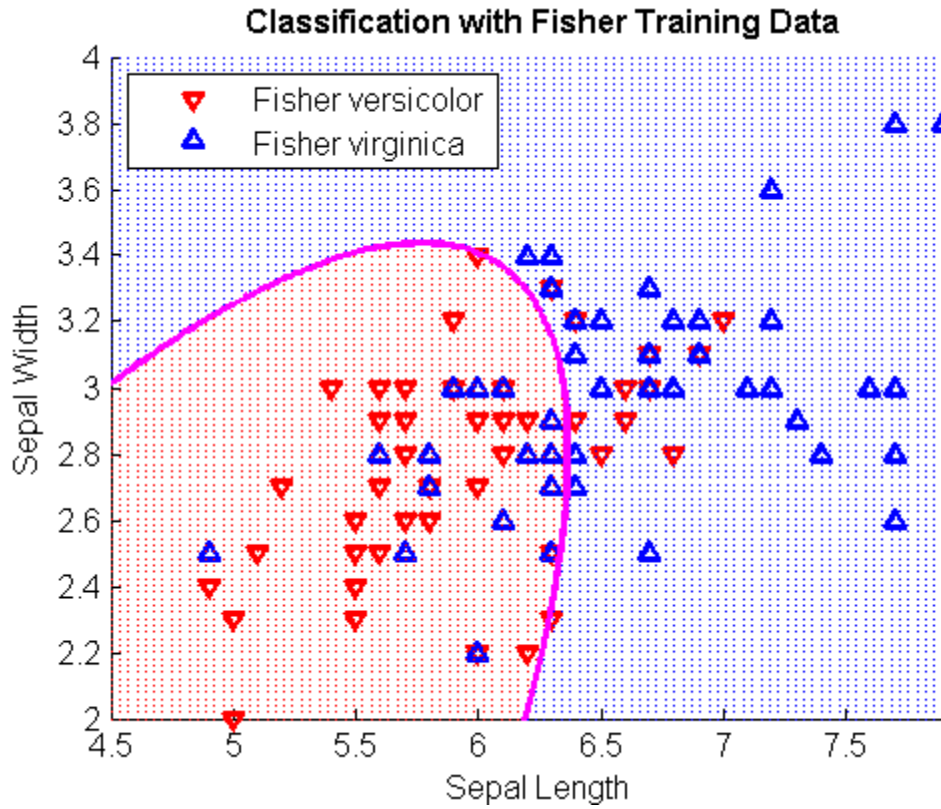


Classify a grid of measurements on the same scale:

```
[X,Y] = meshgrid(linspace(4.5,8),linspace(2,4));
X = X(:); Y = Y(:);
[C,err,P,logp,coeff] = classify([X Y],[SL SW],...
                                 group,'quadratic');
```

Visualize the classification:

```
hold on;
gscatter(X,Y,C,'rb','.',1,'off');
K = coeff(1,2).const;
L = coeff(1,2).linear;
Q = coeff(1,2).quadratic;
% Function to compute K + L*v + v'*Q*v for multiple vectors
% v=[x;y]. Accepts x and y as scalars or column vectors.
f = @(x,y) K + [x y]*L + sum(([x y]*Q) .* [x y], 2);

h2 = ezplot(f,[4.5 8 2 4]);
set(h2,'Color','m','LineWidth',2)
axis([4.5 8 2 4])
xlabel('Sepal Length')
ylabel('Sepal Width')
title('{\bf Classification with Fisher Training Data}')
```



References

[1] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

[2] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

See Also

`classregtree` | `mahal` | `NaiveBayes`

How To

- "Grouped Data" on page 2-34

classregtree.classname

Purpose

Class names for classification decision tree

Syntax

```
CNAMES = classname(T)
CNAMES = classname(T,J)
```

Description

`CNAMES = classname(T)` returns a cell array of strings with class names for this classification decision tree.

`CNAMES = classname(T,J)` takes an array `J` of class numbers and returns the class names for the specified numbers.

See Also

`classregtree`

Purpose

Names of classes

Description

The `ClassNames` property is a cell array containing the class names for the response variable `Y`. This property is empty for regression trees.

classregtree.classprob

Purpose

Class probabilities

Syntax

```
P = classprob(t)
P = classprob(t,nodes)
```

Description

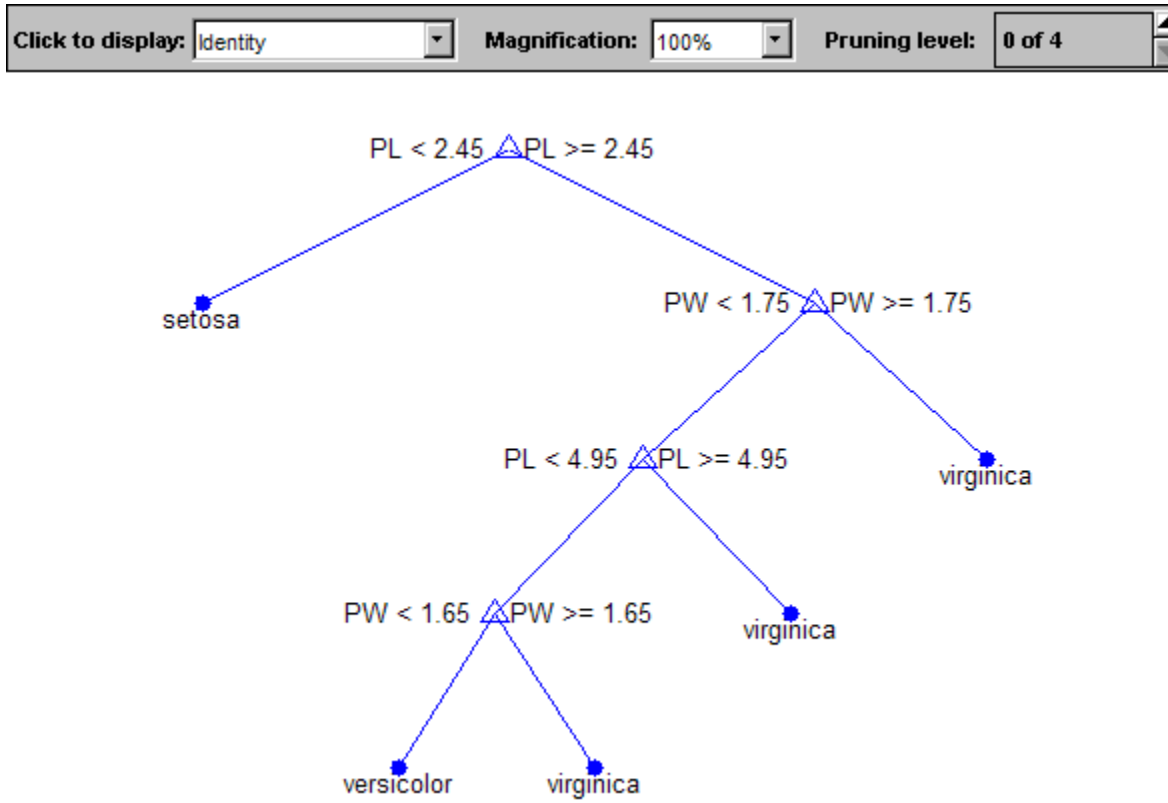
`P = classprob(t)` returns an *n*-by-*m* array `P` of class probabilities for the nodes in the classification tree `t`, where *n* is the number of nodes and *m* is the number of classes. For any node number `i`, the class probabilities `P(i,:)` are the estimated probabilities for each class for a point satisfying the conditions for node `i`.

`P = classprob(t,nodes)` takes a vector `nodes` of node numbers and returns the class probabilities for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
P = classprob(t)
P =
    0.3333    0.3333    0.3333
    1.0000         0         0
         0    0.5000    0.5000
         0    0.9074    0.0926
         0    0.0217    0.9783
         0    0.9792    0.0208
         0    0.3333    0.6667
         0    1.0000         0
```

```
         0         0    1.0000
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes`

Purpose

Classification and regression trees

Construction

classregtree	Construct classification and regression trees

Methods

catsplit	Categorical splits used for branches in decision tree
children	Child nodes
classcount	Class counts
classname	Class names for classification decision tree
classprob	Class probabilities
cutcategories	Cut categories
cutpoint	Decision tree cut point values
cuttype	Cut types
cutvar	Cut variable names
disp	Display `classregtree` object
display	Display `classregtree` object
eval	Predicted responses
isbranch	Test node for branch
meansurrvarassoc	Mean predictive measure of association for surrogate splits in decision tree
nodeclass	Class values of nodes of classification tree
nodeerr	Return vector of node errors

nodemean	Mean values of nodes of regression tree
nodeprob	Node probabilities
nodesize	Return node size
numnodes	Number of nodes
parent	Parent node
prune	Prune tree
prunelist	Pruning levels for decision tree nodes
risk	Node risks
subsasgn	Subscripted reference for `classregtree` object
subsref	Subscripted reference for `classregtree` object
surrcutcategories	Categories used for surrogate splits in decision tree
surrcutflip	Numeric cutpoint assignments used for surrogate splits in decision tree
surrcutpoint	Cutpoints used for surrogate splits in decision tree
surrcuttype	Types of surrogate splits used at branches in decision tree
surrcutvar	Variables used for surrogate splits in decision tree
surrvarassoc	Predictive measure of association for surrogate splits in decision tree
test	Error rate

type	Tree type
varimportance	Compute embedded estimates of input feature importance
view	Plot tree

Properties

Objects of the `classregtree` class have no properties accessible by dot indexing, `get` methods, or `set` methods. To obtain information about a `classregtree` object, use the appropriate method.

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

How To

- "Ensemble Methods" on page 13-51
- "Classification Trees and Regression Trees" on page 13-27
- "Grouped Data" on page 2-34

classregtree

Purpose

Construct classification and regression trees

Syntax

```
t = classregtree(X,y)
t = classregtree(X,y,'Name',value)
```

Description

`t = classregtree(X,y)` creates a decision tree `t` for predicting the response `y` as a function of the predictors in the columns of `X`. `X` is an n-by-m matrix of predictor values. If `y` is a vector of n response values, `classregtree` performs regression. If `y` is a categorical variable, character array, or cell array of strings, `classregtree` performs classification. Either way, `t` is a binary tree where each branching node is split based on the values of a column of `X`. `NaN` values in `X` or `y` are taken to be missing values. Observations with all missing values for `X` or missing values for `y` are not used in the fit. Observations with some missing values for `X` are used to find splits on variables for which these observations have valid values.

`t = classregtree(X,y,'Name',value)` specifies one or more optional parameter name/value pairs. Specify *`Name`* in single quotes. The following options are available:

For all trees:

- `categorical` — Vector of indices of the columns of `X` that are to be treated as unordered categorical variables
- `method` — Either `'classification'` (default if `y` is text or a categorical variable) or `'regression'` (default if `y` is numeric).
- `names` — A cell array of names for the predictor variables, in the order in which they appear in the `X` from which the tree was created.
- `prune` — `'on'` (default) to compute the full tree and the optimal sequence of pruned subtrees, or `'off'` for the full tree without pruning.
- `minparent` — A number *k* such that impure nodes must have *k* or more observations to be split (default is `10`).
- `minleaf` — A minimal number of observations per tree leaf (default is `1`). If you supply both `'minparent'` and `'minleaf'`, `classregtree` uses the setting which results in larger leaves: `minparent = max(minparent,2*minleaf)`
- `mergeleaves` — `'on'` (default) to merge leaves that originate from the same parent node and give the sum of risk values greater or equal to the risk associated with the parent node. If `'off'`, `classregtree` does not merge leaves.
- `nvartosample` — Number of predictor variables randomly selected for each split. By default all variables are considered for each decision split.
- `stream` — Random number stream. Default is the MATLAB default random number stream.
- `surrogate` — `'on'` to find surrogate splits at each branch node. Default is `'off'`. If you set this parameter to `'on'`,`classregtree` can run significantly slower and consume significantly more memory.
- `weights` — Vector of observation weights. By default the weight of every observation is 1. The length of this vector must be equal to the number of rows in `X`.

For regression trees only:

- `qetoler` — Defines tolerance on quadratic error per node for regression trees. Splitting nodes stops when quadratic error per node drops below `qetoler*qed`, where `qed` is the quadratic error for the entire data computed before the decision tree is grown: `qed = norm(y-ybar)` with `ybar` estimated as the average of the input array `Y`. Default value is 1e-6.

For classification trees only:

- `cost` — Square matrix `C`, where `C(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (default has `C(i,j)=1` if `i~=j`, and `C(i,j)=0` if `i=j`). Alternatively, this value can be a structure `S` having two fields: `S.group` containing the group names as a categorical variable, character array, or cell array of strings; and `S.cost` containing the cost matrix C.
- `splitcriterion` — Criterion for choosing a split. One of `'gdi'` (default) or Gini's diversity index, `'twoing'` for the twoing rule, or `'deviance'` for maximum deviance reduction.
- `priorprob` — Prior probabilities for each class, specified as a string (`'empirical'` or `'equal'`) or as a vector (one value for each distinct group name) or as a structure `S` with two fields:
  - `S.group` containing the group names as a categorical variable, character array, or cell array of strings
  - `S.prob` containing a vector of corresponding probabilities.

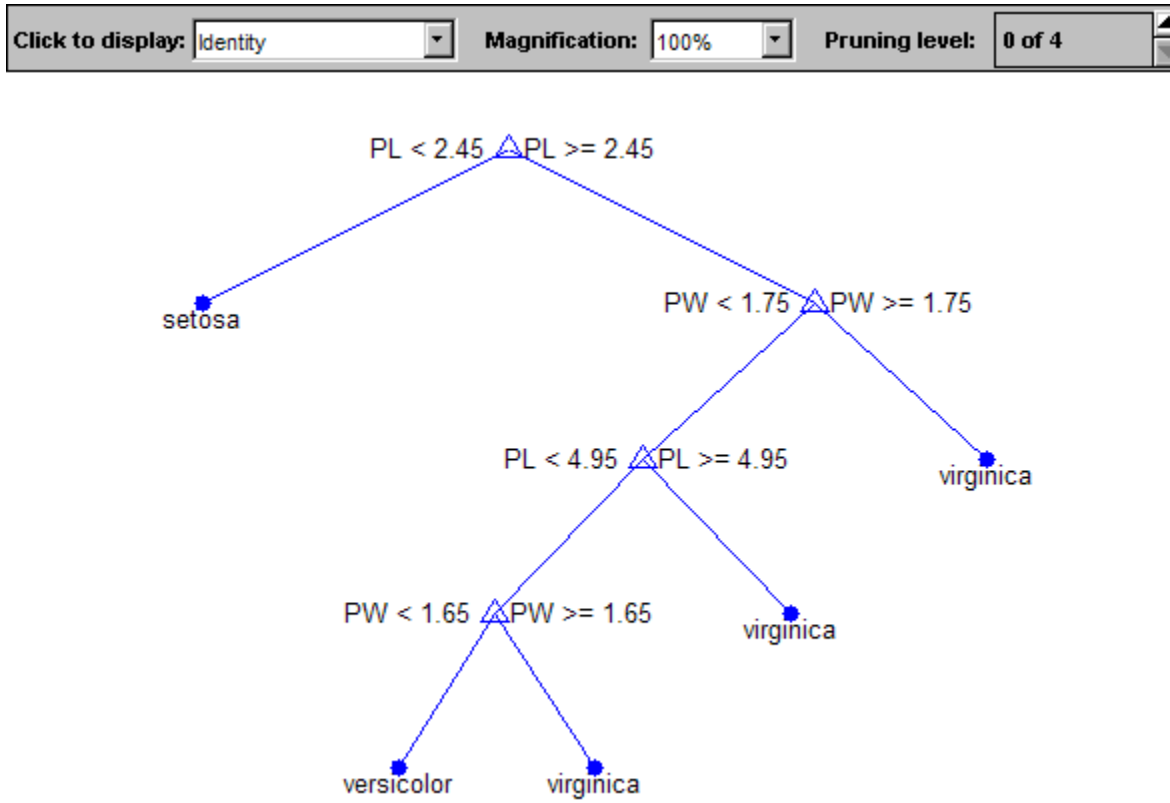
  If the input value is `'empirical'` (default), class probabilities are determined from class frequencies in `Y`. If the input value is `'equal'`, all class probabilities are set equal. If both observation weights and class prior probabilities are supplied, the weights are renormalized to add up to the value of the prior probability in the respective class.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;
```

```
t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`eval` | `prune` | `test` | `view`

How To

- Grouped Data
- “Ensemble Methods” on page 13-51

Purpose

Class levels

Description

The `CLevels` property is a vector of the same type as the grouping variable, containing the unique levels of the grouping variable.

cluster

Purpose

Construct agglomerative clusters from linkages

Syntax

```
T = cluster(Z,'cutoff',c)
T = cluster(Z,'cutoff',c,'depth',d)
T = cluster(Z,'cutoff',c,'criterion',criterion)
T = cluster(Z,'maxclust',n)
```

Description

`T = cluster(Z,'cutoff',c)` constructs clusters from the agglomerative hierarchical cluster tree, `Z`, as generated by the `linkage` function. `Z` is a matrix of size (`m` – 1)-by-3, where `m` is the number of observations in the original data. `c` is a threshold for cutting `Z` into clusters. Clusters are formed when a node and all of its subnodes have `inconsistent` value less than `c`. All leaves at or below the node are grouped into a cluster. `t` is a vector of size `m` containing the cluster assignments of each observation.

If `c` is a vector, `T` is a matrix of cluster assignments with one column per cutoff value.

`T = cluster(Z,'cutoff',c,'depth',d)` evaluates inconsistent values by looking to a depth `d` below each node. The default depth is `2`.

`T = cluster(Z,'cutoff',c,'criterion',criterion)` uses the specified criterion for forming clusters, where `criterion` is one of the strings `'inconsistent'` (default) or `'distance'`. The `'distance'` criterion uses the distance between the two subnodes merged at a node to measure node height. All leaves at or below a node with height less than `c` are grouped into a cluster.

`T = cluster(Z,'maxclust',n)` constructs a maximum of `n` clusters using the `'distance'` criterion. `cluster` finds the smallest height at which a horizontal cut through the tree leaves `n` or fewer clusters.

If `n` is a vector, `T` is a matrix of cluster assignments with one column per maximum value.

Examples

Compare clusters from Fisher iris data with species:

```
load fisheriris
```

```
d = pdist(meas);
Z = linkage(d);
c = cluster(Z,'maxclust',3:5);

crosstab(c(:,1),species)
ans =
     0     0     2
     0    50    48
    50     0     0

crosstab(c(:,2),species)
ans =
     0     0     1
     0    50    47
     0     0     2
    50     0     0

crosstab(c(:,3),species)
ans =
     0     4     0
     0    46    47
     0     0     1
     0     0     2
    50     0     0
```

See Also

clusterdata | cophenet | inconsistent | linkage | pdist

gmdistribution.cluster

Purpose

Construct clusters from Gaussian mixture distribution

Syntax

```
idx = cluster(obj,X)
[idx,nlogl] = cluster(obj,X)
[idx,nlogl,P] = cluster(obj,X)
[idx,nlogl,P,logpdf] = cluster(obj,X)
[idx,nlogl,P,logpdf,M] = cluster(obj,X)
```

Description

`idx = cluster(obj,X)` partitions data in the n-by-d matrix `X`, where n is the number of observations and d is the dimension of the data, into k clusters determined by the k components of the Gaussian mixture distribution defined by `obj`. `obj` is an object created by `gmdistribution` or `fit`. `idx` is an n-by-1 vector, where `idx(I)` is the cluster index of observation `I`. The cluster index gives the component with the largest posterior probability for the observation, weighted by the component probability.

Note The data in `X` is typically the same as the data used to create the Gaussian mixture distribution defined by `obj`. Clustering with `cluster` is treated as a separate step, apart from density estimation. For `cluster` to provide meaningful clustering with new data, `X` should come from the same population as the data used to create `obj`.

`cluster` treats `NaN` values as missing data. Rows of `X` with `NaN` values are excluded from the partition.

`[idx,nlogl] = cluster(obj,X)` also returns `nlogl`, the negative log-likelihood of the data.

`[idx,nlogl,P] = cluster(obj,X)` also returns the posterior probabilities of each component for each observation in the n-by-k matrix `P`. `P(I,J)` is the probability of component `J` given observation `I`.

`[idx,nlogl,P,logpdf] = cluster(obj,X)` also returns the n-by-1 vector `logpdf` containing the logarithm of the estimated probability density function for each observation. The density estimate for

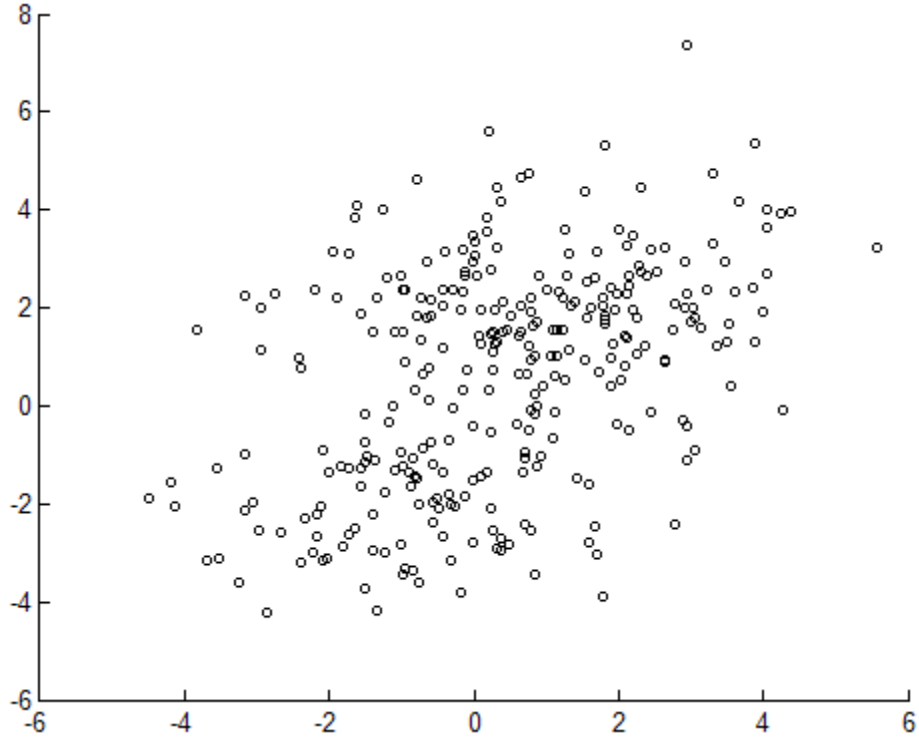
observation `I` is a sum over all components of the component density at `I` times the component probability.

`[idx,nlogl,P,logpdf,M] = cluster(obj,X)` also returns an n-by-k matrix `M` containing Mahalanobis distances in squared units. `M(I,J)` is the Mahalanobis distance of observation `I` from the mean of component `J`.

Examples

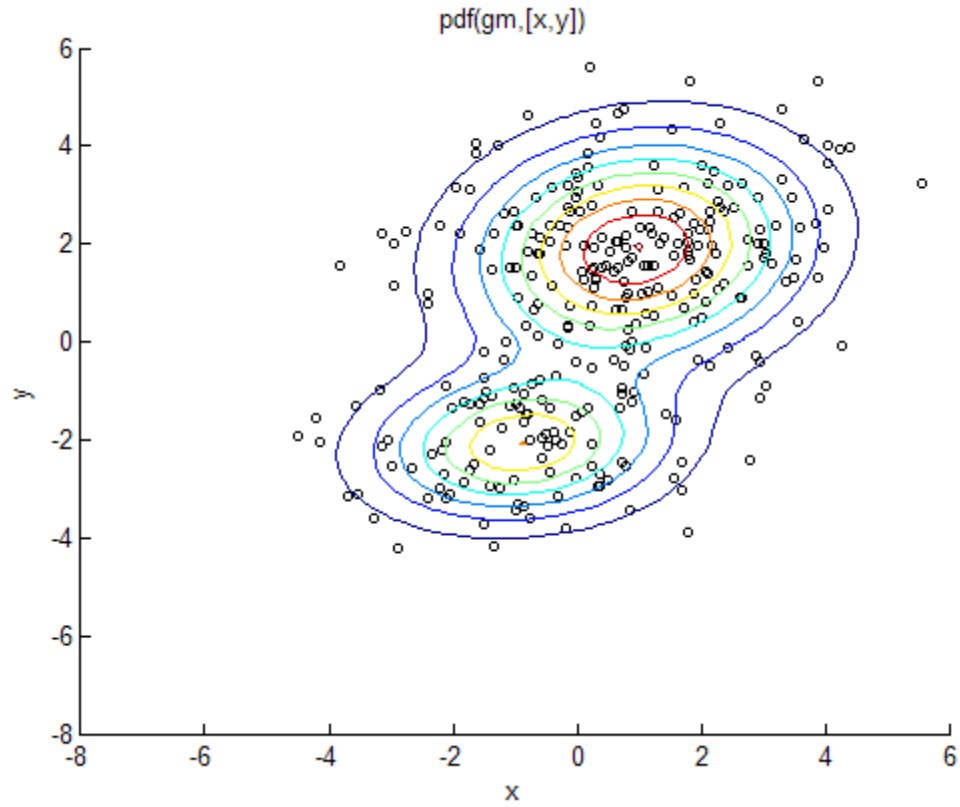
Generate data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function:

```
MU1 = [1 2];
SIGMA1 = [2 0; 0 .5];
MU2 = [-3 -5];
SIGMA2 = [1 0; 0 1];
X = [mvnrnd(MU1,SIGMA1,1000);mvnrnd(MU2,SIGMA2,1000)];

scatter(X(:,1),X(:,2),10,'.')
hold on
```



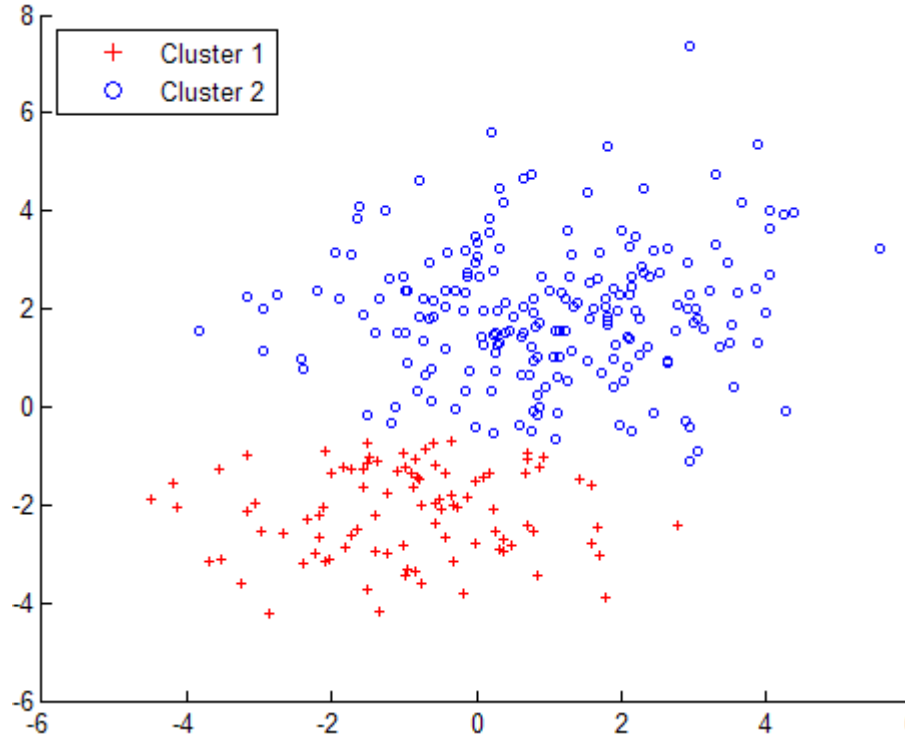
Fit a two-component Gaussian mixture model:

```
obj = gmdistribution.fit(X,2);
h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
```



Use the fit to cluster the data:

```
idx = cluster(obj,X);
cluster1 = X(idx == 1,:);
cluster2 = X(idx == 2,:);

delete(h)
h1 = scatter(cluster1(:,1),cluster1(:,2),10,'r.');
h2 = scatter(cluster2(:,1),cluster2(:,2),10,'g.');
legend([h1 h2],'Cluster 1','Cluster 2','Location','NW')
```



See Also

`fit` | `gmdistribution` | `mahal` | `posterior`

Purpose

Agglomerative clusters from data

Syntax

```
T = clusterdata(X,cutoff)
T = clusterdata(X,Name,Value)
```

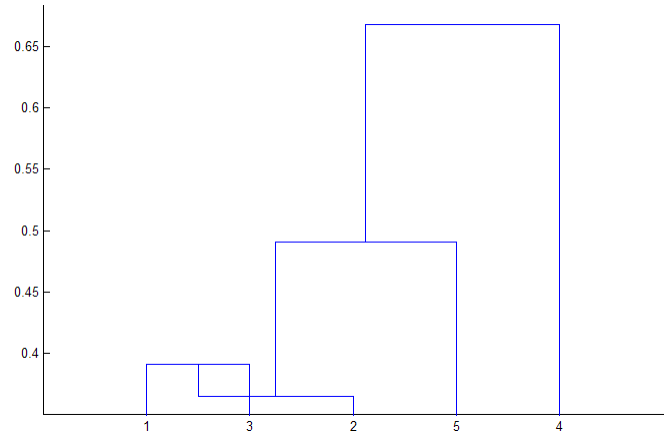
Description

`T = clusterdata(X,cutoff)`

`T = clusterdata(X,Name,Value)` clusters with additional options specified by one or more `Name,Value` pair arguments.

Tips

- The `centroid` and `median` methods can produce a cluster tree that is not monotonic. This occurs when the distance from the union of two clusters, *r* and *s*, to a third cluster is less than the distance between *r* and *s*. In this case, in a dendrogram drawn with the default orientation, the path from a leaf to the root node takes some downward steps. To avoid this, use another method. The following image shows a nonmonotonic cluster tree.



In this case, cluster 1 and cluster 3 are joined into a new cluster, while the distance between this new cluster and cluster 2 is less than the distance between cluster 1 and cluster 3. This leads to a nonmonotonic tree.

- You can provide the output `T` to other functions including `dendrogram` to display the tree, `cluster` to assign points to clusters, `inconsistent` to compute inconsistent measures, and `cophenet` to compute the cophenetic correlation coefficient.

Input Arguments

`X`

Matrix with two or more rows. The rows represent observations, the columns represent categories or dimensions.

`cutoff`

When `0 < cutoff < 2`, `clusterdata` forms clusters when inconsistent values are greater than `cutoff` (see `inconsistent`). When `cutoff` is an integer ≥ 2, `clusterdata` interprets `cutoff` as the maximum number of clusters to keep in the hierarchical tree generated by `linkage`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`criterion`

Either `'inconsistent'` or `'distance'`.

`cutoff`

Cutoff for inconsistent or distance measure, a positive scalar. When `0 < cutoff < 2`, `clusterdata` forms clusters when inconsistent values are greater than `cutoff` (see `inconsistent`). When `cutoff` is an integer ≥ 2, `clusterdata` interprets `cutoff` as the maximum number of clusters to keep in the hierarchical tree generated by `linkage`.

`depth`

Depth for computing inconsistent values, a positive integer.

`distance`

Any of the distance metric names allowed by `pdist` (follow the `'minkowski'` option by the value of the exponent `p`):

Metric	Description
`'euclidean'`	Euclidean distance (default).
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between rows in X is scaled by dividing by the corresponding element of the standard deviation `S=nanstd(X)`. To specify another value for `S`, use `D=pdist(X,'seuclidean',S)`.
`'cityblock'`	City block metric.
`'minkowski'`	Minkowski distance. The default exponent is 2. To specify a different exponent, use `D = pdist(X,'minkowski',P)`, where `P` is a
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'mahalanobis'`	Mahalanobis distance, using the sample covariance of `X` as computed by `nancov`. To compute the distance with a different covariance, use `D = pdist(X,'mahalanobis',C)`, where the matrix `C` is symmetric and positive definite.
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors).
`'correlation'`	One minus the sample correlation between points (treated as sequences of values).
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).

Metric	Description
`'hamming'`	Hamming distance, which is the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.

custom distance function	A distance function specified using @:
	`D = pdist(X,@distfun)`
	A distance function must be of form
	`d2 = distfun(XI,XJ)`
	taking as arguments a 1-by-n vector `XI`, corresponding to a single row of `X`, and an m2-by-n matrix `XJ`, corresponding to multiple rows of `X`. `distfun` must accept a matrix `XJ` with an arbitrary number of rows. `distfun` must return an m2-by-1 vector of distances `d2`, whose kth element is the distance between `XI` and `XJ(k,:)`.

`linkage`

Any of the linkage methods allowed by the `linkage` function:

- `'average'`
- `'centroid'`
- `'complete'`
- `'median'`
- `'single'`
- `'ward'`
- `'weighted'`

For details, see the definitions in the `linkage` function reference page.

`maxclust`

Maximum number of clusters to form, a positive integer.

`savememory`

A string, either `'on'` or `'off'`. When applicable, the `'on'` setting causes `clusterdata` to construct clusters without computing the distance matrix. `savememory` is applicable when:

- `linkage` is `'centroid'`, `'median'`, or `'ward'`
- `distance` is `'euclidean'` (default)

When `savememory` is `'on'`, `linkage` run time is proportional to the number of dimensions (number of columns of `X`). When `savememory` is `'off'`, `linkage` memory requirement is proportional to N^2, where `N` is the number of observations. So choosing the best (least-time) setting for `savememory` depends on the problem dimensions, number of observations, and available memory. The default `savememory` setting is a rough approximation of an optimal setting.

Default: `'on'` when `X` has 20 columns or fewer, or the computer does not have enough memory to store the distance matrix; otherwise `'off'`

Output Arguments

`T`

`T` is a vector of size `m` containing a cluster number for each observation.

- When `0 < cutoff < 2`, `T = clusterdata(X,cutoff)` is equivalent to:

```
Y = pdist(X,'euclid');
```

```
Z = linkage(Y,'single');
T = cluster(Z,'cutoff',cutoff);
```

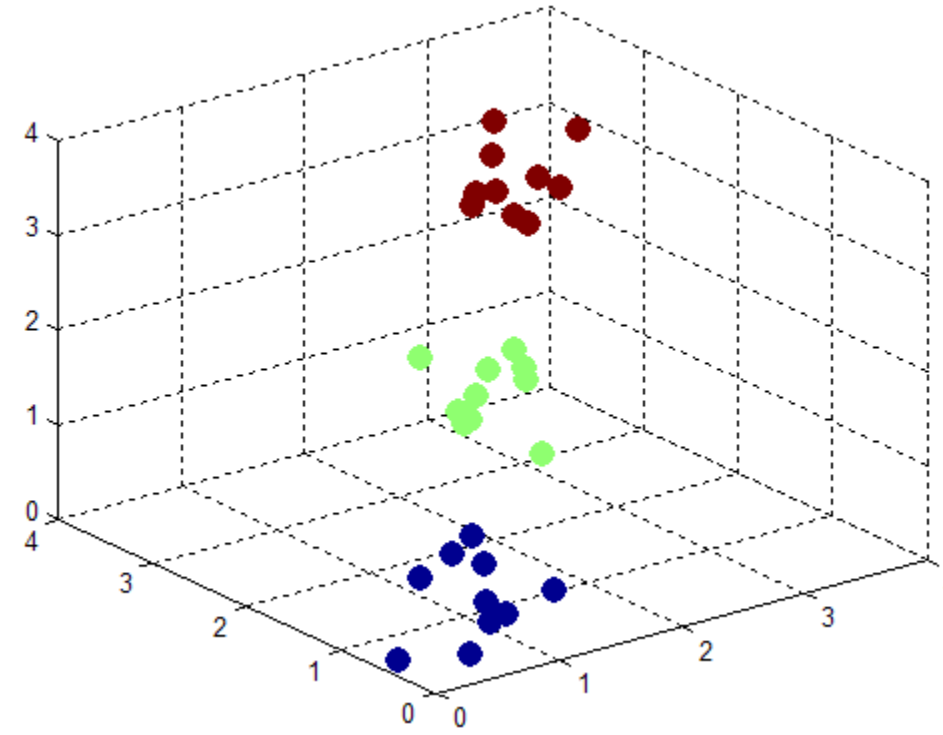
- When `cutoff` is an integer ≥ 2, `T = clusterdata(X,cutoff)` is equivalent to:

```
Y = pdist(X,'euclid');
Z = linkage(Y,'single');
T = cluster(Z,'maxclust',cutoff);
```

Examples

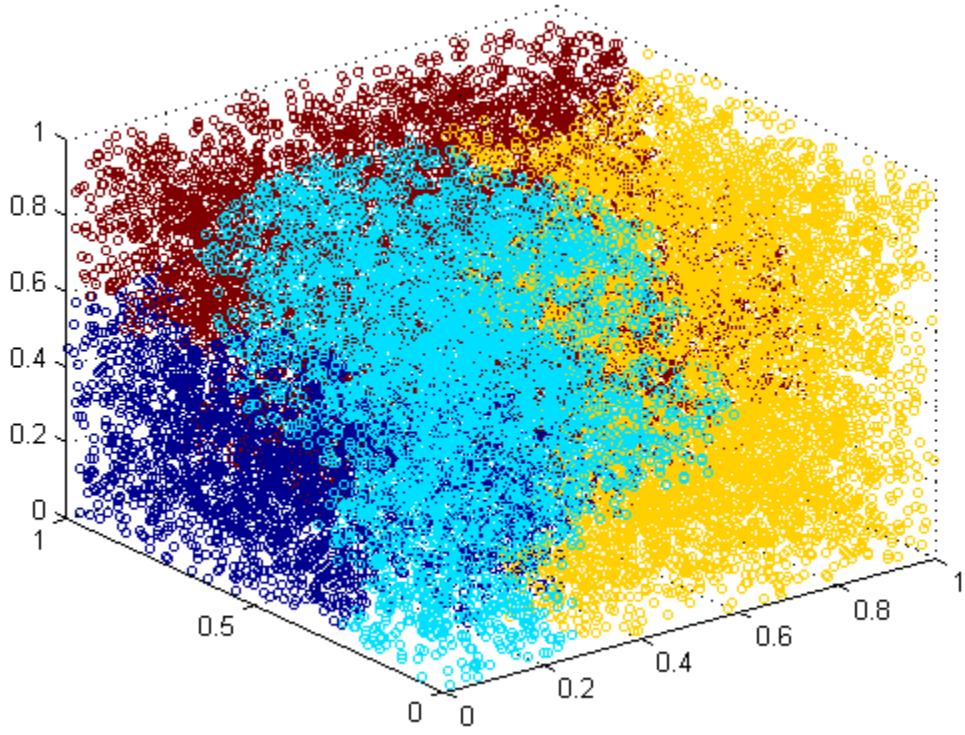
The example first creates a sample data set of random numbers. It then uses `clusterdata` to compute the distances between items in the data set and create a hierarchical cluster tree from the data set. Finally, the `clusterdata` function groups the items in the data set into three clusters. The example uses the `find` function to list all the items in cluster 2, and the `scatter3` function to plot the data with each cluster shown in a different color.

```
X = [gallery('uniformdata',[10 3],12);...
gallery('uniformdata',[10 3],13)+1.2;...
gallery('uniformdata',[10 3],14)+2.5];
T = clusterdata(X,'maxclust',3);
find(T==2)
ans =
  11
  12
  13
  14
  15
  16
  17
  18
  19
  20
scatter3(X(:,1),X(:,2),X(:,3),100,T,'filled')
```



Create a hierarchical cluster tree for a data with 20000 observations using Ward's linkage. If you set `savememory` to `'off'`, you can get an out-of-memory error if your machine doesn't have enough memory to hold the distance matrix.

```
X = rand(20000,3);
c = clusterdata(X,'linkage','ward','savememory','on',...
    'maxclust',4);
scatter3(X(:,1),X(:,2),X(:,3),10,c)
```



See Also `cluster` | `inconsistent` | `kmeans` | `linkage` | `pdist`

Purpose

Classical multidimensional scaling

Syntax

```
Y = cmdscale(D)
[Y,e] = cmdscale(D)
```

Description

`Y = cmdscale(D)` takes an `n`-by-`n` distance matrix `D`, and returns an `n`-by-`p` configuration matrix `Y`. Rows of `Y` are the coordinates of `n` points in `p`-dimensional space for some `p < n`. When `D` is a Euclidean distance matrix, the distances between those points are given by `D`. `p` is the dimension of the smallest space in which the `n` points whose inter-point distances are given by `D` can be embedded.

`[Y,e] = cmdscale(D)` also returns the eigenvalues of `Y*Y'`. When `D` is Euclidean, the first `p` elements of `e` are positive, the rest zero. If the first `k` elements of `e` are much larger than the remaining `(n-k)`, then you can use the first `k` columns of `Y` as `k`-dimensional points whose inter-point distances approximate `D`. This can provide a useful dimension reduction for visualization, e.g., for `k = 2`.

`D` need not be a Euclidean distance matrix. If it is non-Euclidean or a more general dissimilarity matrix, then some elements of `e` are negative, and `cmdscale` chooses `p` as the number of positive eigenvalues. In this case, the reduction to `p` or fewer dimensions provides a reasonable approximation to `D` only if the negative elements of `e` are small in magnitude.

You can specify `D` as either a full dissimilarity matrix, or in upper triangle vector form such as is output by `pdist`. A full dissimilarity matrix must be real and symmetric, and have zeros along the diagonal and positive elements everywhere else. A dissimilarity matrix in upper triangle form must have real, positive entries. You can also specify `D` as a full similarity matrix, with ones along the diagonal and all other elements less than one. `cmdscale` transforms a similarity matrix to a dissimilarity matrix in such a way that distances between the points returned in `Y` equal or approximate `sqrt(1-D)`. To use a different transformation, you must transform the similarities prior to calling `cmdscale`.

Examples

Generate some points in 4-D space, but close to 3-D space, then reduce them to distances only.

```
X = [normrnd(0,1,10,3) normrnd(0,.1,10,1)];
D = pdist(X,'euclidean');
```

Find a configuration with those inter-point distances.

```
[Y,e] = cmdscale(D);

% Four, but fourth one small
dim = sum(e > eps^(3/4))

% Poor reconstruction
maxerr2 = max(abs(pdist(X)-pdist(Y(:,1:2))))

% Good reconstruction
maxerr3 = max(abs(pdist(X)-pdist(Y(:,1:3))))

% Exact reconstruction
maxerr4 = max(abs(pdist(X)-pdist(Y)))

% D is now non-Euclidean
D = pdist(X,'cityblock');
[Y,e] = cmdscale(D);

% One is large negative
min(e)

% Poor reconstruction
maxerr = max(abs(pdist(X)-pdist(Y)))
```

References

[1] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

See Also

`mdscale` | `pdist` | `procrustes`

Purpose

Class names

Description

The `CNames` property is an `NClasses`-by-1 cell array containing the group names, where `NClasses` number of groups in the grouping variable used to create the Naive Bayes classifier.

CompactTreeBagger.combine

Purpose

Combine two ensembles

Syntax

```
B1 = combine(B1,B2)
```

Description

`B1 = combine(B1,B2)` appends decision trees from ensemble `B2` to those stored in `B1` and returns ensemble `B1`. This method requires that the class and variable names be identical in both ensembles.

See Also

`TreeBagger.append`

Purpose

Enumeration of combinations

Syntax

```
C = combnk(v,k)
```

Description

`C = combnk(v,k)` returns all combinations of the n elements in `v` taken `k` at a time.

`C = combnk(v,k)` produces a matrix `C` with `k` columns and $n!/k!(n–k)!$ rows, where each row contains `k` of the elements in the vector `v`.

It is not practical to use this function if `v` has more than about 15 elements.

Examples

Combinations of characters from a string.

```
C = combnk('tendril',4);
last5 = C(31:35,:)
last5 =
tedr
tenl
teni
tenr
tend
```

Combinations of elements from a numeric vector.

```
c = combnk(1:4,2)
c =
   3   4
   2   4
   2   3
   1   4
   1   3
   1   2
```

See Also

`perms`

ClassificationDiscriminant.compact

Purpose

Compact discriminant analysis classifier

Syntax

```
cobj = compact(obj)
```

Description

`cobj = compact(obj)` creates a compact version of `obj`.

Input Arguments

`obj`

Discriminant analysis classifier created using `ClassificationDiscriminant.fit`.

Output Arguments

`cobj`

Compact classifier. `cobj` has class `CompactClassificationDiscriminant`. You can predict classifications using `cobj` exactly as you can using `obj`. However, since `cobj` does not contain training data, you cannot perform some actions, such as cross validation.

Examples

Compare the size of the discriminant analysis classifier for Fisher's iris data to the compact version of the classifier:

```
load fisheriris
fullobj = ClassificationDiscriminant.fit(meas,species);
cobj = compact(fullobj);
b = whos('fullobj'); % b.bytes = size of fullobj
c = whos('cobj'); % c.bytes = size of cobj
[b.bytes c.bytes] % shows cobj uses 60% of the memory

ans =
       18578       11498
```

See Also

`ClassificationDiscriminant`

How To

- "Discriminant Analysis" on page 12-3

Purpose

Compact classification ensemble

Syntax

```
cens = compact(ens)
```

Description

`cens = compact(ens)` creates a compact version of `ens`. You can predict classifications using `cens` exactly as you can using `ens`. However, since `cens` does not contain training data, you cannot perform some actions, such as cross validation.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Output Arguments

`cens`

A compact classification ensemble. `cens` has class `CompactClassificationEnsemble`.

Examples

Compare the size of a classification ensemble for Fisher's iris data to the compact version of the ensemble:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
cens = compact(ens);
b = whos('ens'); % b.bytes = size of ens
c = whos('cens'); % c.bytes = size of ens
[b.bytes c.bytes] % shows cens uses less memory

ans =
      571727      532476
```

See Also

`ClassificationTree` | `fitensemble`

How To

- "Ensemble Methods" on page 13-51

ClassificationTree.compact

Purpose

Compact tree

Syntax

```
ctree = compact(tree)
```

Description

`ctree = compact(tree)` creates a compact version of `tree`.

Input Arguments

`tree`

A classification tree created using `ClassificationTree.fit`.

Output Arguments

`ctree`

A compact decision tree. `ctree` has class `CompactClassificationTree`. You can predict classifications using `ctree` exactly as you can using `tree`. However, since `ctree` does not contain training data, you cannot perform some actions, such as cross validation.

Examples

Compare the size of the classification tree for Fisher's iris data to the compact version of the tree:

```
load fisheriris
fulltree = ClassificationTree.fit(meas,species);
ctree = compact(fulltree);
b = whos('fulltree'); % b.bytes = size of fulltree
c = whos('ctree'); % c.bytes = size of ctree
[b.bytes c.bytes] % shows ctree uses half the memory

ans =
       13913        6818
```

See Also

`CompactClassificationTree` | `ClassificationTree` | `predict`

How To

- Chapter 13, "Nonparametric Supervised Learning"

Purpose

Create compact regression ensemble

Syntax

```
cens = compact(ens)
```

Description

`cens = compact(ens)` creates a compact version of `ens`. You can predict regressions using `cens` exactly as you can using `ens`. However, since `cens` does not contain training data, you cannot perform some actions, such as cross validation.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`.

Output Arguments

`cens`

A compact regression ensemble. `cens` is of class `CompactRegressionEnsemble`.

Examples

Compare the size of a regression ensemble for the `carsmall` data to the compact version of the ensemble:

```
load carsmall
X = [Acceleration Cylinders Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',100,'Tree');
cens = compact(ens);
b = whos('ens'); % b.bytes = size of ens
c = whos('cens'); % c.bytes = size of cens
[b.bytes c.bytes] % shows ctree uses less memory

ans =
      311789      287368
```

See Also

`RegressionEnsemble | CompactRegressionEnsemble`

How To

- Chapter 13, “Nonparametric Supervised Learning”

RegressionTree.compact

Purpose

Compact regression tree

Syntax

```
ctree = compact(tree)
```

Description

`ctree = compact(tree)` creates a compact version of `tree`.

Input Arguments

`tree`

A regression tree created using `RegressionTree.fit`.

Output Arguments

`ctree`

A compact regression tree. `ctree` has class `CompactRegressionTree`. You can predict regressions using `ctree` exactly as you can using `tree`. However, since `ctree` does not contain training data, you cannot perform some actions, such as cross validation.

Examples

Compare the size of a regression tree for the `carsmall` data to the compact version of the tree:

```
load carsmall
X = [Acceleration Cylinders Displacement Horsepower Weight];
fulltree = RegressionTree.fit(X,MPG);
ctree = compact(fulltree);
b = whos('fulltree'); % b.bytes = size of fulltree
c = whos('ctree'); % c.bytes = size of ctree
[b.bytes c.bytes] % shows ctree uses 2/3 the memory

ans =
       15715       10258
```

See Also

`CompactRegressionTree` | `RegressionTree` | `predict`

How To

- Chapter 13, "Nonparametric Supervised Learning"

Purpose

Compact ensemble of decision trees

Description

Return an object of class `CompactTreeBagger` holding the structure of the trained ensemble. The class is more compact than the full `TreeBagger` class because it does not contain information for growing more trees for the ensemble. In particular, it does not contain `X` and `Y` used for training.

See Also

`CompactTreeBagger`

CompactClassificationDiscriminant

Purpose

Compact discriminant analysis class

Description

A `CompactClassificationDiscriminant` object is a compact version of a discriminant analysis classifier. The compact version does not include the data for training the classifier. Therefore, you cannot perform some tasks with a compact classifier, such as cross validation. Use a compact classifier for making predictions (classifications) of new data.

Construction

`cobj = compact(obj)` constructs a compact classifier from a full classifier.

`cobj = ClassificationDiscriminant.make(Mu,Sigma)` constructs a compact discriminant analysis classifier from the class means `Mu` and covariance matrix `Sigma`. For syntax details, see `ClassificationDiscriminant.make`.

Input Arguments

`obj`

Discriminant analysis classifier, created with `ClassificationDiscriminant.fit`.

Properties

`BetweenSigma`

`p`-by-`p` matrix, the between-class covariance, where `p` is the number of predictors.

`CategoricalPredictors`

List of categorical predictors, always empty (`[]`) for discriminant analysis.

`ClassNames`

List of the elements in the training data `Y` with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument `Y`.

`Coeffs`

`k`-by-`k` structure of coefficient matrices, where `k` is the number of classes. `Coeffs(i,j)` contains coefficients of the linear or quadratic boundaries between classes `i` and `j`. Fields in `Coeffs(i,j)`:

- `DiscrimType`
- `Class1` — `ClassNames(i)`
- `Class2` — `ClassNames(j)`
- `Const` — A scalar
- `Linear` — A vector with `p` components, where `p` is the number of columns in `X`
- `Quadratic` — `p`-by-`p` matrix, exists for quadratic `DiscrimType`

The equation of the boundary between class `i` and class `j` is

```
Const + Linear * x + x' * Quadratic * x = 0,
```

where `x` is a column vector of length `p`.

If `ClassificationDiscriminant.fit` had the `FillCoeffs` name-value pair set to `'off'` when constructing the classifier, `Coeffs` is empty (`[]`).

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. `Cost` is `K`-by-`K`, where `K` is the number of classes.

Change a `Cost` matrix using dot addressing:

```
obj.Cost = costMatrix
```

`DiscrimType`

String specifying the discriminant type. One of:

- 'linear'
- 'quadratic'
- 'diagLinear'
- 'diagQuadratic'
- 'pseudoLinear'
- 'pseudoQuadratic'

LogDetSigma

Logarithm of the determinant of the within-class covariance matrix. The type of LogDetSigma depends on the discriminant type:

- Scalar for linear discriminant analysis
- Vector of length K for quadratic discriminant analysis, where K is the number of classes

Mu

Matrix of class means of size K-by-p, where K is the number of classes, and p is the number of predictors. Each row of Mu represents the mean of the multivariate normal distribution of the corresponding class. The class indices are in the ClassNames attribute.

PredictorNames

Cell array of names for the predictor variables, in the order in which they appear in the training data X.

Prior

Prior probabilities for each class. Prior is a numeric vector whose entries relate to the corresponding ClassNames property.

Add or change a Prior vector using dot addressing:

```
obj.Prior = priorVector
```

`ResponseName`

String describing the response variable `Y`.

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `ClassificationDiscriminant.fit`.

Add or change a `ScoreTransform` function by dot addressing:

```
cobj.ScoreTransform = 'function'
```

or

```
cobj.ScoreTransform = @function
```

`Sigma`

Within-class covariance matrix or matrices. The dimensions depend on `DiscrimType`:

- `'linear'` (default) — Matrix of size `p`-by-`p`, where `p` is the number of predictors
- `'quadratic'` — Array of size `p`-by-`p`-by-`K`, where `K` is the number of classes
- `'diagLinear'` — Row vector of length `p`
- `'diagQuadratic'` — Array of size `1`-by-`p`-by-`K`
- `'pseudoLinear'` — Matrix of size `p`-by-`p`
- `'pseudoQuadratic'` — Array of size `p`-by-`p`-by-`K`

Methods

edge	Classification edge
loss	Classification error

mahal	Mahalanobis distance to class means
margin	Classification margins
predict	Predict classification

Definitions

Discriminant Classification

The model for discriminant analysis is:

- Each class (`Y`) generates data (`X`) using a multivariate normal distribution. That is, the model assumes `X` has a Gaussian mixture distribution (`gmdistribution`).
  - For linear discriminant analysis, the model has the same covariance matrix for each class, only the means vary.
  - For quadratic discriminant analysis, both means and covariances of each class vary.

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \underset{y=1,\ldots,K}{\arg\min} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

For details, see “How the predict Method Classifies” on page 12-6.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Construct a compact discriminant analysis classifier for the Fisher iris data, and compare its size to that of the full classifier:

```
load fisheriris
fullobj = ClassificationDiscriminant.fit(meas,species);
cobj = compact(fullobj);
b = whos('fullobj'); % b.bytes = size of fullobj
c = whos('cobj'); % c.bytes = size of cobj
[b.bytes c.bytes] % shows cobj uses 60% of the memory

ans =
       18578       11498
```

Construct a compact discriminant analysis classifier from the means and covariances of the Fisher iris data:

```
load fisheriris
mu(1,:) = mean(meas(1:50,:));
mu(2,:) = mean(meas(51:100,:));
mu(3,:) = mean(meas(101:150,:));

mm1 = repmat(mu(1,:),50,1);
mm2 = repmat(mu(2,:),50,1);
mm3 = repmat(mu(3,:),50,1);
cc = meas;
cc(1:50,:) = cc(1:50,:) - mm1;
cc(51:100,:) = cc(51:100,:) - mm2;
cc(101:150,:) = cc(101:150,:) - mm3;
sigstar = cc' * cc / 147;
cpct = ClassificationDiscriminant.make(mu,sigstar,...
    'ClassNames',{'setosa','versicolor','virginica'});
```

See Also

`ClassificationDiscriminant` | `compact` | `ClassificationDiscriminant.make` | `predict`

How To

- “Discriminant Analysis” on page 12-3

Purpose

Compact classification ensemble class

Description

Compact version of a classification ensemble (of class `ClassificationEnsemble`). The compact version does not include the data for training the classification ensemble. Therefore, you cannot perform some tasks with a compact classification ensemble, such as cross validation. Use a compact classification ensemble for making predictions (classifications) of new data.

Construction

`cens = compact(ens)` constructs a compact decision ensemble from a full decision ensemble.

Input Arguments

`ens`

A classification ensemble created by `fitensemble`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`ClassNames`

List of the elements in `Y` with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument `Y`.

`CombineWeights`

String describing how `ens` combines weak learner weights, either `'WeightedSum'` or `'WeightedAverage'`.

`Cost`

Square matrix where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`.

`NTrained`

Number of trained weak learners in `cens`, a scalar.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`Prior`

Prior probabilities for each class. `Prior` is a numeric vector whose entries relate to the corresponding `ClassNames` property.

`ResponseName`

String with the name of the response variable `Y`.

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `ClassificationTree.fit`.

Add or change a `ScoreTransform` function by dot addressing:

```
cens.ScoreTransform = 'function'
```

or

```
cens.ScoreTransform = @function
```

`Trained`

Trained learners, a cell array of compact classification models.

`TrainedWeights`

Numeric vector of trained weights for the weak learners in `ens`. `TrainedWeights` has `T` elements, where `T` is the number of weak learners in `learners`.

Methods

edge	Classification edge
loss	Classification error
margin	Classification margins
predict	Predict classification
predictorImportance	Estimates of predictor importance

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Create a compact classification ensemble for the `ionosphere` data:

```
load ionosphere
ens = fitensemble(X,Y,'AdaBoostM1',100,'Tree');
cens = compact(ens)

cens =
classreg.learning.classif.CompactClassificationEnsemble:
           PredictorNames: {1x34 cell}
    CategoricalPredictors: []
             ResponseName: 'Y'
                ClassNames: {'b'  'g'}
           ScoreTransform: 'none'
                 NTrained: 100
```

See Also

`fitensemble` | `ClassificationEnsemble` | `predict` | `compact`

How To

- Chapter 13, “Nonparametric Supervised Learning”

CompactClassificationTree

Purpose

Compact classification tree

Description

Compact version of a classification tree (of class `ClassificationTree`). The compact version does not include the data for training the classification tree. Therefore, you cannot perform some tasks with a compact classification tree, such as cross validation. Use a compact classification tree for making predictions (classifications) of new data.

Construction

`ctree = compact(tree)` constructs a compact decision tree from a full decision tree.

Input Arguments

`tree`

A decision tree constructed by `ClassificationTree.fit`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CatSplit`

An *n*-by-2 cell array, where *n* is the number of nodes in `tree`. Each row in `CatSplit` gives left and right values for a categorical split. For each branch node `j` based on a categorical predictor variable `z`, the left child is chosen if `z` is in `CatSplit(j,1)` and the right child is chosen if `z` is in `CatSplit(j,2)`. The splits are in the same order as nodes of the tree. Find the nodes for these splits by selecting `'categorical'` cuts from top to bottom in the `CutType` property.

`Children`

An *n*-by-2 array containing the numbers of the child nodes for each node in `tree`, where *n* is the number of nodes. Leaf nodes have child node `0`.

`ClassCount`

An *n*-by-*k* array of class counts for the nodes in `tree`, where *n* is the number of nodes and *k* is the number of classes. For any node number `i`, the class counts `ClassCount(i,:)` are counts of observations (from the data used in fitting the tree) from each class satisfying the conditions for node `i`.

`ClassNames`

List of the elements in `Y` with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument `Y`.

`ClassProb`

An *n*-by-*k* array of class probabilities for the nodes in `tree`, where *n* is the number of nodes and *k* is the number of classes. For any node number `i`, the class probabilities `ClassProb(i,:)` are the estimated probabilities for each class for a point satisfying the conditions for node `i`.

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`.

`CutCategories`

An *n*-by-2 cell array of the categories used at branches in `tree`, where *n* is the number of nodes. For each branch node `i` based on a categorical predictor variable `x`, the left child is chosen if `x` is among the categories listed in `CutCategories{i,1}`, and the right child is chosen if `x` is among those listed in `CutCategories{i,2}`. Both columns of `CutCategories` are empty for branch nodes based on continuous predictors and for leaf nodes.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutPoint`

An *n*-element vector of the values used as cut points in `tree`, where *n* is the number of nodes. For each branch node `i` based on a continuous predictor variable `x`, the left child is chosen if `x<CutPoint(i)` and the right child is chosen if `x>=CutPoint(i)`. `CutPoint` is `NaN` for branch nodes based on categorical predictors and for leaf nodes.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutType`

An *n*-element cell array indicating the type of cut at each node in `tree`, where *n* is the number of nodes. For each node `i`, `CutType{i}` is:

- `'continuous'` — If the cut is defined in the form `x < v` for a variable `x` and cut point `v`.
- `'categorical'` — If the cut is defined by whether a variable `x` takes a value in a set of categories.
- `''` — If `i` is a leaf node.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutVar`

An *n*-element cell array of the names of the variables used for branching in each node in `tree`, where *n* is the number of nodes. These variables are sometimes known as *cut variables*. For leaf nodes, `CutVar` contains an empty string.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`IsBranch`

An *n*-element logical vector that is `true` for each branch node and `false` for each leaf node of `tree`.

`NodeClass`

An n-element cell array with the names of the most probable classes in each node of `tree`, where n is the number of nodes in the tree. Every element of this array is a string equal to one of the class names in `ClassNames`.

`NodeErr`

An n-element vector of the errors of the nodes in `tree`, where n is the number of nodes. `NodeErr(i)` is the misclassification probability for node `i`.

`NodeProb`

An n-element vector of the probabilities of the nodes in `tree`, where n is the number of nodes. The probability of a node is computed as the proportion of observations from the original data that satisfy the conditions for the node. This proportion is adjusted for any prior probabilities assigned to each class.

`NodeSize`

An n-element vector of the sizes of the nodes in `tree`, where n is the number of nodes. The size of a node is defined as the number of observations from the data used to create the tree that satisfy the conditions for the node.

`NumNodes`

The number of nodes in `tree`.

`Parent`

An n-element vector containing the number of the parent node for each node in `tree`, where n is the number of nodes. The parent of the root node is `0`.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`Prior`

Prior probabilities for each class. `Prior` is a numeric vector whose entries relate to the corresponding `ClassNames` property.

`PruneList`

An *n*-element numeric vector with the pruning levels in each node of `tree`, where *n* is the number of nodes.

`ResponseName`

String describing the response variable `Y`.

`Risk`

An *n*-element vector of the risk of the nodes in `tree`, where *n* is the number of nodes. For each node `i`,

```
Risk(i) = NodeErr(i) * NodeProb(i).
```

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `ClassificationTree.fit`.

Add or change a `ScoreTransform` function by dot addressing:

```
ctree.ScoreTransform = 'function'
or
ctree.ScoreTransform = @function
```

`SurrCutCategories`

An *n*-element cell array of the categories used for surrogate splits in `tree`, where *n* is the number of nodes in `tree`. For each node `k`, `SurrCutCategories{k}` is a cell array. The length of `SurrCutCategories{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutCategories{k}` is either an empty string for a continuous surrogate predictor, or is a two-element cell array with categories

for a categorical surrogate predictor. The first element of this two-element cell array lists categories assigned to the left child by this surrogate split and the second element of this two-element cell array lists categories assigned to the right child by this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutCategories` contains an empty cell.

`SurrCutFlip`

An n-element cell array of the numeric cut assignments used for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutFlip{k}` is a numeric vector. The length of `SurrCutFlip{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutFlip{k}` is either zero for a categorical surrogate predictor, or a numeric cut assignment for a continuous surrogate predictor. The numeric cut assignment can be either –1 or +1. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and the cut assignment for this surrogate split is +1, or if $Z\geq C$ and the cut assignment for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and the cut assignment for this surrogate split is +1, or if $Z<C$ and the cut assignment for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutFlip` contains an empty array.

`SurrCutPoint`

An n-element cell array of the numeric values used for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutPoint{k}` is a numeric vector. The length of `SurrCutPoint{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutPoint{k}` is either `NaN` for a categorical surrogate predictor, or a numeric cut for a continuous surrogate predictor. For every surrogate split with a

numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and `SurrCutFlip` for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and `SurrCutFlip` for this surrogate split is +1, or if $Z<C$ and `SurrCutFlip` for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables returned by `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutPoint` contains an empty cell.

`SurrCutType`

An n-element cell array indicating types of surrogate splits at each node in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutType{k}` is a cell array with the types of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutType` contains an empty cell. A surrogate split type can be either `'continuous'` if the cut is defined in the form `Z<V` for a variable `Z` and cut point `V` or `'categorical'` if the cut is defined by whether `Z` takes a value in a set of categories.

`SurrCutVar`

An n-element cell array of the names of the variables used for surrogate splits in each node in `tree`, where n is the number of nodes in `tree`. Every element of `SurrCutVar` is a cell array with the names of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutVar` contains an empty cell.

`SurrVarAssoc`

An n-element cell array of the predictive measures of association for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrVarAssoc{k}` is a numeric vector. The length of `SurrVarAssoc{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrVarAssoc{k}` gives the predictive measure of association between the optimal split and this surrogate split. The order of the surrogate split variables at each node is the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrVarAssoc` contains an empty cell.

Methods

edge	Classification edge
loss	Classification error
margin	Classification margins
meanSurrVarAssoc	Mean predictive measure of association for surrogate splits in decision tree
predict	Predict classification
predictorImportance	Estimates of predictor importance
view	View tree

Definitions

Impurity and Node Error

`ClassificationTree` splits nodes based on either *impurity* or *node error*. Impurity means one of several things, depending on your choice of the `SplitCriterion` name-value pair:

- Gini's Diversity Index (`gdi`) — The Gini index of a node is

$$1 - \sum_i p^2(i),$$

where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index `0`; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.

- Deviance (`'deviance'`) — With $p(i)$ defined as for the Gini index, the deviance of a node is

  $$-\sum_i p(i)\log p(i).$$

  A pure node has deviance `0`; otherwise, the deviance is positive.

- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

  $$P(L)P(R)\left(\sum_i |L(i)-R(i)|\right)^2,$$

  where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.

- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with largest number of training samples at a node, the node error is

  $$1-p(j).$$

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Construct a compact classification tree for the Fisher iris data, and compare the size of the resulting tree to that of the original tree:

```
load fisheriris
tree = ClassificationTree.fit(meas,species);
ctree = compact(tree);
t = whos('tree'); % t.bytes = size of tree in bytes
c = whos('ctree'); % c.bytes = size of ctree in bytes
[c.bytes t.bytes]

ans =
        6818       13913
```

See Also

`ClassificationTree.fit` | `ClassificationTree` | `compact`

How To

- Chapter 13, “Nonparametric Supervised Learning”

CompactRegressionEnsemble

Purpose

Compact regression ensemble class

Description

Compact version of a regression ensemble (of class `RegressionEnsemble`). The compact version does not include the data for training the regression ensemble. Therefore, you cannot perform some tasks with a compact regression ensemble, such as cross validation. Use a compact regression ensemble for making predictions (regressions) of new data.

Construction

`cens = compact(ens)` constructs a compact decision ensemble from a full decision ensemble.

Input Arguments

`ens`

A regression ensemble created by `fitensemble`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CombineWeights`

A string describing how the ensemble combines learner predictions.

`NTrained`

Number of trained learners in the ensemble, a positive scalar.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`ResponseName`

A string with the name of the response variable `Y`.

`ResponseTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`.

Add or change a `ResponseTransform` function by dot addressing:

```
cens.ResponseTransform = @function
```

`Trained`

The trained learners, a cell array of compact regression models.

`TrainedWeights`

A numeric vector of weights the ensemble assigns to its learners. The ensemble computes predicted response by aggregating weighted predictions from its learners.

Methods

loss	Regression error
predict	Predict response of ensemble
predictorImportance	Estimates of predictor importance

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Construct a regression ensemble for the `carsmall` data. Make a compact version of the ensemble, and compare its size to that of the full ensemble:

```
load carsmall
learner = RegressionTree.template('MinParent',20);
ens = fitensemble([Weight, Cylinders],MPG,...
    'LSBoost',100,learner,'PredictorNames',{'W','C'},...
    'categoricalpredictors',2);
cens = compact(ens);
ee = whos('ens'); % ee.bytes = size of ensemble in bytes
cee = whos('cens');
```

```
[ee.bytes cee.bytes]

ans =
      606903      587096
```

See Also

`fitensemble` | `RegressionEnsemble` | `predict` | `compact`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Compact regression tree

Description

Compact version of a regression tree (of class `RegressionTree`). The compact version does not include the data for training the regression tree. Therefore, you cannot perform some tasks with a compact regression tree, such as cross validation. Use a compact regression tree for making predictions (regressions) of new data.

Construction

`ctree = compact(tree)` constructs a compact decision tree from a full decision tree.

Input Arguments

`tree`

A decision tree constructed by `RegressionTree.fit`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CatSplit`

An *n*-by-2 cell array, where *n* is the number of nodes in `tree`. Each row in `CatSplit` gives left and right values for a categorical split. For each branch node `j` based on a categorical predictor variable `z`, the left child is chosen if `z` is in `CatSplit(j,1)` and the right child is chosen if `z` is in `CatSplit(j,2)`. The splits are in the same order as nodes of the tree. Nodes for these splits can be found by running `cuttype` and selecting `'categorical'` cuts from top to bottom.

`Children`

An *n*-by-2 array containing the numbers of the child nodes for each node in `tree`, where *n* is the number of nodes. Leaf nodes have child node `0`.

`CutCategories`

An *n*-by-2 cell array of the categories used at branches in `tree`, where *n* is the number of nodes. For each branch node `i` based on a categorical predictor variable `x`, the left child is chosen if `x` is among the categories listed in `CutCategories{i,1}`, and the right child is chosen if `x` is among those listed in `CutCategories{i,2}`. Both columns of `CutCategories` are empty for branch nodes based on continuous predictors and for leaf nodes.

`CutVar` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutPoint`

An *n*-element vector of the values used as cut points in `tree`, where *n* is the number of nodes. For each branch node `i` based on a continuous predictor variable `x`, the left child is chosen if `CutPoint<v(i)` and the right child is chosen if `x>=CutPoint(i)`. `CutPoint` is `NaN` for branch nodes based on categorical predictors and for leaf nodes.

`CutType`

An *n*-element cell array indicating the type of cut at each node in `tree`, where *n* is the number of nodes. For each node `i`, `CutType{i}` is:

- `'continuous'` — If the cut is defined in the form `x < v` for a variable `x` and cut point `v`.
- `'categorical'` — If the cut is defined by whether a variable `x` takes a value in a set of categories.
- `''` — If `i` is a leaf node.

`CutVar` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutVar`

An *n*-element cell array of the names of the variables used for branching in each node in `tree`, where *n* is the number of nodes.

These variables are sometimes known as *cut variables*. For leaf nodes, `CutVar` contains an empty string.

`CutVar` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`IsBranch`

An *n*-element logical vector `ib` that is `true` for each branch node and `false` for each leaf node of `tree`.

`NodeErr`

An *n*-element vector `e` of the errors of the nodes in `tree`, where *n* is the number of nodes. `e(i)` is the misclassification probability for node `i`.

`NodeMean`

An *n*-element numeric array with mean values in each node of `tree`, where *n* is the number of nodes in the tree. Every element in `NodeMean` is the average of the true `Y` values over all observations in the node.

`NodeProb`

An *n*-element vector `p` of the probabilities of the nodes in `tree`, where *n* is the number of nodes. The probability of a node is computed as the proportion of observations from the original data that satisfy the conditions for the node. This proportion is adjusted for any prior probabilities assigned to each class.

`NodeSize`

An *n*-element vector `sizes` of the sizes of the nodes in `tree`, where *n* is the number of nodes. The size of a node is defined as the number of observations from the data used to create the tree that satisfy the conditions for the node.

`NumNodes`

The number of nodes `n` in `tree`.

`Parent`

An *n*-element vector `p` containing the number of the parent node for each node in `tree`, where *n* is the number of nodes. The parent of the root node is `0`.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`PruneList`

An *n*-element numeric vector with the pruning levels in each node of `tree`, where *n* is the number of nodes.

`ResponseName`

Name of the response variable `Y`, a string.

`ResponseTransform`

Function handle for transforming the raw response values (mean squared error). The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function by dot addressing:

```
ctree.ResponseTransform = @function
```

`Risk`

An *n*-element vector `r` of the risk of the nodes in `tree`, where *n* is the number of nodes. The risk `r(i)` for node `i` is the node error `NodeErr(i)` multiplied by the node probability `NodeProb(i)`.

`SurrCutCategories`

An *n*-element cell array of the categories used for surrogate splits in `tree`, where *n* is the number of nodes in `tree`. For each node `k`, `SurrCutCategories{k}` is a cell array. The length of `SurrCutCategories{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutCategories{k}` is either an empty string for a continuous

surrogate predictor, or is a two-element cell array with categories for a categorical surrogate predictor. The first element of this two-element cell array lists categories assigned to the left child by this surrogate split, and the second element of this two-element cell array lists categories assigned to the right child by this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutCategories` contains an empty cell.

`SurrCutFlip`

An n-element cell array of the numeric cut assignments used for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutFlip{k}` is a numeric vector. The length of `SurrCutFlip{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutFlip{k}` is either zero for a categorical surrogate predictor, or a numeric cut assignment for a continuous surrogate predictor. The numeric cut assignment can be either –1 or +1. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and the cut assignment for this surrogate split is +1, or if $Z\geq C$ and the cut assignment for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and the cut assignment for this surrogate split is +1, or if $Z<C$ and the cut assignment for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutFlip` contains an empty array.

`SurrCutPoint`

An n-element cell array of the numeric values used for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutPoint{k}` is a numeric vector. The length of `SurrCutPoint{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutPoint{k}` is either `NaN` for a categorical surrogate predictor, or a numeric cut for a

continuous surrogate predictor. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and `SurrCutFlip` for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and `SurrCutFlip` for this surrogate split is +1, or if $Z<C$ and `SurrCutFlip` for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables returned by `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutPoint` contains an empty cell.

`SurrCutType`

An n-element cell array indicating types of surrogate splits at each node in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutType{k}` is a cell array with the types of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutType` contains an empty cell. A surrogate split type can be either `'continuous'` if the cut is defined in the form `Z<V` for a variable `Z` and cut point `V` or `'categorical'` if the cut is defined by whether `Z` takes a value in a set of categories.

`SurrCutVar`

An n-element cell array of the names of the variables used for surrogate splits in each node in `tree`, where n is the number of nodes in `tree`. Every element of `SurrCutVar` is a cell array with the names of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutVar` contains an empty cell.

`SurrVarAssoc`

An n-element cell array of the predictive measures of association for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrVarAssoc{k}` is a numeric vector. The length of `SurrVarAssoc{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrVarAssoc{k}` gives the predictive measure of association between the optimal split and this surrogate split. The order of the surrogate split variables at each node is the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrVarAssoc` contains an empty cell.

Methods

loss	Regression error
meanSurrVarAssoc	Mean predictive measure of association for surrogate splits in decision tree
predict	Predict response of regression tree
predictorImportance	Estimates of predictor importance
view	View tree

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Construct a regression tree for the `carsmall` data. Make a compact version of the tree, and compare its size to that of the full tree:

```
load carsmall
tree = RegressionTree.fit([Weight, Cylinders],MPG,...
    'MinParent',20,...
    'PredictorNames',{'W','C'});
ctree = compact(tree);
t = whos('tree'); % t.bytes = size of tree in bytes
```

```
c = whos('ctree'); % c.bytes = size of ctree in bytes
[c.bytes t.bytes]

ans =
        4972        8173
```

See Also

`RegressionTree.fit` | `RegressionTree` | `compact`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Compact ensemble of decision trees grown by bootstrap aggregation

Description

`CompactTreeBagger` class is a lightweight class that contains the trees grown using `TreeBagger`. `CompactTreeBagger` does not preserve any information about how `TreeBagger` grew the decision trees. It does not contain the input data used for growing trees, nor does it contain training parameters such as minimal leaf size or number of variables sampled for each decision split at random. You can only use `CompactTreeBagger` for predicting the response of the trained ensemble given new data `X`, and other related functions.

`CompactTreeBagger` lets you save the trained ensemble to disk, or use it in any other way, while discarding training data and various parameters of the training configuration irrelevant for predicting response of the fully grown ensemble. This reduces storage and memory requirements, especially for ensembles trained on large datasets.

Construction

CompactTreeBagger	Create CompactTreeBagger object

Methods

combine	Combine two ensembles
error	Error (misclassification probability or MSE)
margin	Classification margin
mdsProx	Multidimensional scaling of proximity matrix
meanMargin	Mean classification margin
outlierMeasure	Outlier measure for data
predict	Predict response

proximity	Proximity matrix for data
SetDefaultYfit	Set default value for `predict`

Properties

`ClassNames`

The `ClassNames` property is a cell array containing the class names for the response variable `Y` supplied to `TreeBagger`. This property is empty for regression trees.

`DeltaCritDecisionSplit`

The `DeltaCritDecisionSplit` property is a numeric array of size 1-by-`Nvars` of changes in the split criterion summed over splits on each variable, averaged across the entire ensemble of grown trees.

See also `TreeBagger.DeltaCritDecisionSplit`, `classregtree.varimportance`

`DefaultYfit`

The `DefaultYfit` property controls what predicted value `CompactTreeBagger` returns when no prediction is possible, for example when the `predict` method needs to predict for an observation which has only false values in the matrix supplied through `'useifort'` argument.

For classification, you can set this property to either `''` or `'MostPopular'`. If you choose `'MostPopular'` (default), the property value becomes the name of the most probable class in the training data.

For regression, you can set this property to any numeric scalar. The default is the mean of the response for the training data.

See also `predict`, `setDefaultYfit`, `TreeBagger.DefaultYfit`.

`Method`

The `Method` property is `'classification'` for classification ensembles and `'regression'` for regression ensembles.

`NTrees`

The `NTrees` property is a scalar equal to the number of decision trees in the ensemble.

`NVarSplit`

The `NVarSplit` property is a numeric array of size 1-by-*Nvars*, where every element gives a number of splits on this predictor summed over all trees.

`Trees`

The `Trees` property is a cell array of size `NTrees`-by-1 containing the trees in the ensemble.

`VarAssoc`

The `VarAssoc` property is a matrix of size *Nvars*-by-*Nvars* with predictive measures of variable association, averaged across the entire ensemble of grown trees. If you grew the ensemble setting `'surrogate'` to `'on'`, this matrix for each tree is filled with predictive measures of association averaged over the surrogate splits. If you grew the ensemble setting `'surrogate'` to `'off'` (default), `VarAssoc` is diagonal.

See also `classregtree.MeanSurrVarAssoc`

`VarNames`

The `VarNames` property is a cell array containing the names of the predictor variables (features). These names are taken from the optional `'names'` parameter that supplied to `TreeBagger`. The default names are `'x1'`, `'x2'`, etc.

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

See Also

`classregtree`

How To

- "Ensemble Methods" on page 13-51
- "Classification Trees and Regression Trees" on page 13-27
- "Grouped Data" on page 2-34

Purpose

Create CompactTreeBagger object

Description

When you use the `TreeBagger` constructor to grow trees, it creates a `CompactTreeBagger` object. You can obtain the compact object from the full `TreeBagger` object using the `TreeBagger/compact` method. You do not create an instance of `CompactTreeBagger` directly.

See Also

`TreeBagger`

How To

- Grouped Data
- “Ensemble Methods” on page 13-51

TreeBagger.ComputeOOBPrediction property

Purpose

Flag to compute out-of-bag predictions

Description

The `ComputeOOBPrediction` property is a logical flag specifying whether out-of-bag predictions for training observations should be computed. The default is `false`.

If this flag is true, the following properties are available:

- `OOBIndices`
- `OOBInstanceWeight`

If this flag is true, the following methods can be called:

- `oobError`
- `oobMargin`
- `oobMeanMargin`

See Also

`oobError` | `OOBIndices` | `OOBInstanceWeight` | `oobMargin` | `oobMeanMargin`

Purpose

Flag to compute out-of-bag variable importance

Description

The `ComputeOOBVarImp` property is a logical flag specifying whether `TreeBagger` should compute out-of-bag estimates of variable importance. The default is false.

If this flag is true, the following properties are available:

- `OOBPermutedVarDeltaError`
- `OOBPermutedVarDeltaMeanMargin`
- `OOBPermutedVarCountRaiseMargin`

See Also

`ComputeOOBPrediction` | `OOBPermutedVarDeltaError` | `OOBPermutedVarDeltaMeanMargin` | `OOBPermutedVarCountRaiseMargin` | `oobMeanMargin` | `TreeBagger`

Purpose

Confusion matrix

Syntax

```
C = confusionmat(group,grouphat)
C = confusionmat(group,grouphat,'order',grouporder)
[C,order] = confusionmat(...)
```

Description

`C = confusionmat(group,grouphat)` returns the confusion matrix `C` determined by the known and predicted groups in `group` and `grouphat`, respectively. `group` and `grouphat` are grouping variables with the same number of observations, as described in "Grouped Data" on page 2-34. Input vectors must be of the same type. `C` is a square matrix with size equal to the total number of distinct elements in `group` and `grouphat`. `C(i,j)` is a count of observations known to be in group `i` but predicted to be in group `j`. Group indices and their order are the same for the rows and columns of `C`, computed by `grp2idx` using `grp2idx(group;grouphat)`. `NaN`, empty, or `'undefined'` groups are not counted.

`C = confusionmat(group,grouphat,'order',grouporder)` uses `grouporder` to order the rows and columns of `C`. `grouporder` is a grouping variable containing all of the distinct elements in `group` and `grouphat`. If `grouporder` contains elements that are not in `group` or `grouphat`, the corresponding entries in `C` will be `0`.

`[C,order] = confusionmat(...)` also returns the order of the rows and columns of `C` in a variable `order` the same type as `group` and `grouphat`.

Examples

Example 1

Display the confusion matrix for data with two misclassifications and one missing classification:

```
g1 = [1 1 2 2 3 3]';  % Known groups
g2 = [1 1 2 3 4 NaN]'; % Predicted groups

[C,order] = confusionmat(g1,g2)
C =
```

```
     2     0     0     0
     0     1     1     0
     0     0     0     1
     0     0     0     0
order =
     1
     2
     3
     4
```

Example 2

Randomize the measurements and groups in Fisher's iris data:

```
load fisheriris
numObs = length(species);
p = randperm(numObs);
meas = meas(p,:);
species = species(p);
```

Use `classify` to classify measurements in the second half of the data, using the first half of the data for training:

```
half = floor(numObs/2);
training = meas(1:half,:);
trainingSpecies = species(1:half);
sample = meas(half+1:end,:);
grouphat = classify(sample,training,trainingSpecies);
```

Display the confusion matrix for the resulting classification:

```
group = species(half+1:end);
[C,order] = confusionmat(group,grouphat)
C =
    22     0     0
     2    22     0
     0     0    29
order =
    'virginica'
```

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

See Also

`crosstab` | `grp2idx`

How To

- "Grouped Data" on page 2-34

Purpose

Shewhart control charts

Syntax

```
controlchart(X)
controlchart(x,group)
controlchart(X,group)
[stats,plotdata] = controlchart(x,[group])
controlchart(x,group,'name',value)
```

Description

`controlchart(X)` produces an xbar chart of the measurements in matrix `X`. Each row of `X` is considered to be a subgroup of measurements containing replicate observations taken at the same time. The rows should be in time order. If `X` is a time series object, the time samples should contain replicate observations.

The chart plots the means of the subgroups in time order, a center line (`CL`) at the average of the means, and upper and lower control limits (`UCL`, `LCL`) at three standard errors from the center line. The standard error is the estimated process standard deviation divided by the square root of the subgroup size. Process standard deviation is estimated from the average of the subgroup standard deviations. Out of control measurements are marked as violations and drawn with a red circle. Data cursor mode is enabled, so clicking any data point displays information about that point.

`controlchart(x,group)` accepts a grouping variable `group` for a vector of measurements `x`. (See "Grouped Data" on page 2-34.) `group` is a categorical variable, vector, string array, or cell array of strings the same length as `x`. Consecutive measurements `x(n)` sharing the same value of `group(n)` for $1 \le n \le$ `length(x)` are defined to be a subgroup. Subgroups can have different numbers of observations.

`controlchart(X,group)` accepts a grouping variable `group` for a matrix of measurements in `X`. In this case, `group` is only used to label the time axis; it does not change the default grouping by rows.

`[stats,plotdata] = controlchart(x,[group])` returns a structure `stats` of subgroup statistics and parameter estimates, and a structure `plotdata` of plotted values. `plotdata` contains one record for each chart.

The fields in `stats` and `plotdata` depend on the chart type.

The fields in `stats` are selected from the following:

- `mean` — Subgroup means
- `std` — Subgroup standard deviations
- `range` — Subgroup ranges
- `n` — Subgroup size, or total inspection size or area
- `i` — Individual data values
- `ma` — Moving averages
- `mr` — Moving ranges
- `count` — Count of defects or defective items
- `mu` — Estimated process mean
- `sigma` — Estimated process standard deviation
- `p` — Estimated proportion defective
- `m` — Estimated mean defects per unit

The fields in `plotdata` are the following:

- `pts` — Plotted point values
- `cl` — Center line
- `lcl` — Lower control limit
- `ucl` — Upper control limit
- `se` — Standard error of plotted point
- `n` — Subgroup size
- `ooc` — Logical that is true for points that are out of control

`controlchart(x,group,'name',value)` specifies one or more of the following optional parameter name/value pairs, with *`name`* in single quotes:

- `charttype` — The name of a chart type chosen from among the following:
  - `'xbar'` — Xbar or mean
  - `'s'` — Standard deviation
  - `'r'` — Range
  - `'ewma'` — Exponentially weighted moving average
  - `'i'` — Individual observation
  - `'mr'` — Moving range of individual observations
  - `'ma'` — Moving average of individual observations
  - `'p'` — Proportion defective
  - `'np'` — Number of defectives
  - `'u'` — Defects per unit
  - `'c'` — Count of defects

  Alternatively, a parameter can be a cell array listing multiple compatible chart types. There are four sets of compatible types:
  - `'xbar'`, `'s'`, `'r'`, and `'ewma'`
  - `'i'`, `'mr'`, and `'ma'`
  - `'p'` and `'np'`
  - `'u'` and `'c'`
- `display` — Either `'on'` (default) to display the control chart, or `'off'` to omit the display
- `label` — A string array or cell array of strings, one per subgroup. This label is displayed as part of the data cursor for a point on the plot.

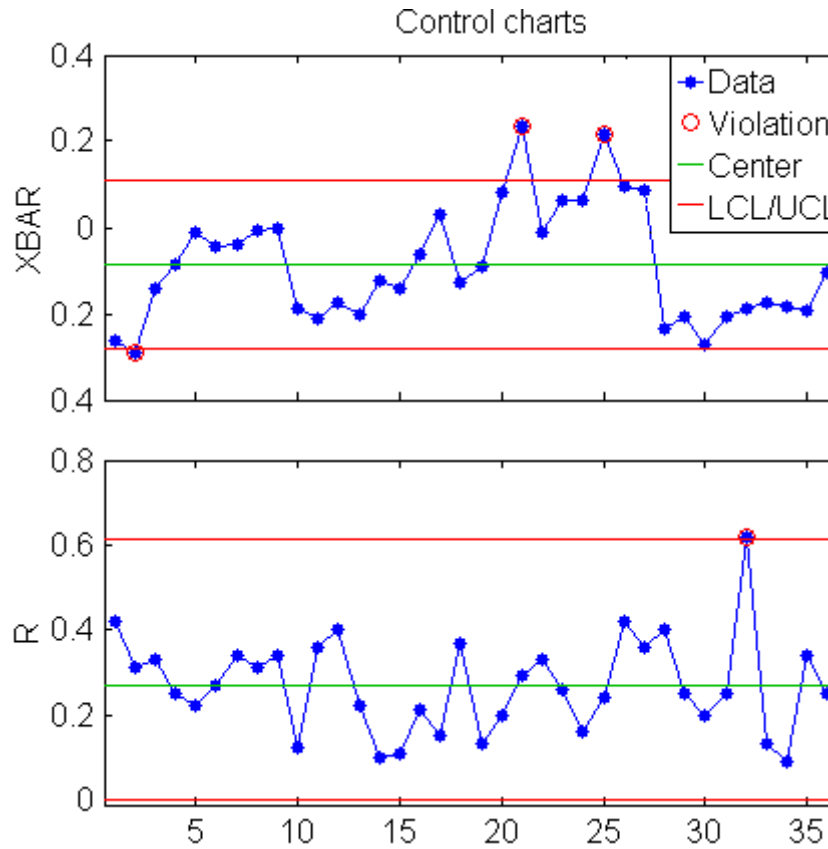
- `lambda` — A parameter between 0 and 1 controlling how much the current prediction is influenced by past observations in an EWMA plot. Higher values of `'lambda'` give less weight to past observations and more weight to the current observation. The default is 0.4.
- `limits'` — A three-element vector specifying the values of the lower control limit, center line, and upper control limits. Default is to estimate the center line and to compute control limits based on the estimated value of sigma. Not permitted if there are multiple chart types.
- `mean` — Value for the process mean, or an empty value (default) to estimate the mean from `X`. This is the `p` parameter for `p` and `np` charts, the mean defects per unit for `u` and `c` charts, and the normal `mu` parameter for other charts.
- `nsigma` — The number of sigma multiples from the center line to a control limit. Default is 3.
- `parent` — The handle of the axes to receive the control chart plot. Default is to create axes in a new figure. Not permitted if there are multiple chart types.
- `rules` — The name of a control rule, or a cell array containing multiple control rule names. These rules, together with the control limits, determine if a point is marked as out of control. The default is to apply no control rules, and to use only the control limits to decide if a point is out of control. See `controlrules` for more information. Control rules are applied to charts that measure the process level (`xbar`, `i`, `c`, `u`, `p`, and `np`) rather than the variability (`r`, `s`), and they are not applied to charts based on moving statistics (`ma`, `mr`, `ewma`).
- `sigma` — Either a value for sigma, or a method of estimating sigma chosen from among `'std'` (the default) to use the average within-subgroup standard deviation, `'range'` to use the average subgroup range, and `'variance'` to use the square root of the pooled variance. When creating `i`, `mr`, or `ma` charts for data not in subgroups, the estimate is always based on a moving range.

- `specs` — A vector specifying specification limits. Typically this is a two-element vector of lower and upper specification limits. Since specification limits typically apply to individual measurements, this parameter is primarily suitable for `i` charts. These limits are not plotted on `r`, `s`, or `mr` charts.
- `unit` — The total number of inspected items for `p` and `np` charts, and the size of the inspected unit for `u` and `c` charts. In both cases `X` must be the count of the number of defects or defectives found. Default is 1 for `u` and `c` charts. This argument is required (no default) for `p` and `np` charts.
- `width` — The width of the window used for computing the moving ranges and averages in `mr` and `ma` charts, and for computing the sigma estimate in `i`, `mr`, and `ma` charts. Default is 5.

Examples

Create `xbar` and `r` control charts for the data in `parts.mat`:

```
load parts
st = controlchart(runout,'chart',{'xbar' 'r'});
```



Display the process mean and standard deviation:

```
fprintf('Parameter estimates:  mu = %g, sigma = %g\n',st.mu,st.sigma);
Parameter estimates:  mu = -0.0863889, sigma = 0.130215
```

See Also

`controlrules`

How To

- “Grouped Data” on page 2-34

Purpose

Western Electric and Nelson control rules

Syntax

```
R = controlrules('rules',x,cl,se)
[R,RULES] = controlrules('rules',x,cl,se)
```

Description

`R = controlrules('rules',x,cl,se)` determines which points in the vector `x` violate the control rules in *`rules`*. `cl` is a vector of center-line values. `se` is a vector of standard errors. (Typically, control limits on a control chart are at the values `cl – 3*se` and `cl + 3*se`.) `rules` is the name of a control rule, or a cell array containing multiple control rule names, from the list below. If `x` has n values and *`rules`* contains m rules, then `R` is an n-by-m logical array, with `R(i,j)` assigned the value `1` if point `i` violates rule `j`, `0` if it does not.

The following are accepted values for *`rules`* (specified inside single quotes):

- `we1` — 1 point above `cl + 3*se`
- `we2` — 2 of 3 above `cl + 2*se`
- `we3` — 4 of 5 above `cl + se`
- `we4` — 8 of 8 above `cl`
- `we5` — 1 below `cl  3*se`
- `we6` — 2 of 3 below `cl  2*se`
- `we7` — 4 of 5 below `cl  se`
- `we8` — 8 of 8 below `cl`
- `we9` — 15 of 15 between `cl  se` and `cl + se`
- `we10` — 8 of 8 below `cl  se` or above `cl + se`
- `n1` — 1 point below `cl  3*se` or above `cl + 3*se`
- `n2` — 9 of 9 on the same side of `cl`
- `n3` — 6 of 6 increasing or decreasing
- `n4` — 14 alternating up/down

- `n5` — 2 of 3 below `cl  2*se` or above `cl + 2*se`, same side
- `n6` — 4 of 5 below `cl  se` or above `cl + se`, same side
- `n7` — 15 of 15 between `cl  se` and `cl + se`
- `n8` — 8 of 8 below `cl  se` or above `cl + se`, either side
- `we` — All Western Electric rules
- `n` — All Nelson rules

For multi-point rules, a rule violation at point `i` indicates that the set of points ending at point `i` triggered the rule. Point `i` is considered to have violated the rule only if it is one of the points violating the rule's condition.

Any points with `NaN` as their `x`, `cl`, or `se` values are not considered to have violated rules, and are not counted in the rules for other points.

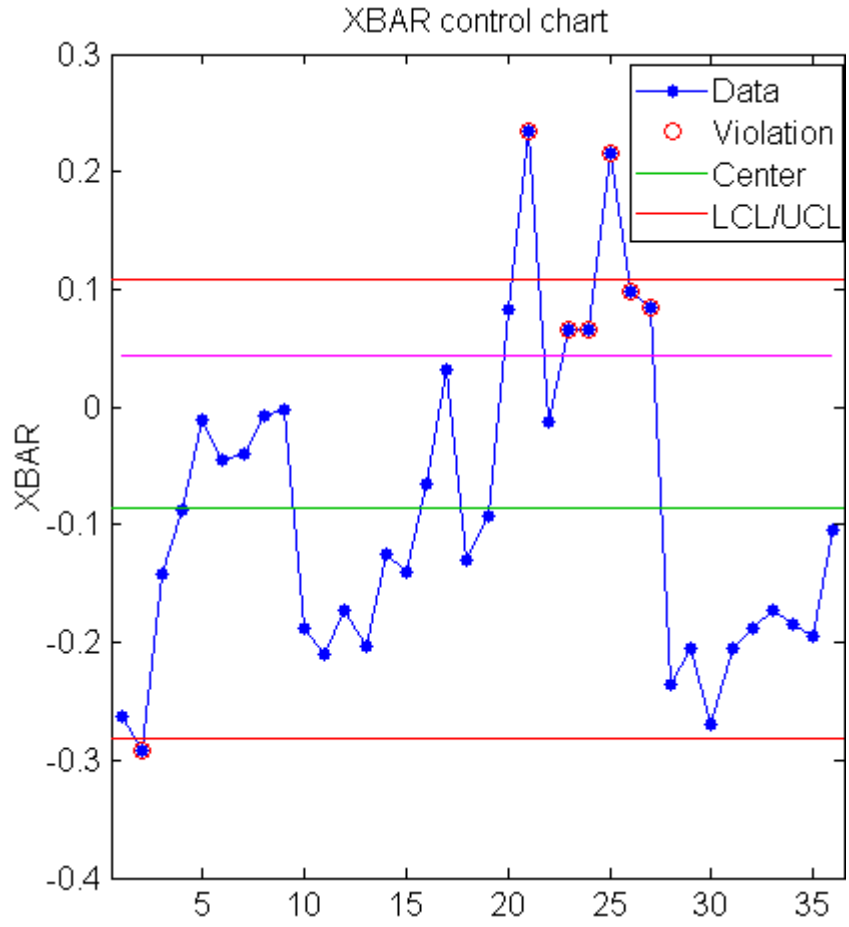
Control rules can be specified in the `controlchart` function as values for the `'rules'` parameter.

`[R,RULES] = controlrules('rules',x,cl,se)` returns a cell array of text strings `RULES` listing the rules applied.

Examples

Create an xbar chart using the `we2` rule to mark out of control measurements:

```
load parts;
st = controlchart(runout,'rules','we2');
x = st.mean;
cl = st.mu;
se = st.sigma./sqrt(st.n);
hold on
plot(cl+2*se,'m')
```



Use `controlrules` to identify the measurements that violate the control rule:

```
R = controlrules('we2',x,cl,se);
I = find(R)
I =
   21
   23
```

```
    24
    25
    26
    27
```

See Also

controlchart

Purpose

Determine if algorithm converged

Description

Logical `true` if the algorithm has converged; logical `false` if the algorithm has not converged.

Note This property applies only to gmdistribution objects constructed with `fit`.

---

cophenet

Purpose

Cophenetic correlation coefficient

Syntax

```
c = cophenet(Z,Y)
[c,d] = cophenet(Z,Y)
```

Description

`c = cophenet(Z,Y)` computes the cophenetic correlation coefficient for the hierarchical cluster tree represented by `Z`. `Z` is the output of the `linkage` function. `Y` contains the distances or dissimilarities used to construct `Z`, as output by the `pdist` function. `Z` is a matrix of size (m–1)-by-3, with distance information in the third column. `Y` is a vector of size m*(m–1)/2.

`[c,d] = cophenet(Z,Y)` returns the cophenetic distances `d` in the same lower triangular distance vector format as `Y`.

The cophenetic correlation for a cluster tree is defined as the linear correlation coefficient between the cophenetic distances obtained from the tree, and the original distances (or dissimilarities) used to construct the tree. Thus, it is a measure of how faithfully the tree represents the dissimilarities among observations.

The cophenetic distance between two observations is represented in a dendrogram by the height of the link at which those two observations are first joined. That height is the distance between the two subclusters that are merged by that link.

The output value, `c`, is the cophenetic correlation coefficient. The magnitude of this value should be very close to 1 for a high-quality solution. This measure can be used to compare alternative cluster solutions obtained using different algorithms.

The cophenetic correlation between `Z(:,3)` and `Y` is defined as

$$c = \frac{\sum_{i<j}(Y_{ij} - y)(Z_{ij} - z)}{\sqrt{\sum_{i<j}(Y_{ij} - y)^2 \sum_{i<j}(Z_{ij} - z)^2}}$$

where:

- Y_{ij} is the distance between objects i and j in `Y`.
- Z_{ij} is the cophenetic distance between objects i and j, from `Z(:,3)`.
- y and z are the average of `Y` and `Z(:,3)`, respectively.

Examples

```
X = [rand(10,3); rand(10,3)+1; rand(10,3)+2];
Y = pdist(X);
Z = linkage(Y,'average');

% Compute Spearman's rank correlation between the
% dissimilarities and the cophenetic distances
[c,D] = cophenet(Z,Y);
r = corr(Y',D','type','spearman')
r =
   0.8279
```

See Also

`cluster` | `dendrogram` | `inconsistent` | `linkage` | `pdist` | `squareform`

copulacdf

Purpose

Copula cumulative distribution function

Syntax

```
Y = copulacdf('Gaussian',U,rho)
Y = copulacdf('t',U,rho,NU)
Y = copulacdf('family',U,alpha)
```

Description

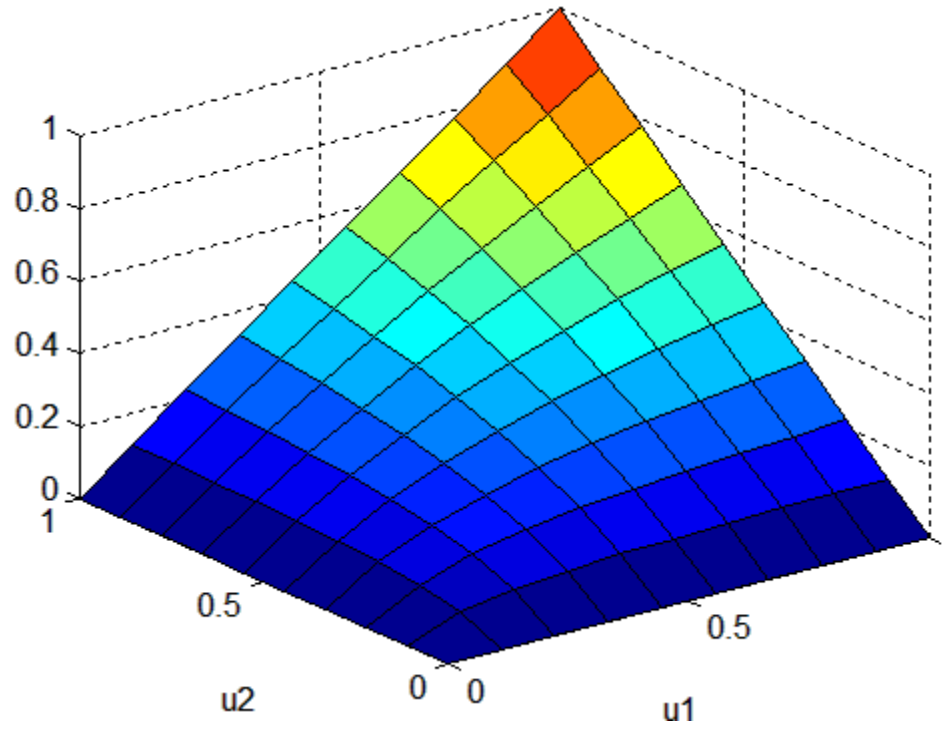
`Y = copulacdf('Gaussian',U,rho)` returns the cumulative probability of the Gaussian copula with linear correlation parameters `rho`, evaluated at the points in `U`. `U` is an `n`-by-`p` matrix of values in `[0,1]`, representing `n` points in the `p`-dimensional unit hypercube. `rho` is a `p`-by-`p` correlation matrix. If `U` is an `n`-by-`2` matrix, `rho` may also be a scalar correlation coefficient.

`Y = copulacdf('t',U,rho,NU)` returns the cumulative probability of the `t` copula with linear correlation parameters `rho` and degrees of freedom parameter `NU`, evaluated at the points in `U`. `U` is an `n`-by-`p` matrix of values in `[0,1]`. `rho` is a `p`-by-`p` correlation matrix. If `U` is an `n`-by-`2` matrix, `rho` may also be a scalar correlation coefficient.

`Y = copulacdf('family',U,alpha)` returns the cumulative probability of the bivariate Archimedean copula determined by *`family`*, with scalar parameter `alpha`, evaluated at the points in `U`. *`family`* is `Clayton`, `Frank`, or `Gumbel`. `U` is an `n`-by-`2` matrix of values in `[0,1]`.

Examples

```
u = linspace(0,1,10);
[U1,U2] = meshgrid(u,u);
F = copulacdf('Clayton',[U1(:) U2(:)],1);
surf(U1,U2,reshape(F,10,10))
xlabel('u1')
ylabel('u2')
```



See Also

`copulapdf` | `copularnd` | `copulastat` | `copulaparam`

copulafit

Purpose

Fit copula to data

Syntax

```
RHOHAT = copulafit('Gaussian',U)
[RHOHAT,nuhat] = copulafit('t',U)
[RHOHAT,nuhat,nuci] = copulafit('t',U)
paramhat = copulafit('family',U)
[paramhat,paramci] = copulafit('family',U)
[...] = copulafit(...,'alpha',alpha)
[...] = copulafit('t',U,'Method','ApproximateML')
[...] = copulafit(...,'Options',options)
```

Description

`RHOHAT = copulafit('Gaussian',U)` returns an estimate `RHOHAT` of the matrix of linear correlation parameters for a Gaussian copula, given data in `U`. `U` is an n-by-p matrix of values in the open interval (0,1) representing n points in the p-dimensional unit hypercube.

`[RHOHAT,nuhat] = copulafit('t',U)` returns an estimate `RHOHAT` of the matrix of linear correlation parameters for a t copula and an estimate `nuhat` of the degrees of freedom parameter, given data in `U`. `U` is an n-by-p matrix of values in the open interval (0,1) representing n points in the p-dimensional unit hypercube.

`[RHOHAT,nuhat,nuci] = copulafit('t',U)` also returns an approximate 95% confidence interval `nuci` for the degrees of freedom parameter estimated in `nuhat`.

`paramhat = copulafit('family',U)` returns an estimate `paramhat` of the copula parameter for an Archimedean copula specified by *`family`*, given data in `U`. `U` is an n-by-2 matrix of values in the open interval (0,1) representing n points in the unit square. *`family`* is one of `Clayton`, `Frank`, or `Gumbel`.

`[paramhat,paramci] = copulafit('family',U)` also returns an approximate 95% confidence interval `paramci` for the copula parameter estimated in `paramhat`.

`[...] = copulafit(...,'alpha',alpha)` returns approximate `100*(1-alpha)`% confidence intervals in `nuci` or `paramci`.

Note By default, `copulafit` uses maximum likelihood to fit a copula to `U`. When `U` contains data transformed to the unit hypercube by parametric estimates of their marginal cumulative distribution functions, this is known as the *Inference Functions for Margins (IFM)* method. When `U` contains data transformed by the empirical cdf (see `ecdf`), this is known as *Canonical Maximum Likelihood (CML)*.

`[...] = copulafit('t',U,'Method','ApproximateML')` fits a *t* copula for large samples `U` by maximizing an objective function that approximates the profile log-likelihood for the degrees of freedom parameter (see [1]). This method can be significantly faster than maximum likelihood, but the estimates and confidence limits may not be accurate for small to moderate sample sizes.

`[...] = copulafit(...,'Options',options)` specifies control parameters for the iterative parameter estimation algorithm using an options structure `options` as created by `statset`. Type `statset('copulafit')` at the command prompt for fields and default values used by `copulafit`. This argument is not applicable to the `'Gaussian'` family.

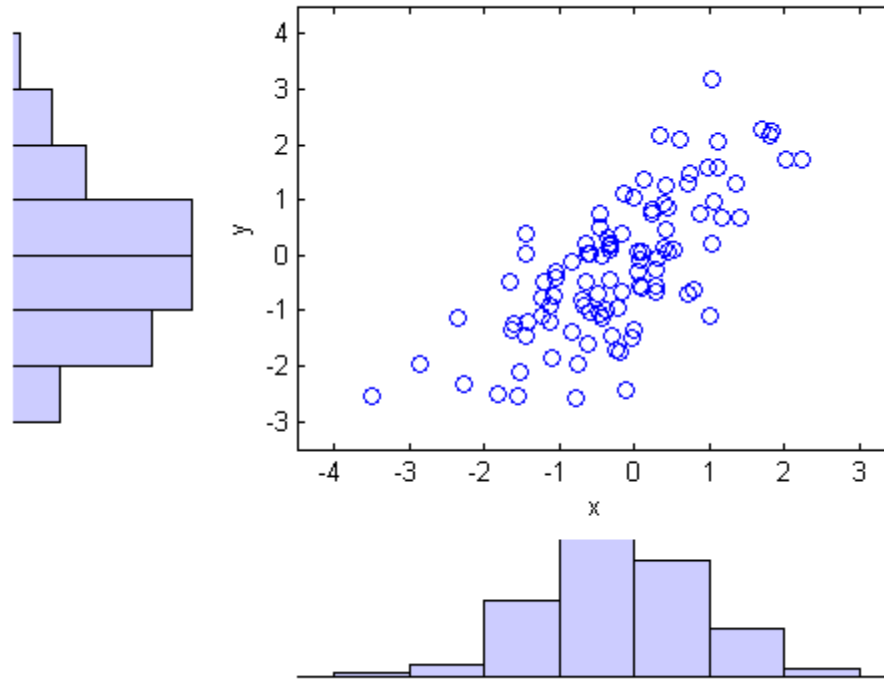
References

[1] Bouye, E., V. Durrleman, A. Nikeghbali, G. Riboulet, and T. Roncalli. "Copulas for Finance: A Reading Guide and Some Applications." Working Paper. Groupe de Recherche Operationnelle, Credit Lyonnais, 2000.

Examples

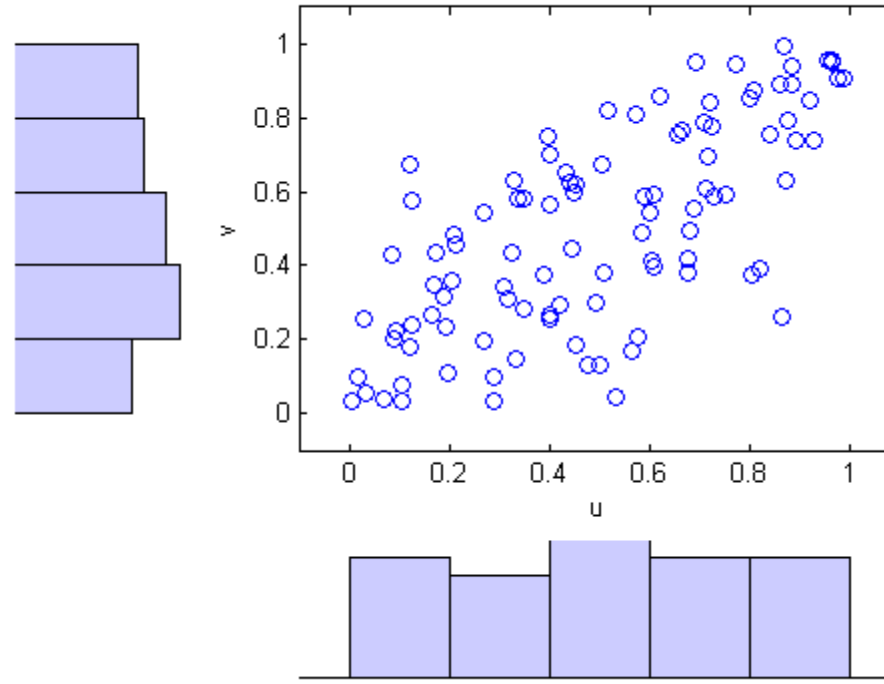
Load and plot simulated stock return data:

```
load stockreturns
x = stocks(:,1);
y = stocks(:,2);

scatterhist(x,y)
```



Transform the data to the copula scale (unit square) using a kernel estimator of the cumulative distribution function:

```
u = ksdensity(x,x,'function','cdf');
v = ksdensity(y,y,'function','cdf');

scatterhist(u,v)
xlabel('u')
ylabel('v')
```



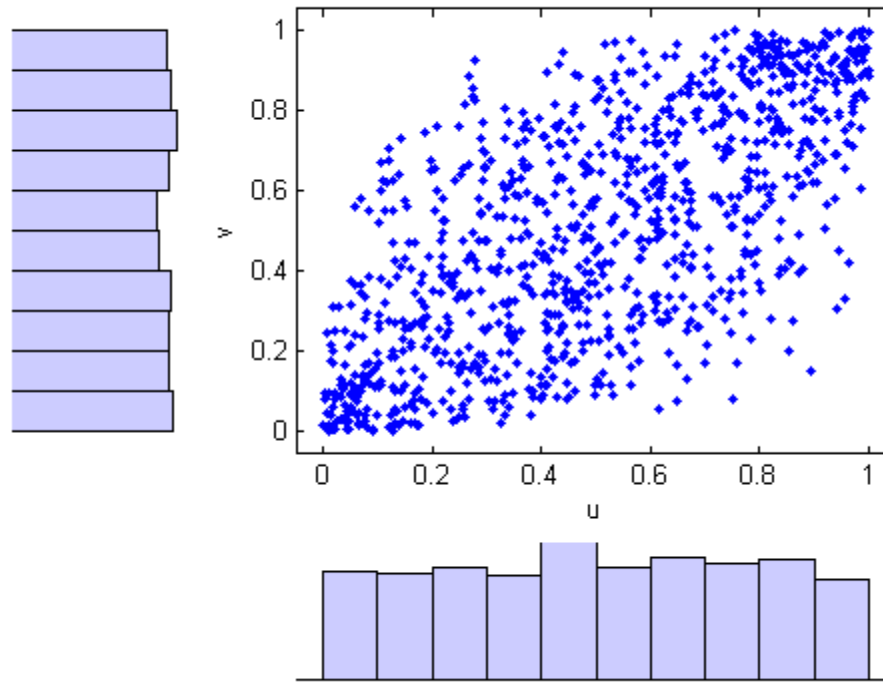
Fit a t copula:

```
[Rho,nu] = copulafit('t',[u v],'Method','ApproximateML')
Rho =
    1.0000    0.7220
    0.7220    1.0000
nu =
  2.8934e+006
```

Generate a random sample from the t copula:

```
r = copularnd('t',Rho,nu,1000);
```

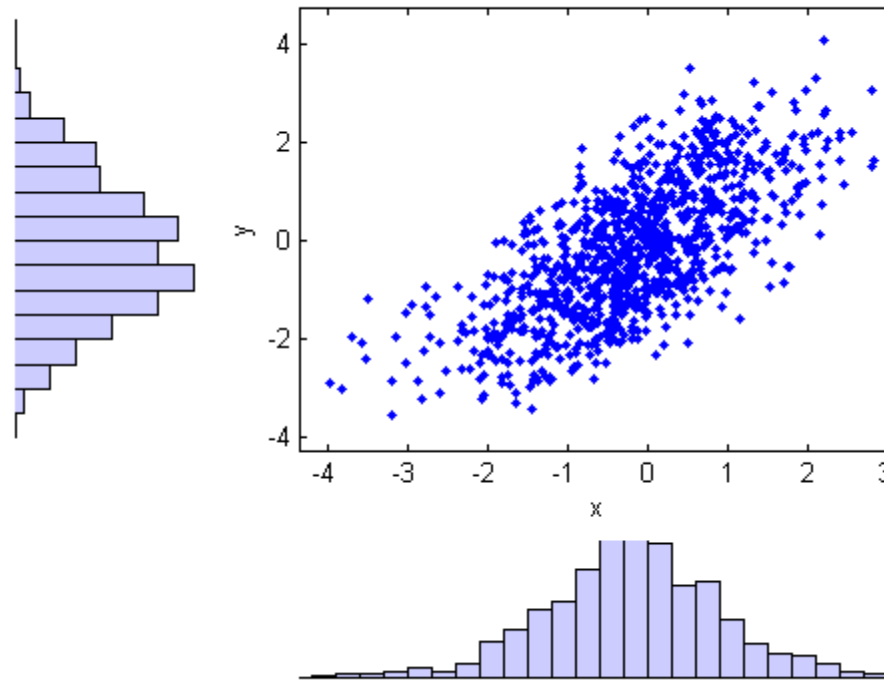
```
u1 = r(:,1);
v1 = r(:,2);

scatterhist(u1,v1)
xlabel('u')
ylabel('v')
set(get(gca,'children'),'marker','.')
```



Transform the random sample back to the original scale of the data:

```
x1 = ksdensity(x,u1,'function','icdf');
```

```
y1 = ksdensity(y,v1,'function','icdf');

scatterhist(x1,y1)
set(get(gca,'children'),'marker','.')
```



See Also

ecdf | copulacdf | copulaparam | copulapdf | copularnd | copulastat

copulaparam

Purpose

Copula parameters as function of rank correlation

Syntax

```
rho = copulaparam('Gaussian',R)
rho = copulaparam('t',R,NU)
alpha = copulaparam('family',R)
[...] = copulaparam(...,'type',type)
```

Description

`rho = copulaparam('Gaussian',R)` returns the linear correlation parameters `rho` corresponding to a Gaussian copula having Kendall's rank correlation `R`. If `R` is a scalar correlation coefficient, `rho` is a scalar correlation coefficient corresponding to a bivariate copula. If `R` is a `p`-by-`p` correlation matrix, `rho` is a `p`-by-`p` correlation matrix.

`rho = copulaparam('t',R,NU)` returns the linear correlation parameters `rho` corresponding to a `t` copula having Kendall's rank correlation `R` and degrees of freedom `NU`. If `R` is a scalar correlation coefficient, `rho` is a scalar correlation coefficient corresponding to a bivariate copula. If `R` is a `p`-by-`p` correlation matrix, `rho` is a `p`-by-`p` correlation matrix.

`alpha = copulaparam('family',R)` returns the copula parameter `alpha` corresponding to a bivariate Archimedean copula having Kendall's rank correlation `R`. `R` is a scalar. *`family`* is one of `Clayton`, `Frank`, or `Gumbel`.

`[...] = copulaparam(...,'type',type)` assumes `R` is the specified type of rank correlation. `type` is `'Kendall'` for Kendall's tau or `'Spearman'` for Spearman's rho.

`copulaparam` uses an approximation to Spearman's rank correlation for some copula families when no analytic formula exists. The approximation is based on a smooth fit to values computed using Monte Carlo simulations.

Examples

Get the linear correlation coefficient corresponding to a bivariate Gaussian copula having a rank correlation of `-0.5`.

```
tau = -0.5
rho = copulaparam('gaussian',tau)
```

```
rho =
   -0.7071

% Generate dependent beta random values using that copula
u = copularnd('gaussian',rho,100);
b = betainv(u,2,2);

% Verify that the sample has a rank correlation
% approximately equal to tau
tau_sample = corr(b,'type','k')
tau_sample =
    1.0000   -0.4638
   -0.4638    1.0000
```

See Also

copulacdf | copulapdf | copularnd | copulastat

copulapdf

Purpose

Copula probability density function

Syntax

```
Y = copulapdf('Gaussian',U,rho)
Y = copulapdf('t',U,rho,NU)
Y = copulapdf('family',U,alpha)
```

Description

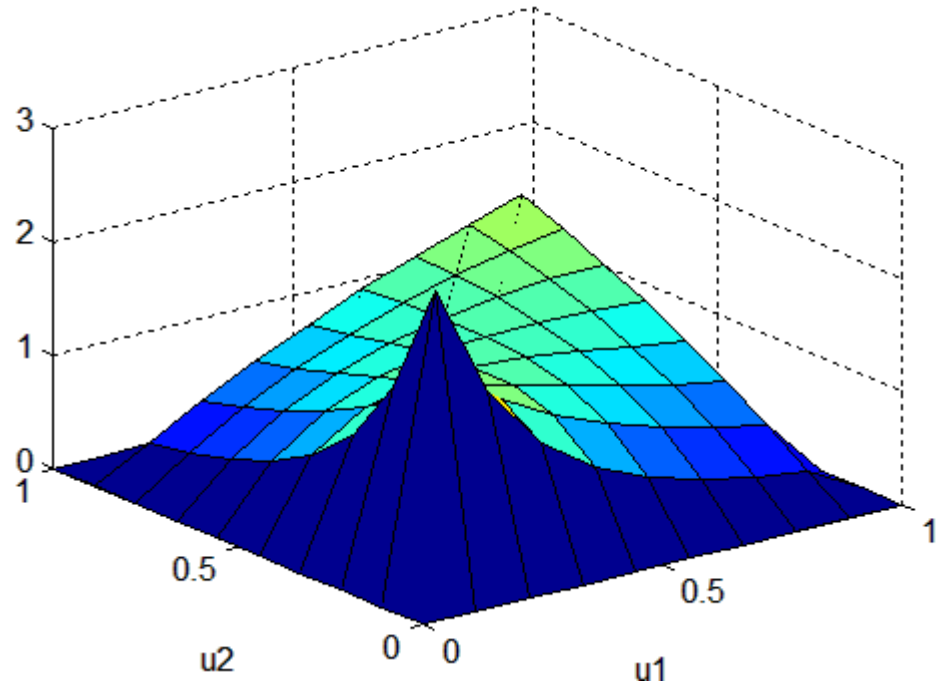
`Y = copulapdf('Gaussian',U,rho)` returns the probability density of the Gaussian copula with linear correlation parameters `rho`, evaluated at the points in `U`. `U` is an `n`-by-`p` matrix of values in `[0,1]`, representing `n` points in the `p`-dimensional unit hypercube. `rho` is a `p`-by-`p` correlation matrix. If `U` is an `n`-by-2 matrix, `rho` may also be a scalar correlation coefficient.

`Y = copulapdf('t',U,rho,NU)` returns the probability density of the `t` copula with linear correlation parameters `rho` and degrees of freedom parameter `NU`, evaluated at the points in `U`. `U` is an `n`-by-`p` matrix of values in `[0,1]`. `rho` is a `p`-by-`p` correlation matrix. If `U` is an `n`-by-2 matrix, `rho` may also be a scalar correlation coefficient.

`Y = copulapdf('family',U,alpha)` returns the probability density of the bivariate Archimedean copula determined by *`family`*, with scalar parameter `alpha`, evaluated at the points in `U`. *`family`* is `Clayton`, `Frank`, or `Gumbel`. `U` is an `n`-by-2 matrix of values in `[0,1]`.

Examples

```
u = linspace(0,1,10);
[U1,U2] = meshgrid(u,u);
F = copulapdf('Clayton',[U1(:) U2(:)],1);
surf(U1,U2,reshape(F,10,10))
xlabel('u1')
ylabel('u2')
```



See Also

`copulacdf` | `copulaparam` | `copularnd` | `copulastat`

Purpose

Copula rank correlation

Syntax

```
R = copulastat('Gaussian',rho)
R = copulastat('t',rho,NU)
R = copulastat('family',alpha)
R = copulastat(...,'type','type')
```

Description

`R = copulastat('Gaussian',rho)` returns the Kendall's rank correlation `R` that corresponds to a Gaussian copula having linear correlation parameters `rho`. If `rho` is a scalar correlation coefficient, `R` is a scalar correlation coefficient corresponding to a bivariate copula. If `rho` is a `p`-by-`p` correlation matrix, `R` is a `p`-by-`p` correlation matrix.

`R = copulastat('t',rho,NU)` returns the Kendall's rank correlation R that corresponds to a `t` copula having linear correlation parameters `rho` and degrees of freedom `NU`. If `rho` is a scalar correlation coefficient, `R` is a scalar correlation coefficient corresponding to a bivariate copula. If `rho` is a `p`-by-`p` correlation matrix, `R` is a `p`-by-`p` correlation matrix.

`R = copulastat('family',alpha)` returns the Kendall's rank correlation `R` that corresponds to a bivariate Archimedean copula with scalar parameter `alpha`. *`family`* is one of `Clayton`, `Frank`, or `Gumbel`.

`R = copulastat(...,'type','type')` returns the specified type of rank correlation. *`type`* is `Kendall` to compute Kendall's tau, or `Spearman` to compute Spearman's rho.

`copulastat` uses an approximation to Spearman's rank correlation for some copula families when no analytic formula exists. The approximation is based on a smooth fit to values computed using Monte-Carlo simulations.

Examples

Get the theoretical rank correlation coefficient for a bivariate.

```
% Gaussian copula with linear correlation parameter rho
rho = -.7071;
tau = copulastat('gaussian',rho)
tau =
   -0.5000
```

```
% Generate dependent beta random values using that copula
u = copularnd('gaussian',rho,100);
b = betainv(u,2,2);

% Verify that the sample has a rank correlation
% approximately equal to tau
tau_sample = corr(b,'type','k')
tau_sample =
    1.0000   -0.5265
   -0.5265    1.0000
```

See Also

copulacdf | copulaparam | copulapdf | copularnd

copularnd

Purpose

Copula random numbers

Syntax

```
U = copularnd('Gaussian',rho,N)
U = copularnd('t',rho,NU,N)
U = copularnd('family',alpha,N)
```

Description

`U = copularnd('Gaussian',rho,N)` returns `N` random vectors generated from a Gaussian copula with linear correlation parameters `rho`. If `rho` is a `p`-by-`p` correlation matrix, `U` is an `n`-by-`p` matrix. If `rho` is a scalar correlation coefficient, `copularnd` generates `U` from a bivariate Gaussian copula. Each column of `U` is a sample from a `Uniform(0,1)` marginal distribution.

`U = copularnd('t',rho,NU,N)` returns `N` random vectors generated from a `t` copula with linear correlation parameters `rho` and degrees of freedom `NU`. If `rho` is a `p`-by-`p` correlation matrix, `U` is an `n`-by-`p` matrix. If `rho` is a scalar correlation coefficient, `copularnd` generates `U` from a bivariate `t` copula. Each column of `U` is a sample from a `Uniform(0,1)` marginal distribution.

`U = copularnd('family',alpha,N)` returns `N` random vectors generated from the bivariate Archimedean copula determined by *`family`*, with scalar parameter `alpha`. *`family`* is `Clayton`, `Frank`, or `Gumbel`. `U` is an `n`-by-`2` matrix. Each column of `U` is a sample from a `Uniform(0,1)` marginal distribution.

Examples

Determine the linear correlation parameter corresponding to a bivariate Gaussian copula having a rank correlation of `-0.5`.

```
tau = -0.5
rho = copulaparam('gaussian',tau)
 rho =
   -0.7071

% Generate dependent beta random values using that copula
u = copularnd('gaussian',rho,100);
b = betainv(u,2,2);
```

```
% Verify that the sample has a rank correlation
% approximately equal to tau
tau_sample = corr(b,'type','kendall')
tau_sample =
    1.0000   -0.4537
   -0.4537    1.0000
```

See Also

copulacdf | copulaparam | copulapdf | copulastat

cordexch

Purpose

Coordinate exchange

Syntax

```
dCE = cordexch(nfactors,nruns)
[dCE,X] = cordexch(nfactors,nruns)
[dCE,X] = cordexch(nfactors,nruns,'model')
[dCE,X] = cordexch(...,'name',value)
```

Description

`dCE = cordexch(nfactors,nruns)` uses a coordinate-exchange algorithm to generate a *D*-optimal design `dCE` with `nruns` runs (the rows of `dCE`) for a linear additive model with `nfactors` factors (the columns of `dCE`). The model includes a constant term.

`[dCE,X] = cordexch(nfactors,nruns)` also returns the associated design matrix `X`, whose columns are the model terms evaluated at each treatment (row) of `dCE`.

`[dCE,X] = cordexch(nfactors,nruns,'model')` uses the linear regression model specified in *`model`*. *`model`* is one of the following strings, specified inside single quotes:

- `linear` — Constant and linear terms. This is the default.
- `interaction` — Constant, linear, and interaction terms
- `quadratic` — Constant, linear, interaction, and squared terms
- `purequadratic` — Constant, linear, and squared terms

The order of the columns of `X` for a full quadratic model with n terms is:

1. The constant term
2. The linear terms in order 1, 2, ..., n
3. The interaction terms in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n–1, n)
4. The squared terms in order 1, 2, ..., n

Other models use a subset of these terms, in the same order.

Alternatively, *model* can be a matrix specifying polynomial terms of arbitrary order. In this case, *model* should have one column for each factor and one row for each term in the model. The entries in any row of *model* are powers for the factors in the columns. For example, if a model has factors X1, X2, and X3, then a row [0 1 2] in *model* specifies the term (X1.^0).*(X2.^1).*(X3.^2). A row of all zeros in *model* specifies a constant term, which can be omitted.

[dCE,X] = cordexch(...,'*name*',*value*) specifies one or more optional name/value pairs for the design. Valid parameters and their values are listed in the following table. Specify *name* inside single quotes.

name	Value
bounds	Lower and upper bounds for each factor, specified as a 2-by-nfactors matrix. Alternatively, this value can be a cell array containing nfactors elements, each element specifying the vector of allowable values for the corresponding factor.
categorical	Indices of categorical predictors.
display	Either 'on' or 'off' to control display of the iteration counter. The default is 'on'.
excludefun	Handle to a function that excludes undesirable runs. If the function is *f*, it must support the syntax $b = f(S)$, where S is a matrix of treatments with nfactors columns and b is a vector of Boolean values with the same number of rows as S. $b(i)$ is true if the method should exclude ith row S.
init	Initial design as a nruns-by-nfactors matrix. The default is a randomly selected set of points.
levels	Vector of number of levels for each factor.
maxiter	Maximum number of iterations. The default is 10.

name	Value
`tries`	Number of times to try to generate a design from a new starting point. The algorithm uses random points for each try, except possibly the first. The default is `1`.
`options`	A structure that specifies whether to run in parallel, and specifies the random stream or streams. Create the `options` structure with `statset`. Option fields: • `UseParallel` — Set to `'always'` to compute in parallel. Default is `'never'`. • `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. Default is `'never'`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. • `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `cordexch` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case - You have an open MATLAB pool - `UseParallel` is `'always'` - `UseSubstreams` is `'never'` In that case, use a cell array the same size as the MATLAB pool. For more information on using parallel computing, see Chapter 17, “Parallel Statistics”.

Algorithms

Both `cordexch` and `rowexch` use iterative search algorithms. They operate by incrementally changing an initial design matrix X to increase $D = |X^TX|$ at each step. In both algorithms, there is randomness

built into the selection of the initial design and into the choice of the incremental changes. As a result, both algorithms may return locally, but not globally, *D*-optimal designs. Run each algorithm multiple times and select the best result for your final design. Both functions have a `'tries'` parameter that automates this repetition and comparison.

Unlike the row-exchange algorithm used by `rowexch`, `cordexch` does not use a candidate set. (Or rather, the candidate set is the entire design space.) At each step, the coordinate-exchange algorithm exchanges a single element of X with a new element evaluated at a neighboring point in design space. The absence of a candidate set reduces demands on memory, but the smaller scale of the search means that the coordinate-exchange algorithm is more likely to become trapped in a local minimum.

Examples

Suppose you want a design to estimate the parameters in the following three-factor, seven-term interaction model:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_{12} x_1 x_2 + \beta_{13} x_1 x_3 + \beta_{23} x_2 x_3 + \varepsilon$$

Use `cordexch` to generate a *D*-optimal design with seven runs:

```
nfactors = 3;
nruns = 7;
[dCE,X] = cordexch(nfactors,nruns,'interaction','tries',10)
dCE =
    -1     1     1
    -1    -1    -1
     1     1     1
    -1     1    -1
     1    -1     1
     1    -1    -1
    -1    -1     1
X =
     1    -1     1     1    -1    -1     1
     1    -1    -1    -1     1     1     1
     1     1     1     1     1     1     1
     1    -1     1    -1    -1     1    -1
```

```
     1     1    -1     1    -1     1    -1
     1     1    -1    -1    -1    -1     1
     1    -1    -1     1     1    -1    -1
```

Columns of the design matrix `X` are the model terms evaluated at each row of the design `dCE`. The terms appear in order from left to right: constant term, linear terms (1, 2, 3), interaction terms (12, 13, 23). Use `X` to fit the model, as described in "Linear Regression" on page 9-3, to response data measured at the design points in `dCE`.

See Also

`rowexch` | `daugment` | `dcovary`

Purpose

Linear or rank correlation

Syntax

```
RHO = corr(X)
RHO = corr(X,Y)
[RHO,PVAL] = corr(X,Y)
[RHO,PVAL] = corr(X,Y,'name',value)
```

Description

`RHO = corr(X)` returns a p-by-p matrix containing the pairwise linear correlation coefficient between each pair of columns in the n-by-p matrix `X`.

`RHO = corr(X,Y)` returns a $p1$-by-$p2$ matrix containing the pairwise correlation coefficient between each pair of columns in the n-by-$p1$ and n-by-$p2$ matrices `X` and `Y`.

`[RHO,PVAL] = corr(X,Y)` also returns `PVAL`, a matrix of p-values for testing the hypothesis of no correlation against the alternative that there is a nonzero correlation. Each element of `PVAL` is the p value for the corresponding element of `RHO`. If `PVAL(i, j)` is small, say less than `0.05`, then the correlation `RHO(i,j)` is significantly different from zero.

`[RHO,PVAL] = corr(X,Y,'name',value)` specifies one or more optional name/value pairs. Specify *`name`* inside single quotes. The following table lists valid parameters and their values.

Parameter	Values
`type`	• `'Pearson'` (the default) computes Pearson's linear correlation coefficient • `'Kendall'` computes Kendall's tau • `'Spearman'` computes Spearman's rho
`rows`	• `'all'` (the default) uses all rows regardless of missing values (`NaN`s) • `'complete'` uses only rows with no missing values

Parameter	Values
	• 'pairwise'computes RHO(i,j) using rows with no missing values in column i or j
tail — The alternative hypothesis against which to compute *p*-values for testing the hypothesis of no correlation	• 'both' — Correlation is not zero (the default) • 'right' — Correlation is greater than zero • 'left' — Correlation is less than zero

Using the 'pairwise' option for the rows parameter may return a matrix that is not positive definite. The 'complete' option always returns a positive definite matrix, but in general the estimates are based on fewer observations.

corr computes *p*-values for Pearson's correlation using a Student's t distribution for a transformation of the correlation. This correlation is exact when X and Y are normal. corr computes *p*-values for Kendall's tau and Spearman's rho using either the exact permutation distributions (for small sample sizes), or large-sample approximations.

corr computes *p*-values for the two-tailed test by doubling the more significant of the two one-tailed *p*-values.

References

[1] Gibbons, J.D. (1985) Nonparametric Statistical Inference, 2nd ed., M. Dekker.

[2] Hollander, M. and D.A. Wolfe (1973) Nonparametric Statistical Methods, Wiley.

[3] Kendall, M.G. (1970) Rank Correlation Methods, Griffin.

[4] Best, D.J. and D.E. Roberts (1975) "Algorithm AS 89: The Upper Tail Probabilities of Spearman's rho", Applied Statistics, 24:377-379.

See Also

corrcoef | partialcorr | corrcov | tiedrank

Purpose

Convert covariance matrix to correlation matrix

Syntax

```
R = corrcov(C)
[R,sigma] = corrcov(C)
```

Description

`R = corrcov(C)` computes the correlation matrix `R` corresponding to the covariance matrix `C`. `C` must be square, symmetric, and positive semi-definite.

`[R,sigma] = corrcov(C)` also computes the vector of standard deviations `sigma`.

Examples

Use `cov` and `corrcoef` to compute covariances and correlations, respectively, for sample data on weight and blood pressure (systolic, diastolic) in `hospital.mat`:

```
load hospital
X = [hospital.Weight hospital.BloodPressure];
C = cov(X)
C =
  706.0404   27.7879   41.0202
   27.7879   45.0622   23.8194
   41.0202   23.8194   48.0590
R = corrcoef(X)
R =
    1.0000    0.1558    0.2227
    0.1558    1.0000    0.5118
    0.2227    0.5118    1.0000
```

Compare `R` with the correlation matrix computed from `C` by `corrcov`:

```
corrcov(C)
ans =
    1.0000    0.1558    0.2227
    0.1558    1.0000    0.5118
    0.2227    0.5118    1.0000
```

See Also

`cov` | `corrcoef` | `corr` | `cholcov`

Purpose

Misclassification costs

Description

The `Cost` property is a matrix with misclassification costs. This property is empty for ensembles of regression trees.

See Also

`classregtree`

gmdistribution.CovType property

Purpose

Type of covariance matrices

Description

The string `'diagonal'` if the covariance matrices are restricted to be diagonal; the string `'full'` otherwise.

Purpose

Cox proportional hazards regression

Syntax

```
b = coxphfit(X,y)
b = coxphfit(X,y,'name',value)
[b,logl,H,stats] = coxphfit(...)
```

Description

`b = coxphfit(X,y)` returns a p-by-1 vector `b` of coefficient estimates for a Cox proportional hazards regression of the responses in `y` on the predictors in `X`. `X` is an n-by-p matrix of p predictors at each of n observations. `y` is an n-by-1 vector of observed responses.

The phrase `h(t)*exp(X*b)` models the hazard rate for the distribution of `y`, where `h(t)` is a common baseline hazard function. The model does not include a constant term, and `X` cannot contain a column of 1s.

`b = coxphfit(X,y,'name',value)` specifies one or more optional parameter name/value pairs chosen from the following table. Specify *name* inside single quotes.

Name	Value
`baseline`	The `X` values at which to compute the baseline hazard. Default is `mean(X)`, so the hazard at `X` is `h(t)*exp((X-mean(X))*b)`. Enter `0` to compute the baseline relative to 0, so the hazard at `X` is `h(t)*exp(X*b)`.
`censoring`	A Boolean array of the same size as `y` that is 1 for observations that are right-censored and 0 for observations that are observed exactly. Default is all observations observed exactly.
`frequency`	An array of the same size as `y` containing nonnegative integer counts. The j^{th} element of this vector gives the number of times the method observes the j^{th} element of `y` and the j^{th} row of `X`. Default is one observation per row of `X` and `y`.

Name	Value
`init`	A vector containing initial values for the estimated coefficients `b`.
`options`	A structure specifying control parameters for the iterative algorithm used to estimate `b`. A call to `statset` can create this argument. For parameter names and default values, type `statset('coxphfit')`.

`[b,logl,H,stats] = coxphfit(...)` returns additional results. `logl` is the log likelihood. `H` is a two-column matrix containing `y` values in the first column and the estimated baseline cumulative hazard evaluated at those values in the second column. `stats` is a structure that contains the fields:

- `beta` — Coefficient estimates (same as `b`)
- `se` — Standard errors of coefficient estimates `b`
- `z` — *z* statistics for `b` (`b` divided by standard error)
- `p` — *p*-values for `b`
- `covb` — Estimated covariance matrix for `b`

Examples

Generate Weibull data depending on predictor `x`:

```
x = 4*rand(100,1);
A = 50*exp(-0.5*x); B = 2;
y = wblrnd(A,B);
```

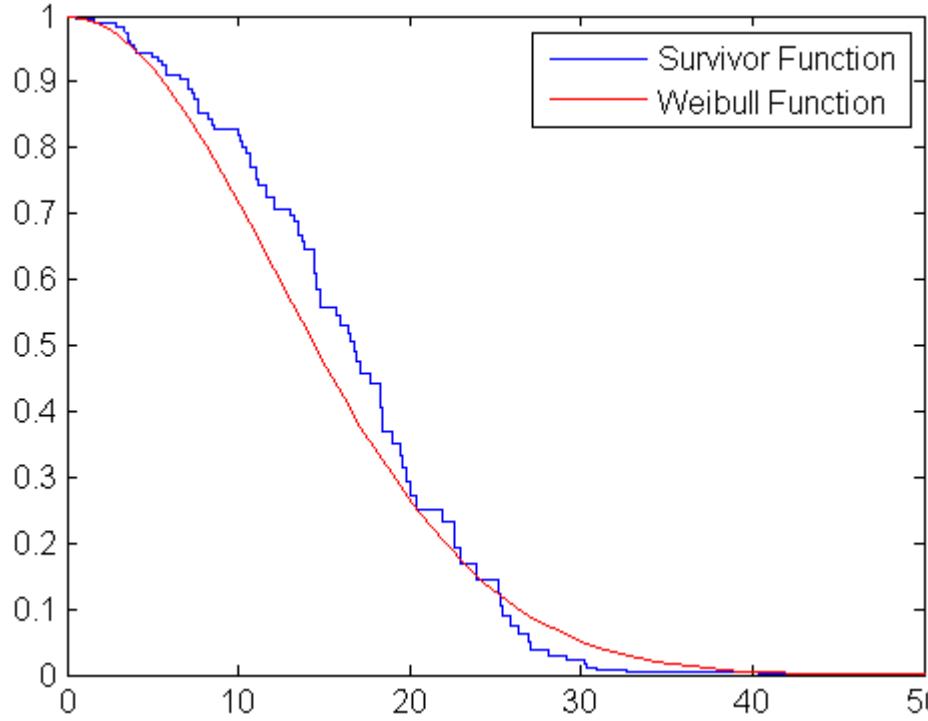
Fit a Cox model :

```
[b,logL,H,stats] = coxphfit(x,y);
```

Show the Cox estimate of the baseline survivor function together with the known Weibull function:

```
stairs(H(:,1),exp(-H(:,2)))
```

```
xx = linspace(0,100);
line(xx,1-wblcdf(xx,50*exp(-0.5*mean(x)),B),'color','r')
xlim([0,50])
legend('Survivor Function','Weibull Function')
```



References

[1] Cox, D.R., and D. Oakes. *Analysis of Survival Data.* London: Chapman & Hall, 1984.

[2] Lawless, J. F. *Statistical Models and Methods for Lifetime Data.* Hoboken, NJ: Wiley-Interscience, 2002.

See Also

`ecdf` | `statset` | `wblfit`

NaiveBayes.CPrior property

Purpose

Class priors

Description

The `CPrior` property is a vector of length `NClasses` containing the class priors. The priors for empty classes are zero.

Purpose

Create object to use in *k*-nearest neighbors search

Syntax

```
NS = createns(X)
NS = createns(X,'Name',Value)
```

Description

`NS = createns(X)` uses the data observations in an *mx*-by-*n* matrix `X` to create an object `NS`. Rows of `X` correspond to observations and columns correspond to variables. `NS` is either an `ExhaustiveSearcher` or a `KDTreeSearcher` object which you can use to find nearest neighbors in `X` for desired query points. When `NS` is an `ExhaustiveSearcher` object, `knnsearch` uses the exhaustive search algorithm to find nearest neighbors. When `NS` is a `KDTreeSearcher`, `createns` creates and saves a *k*d-tree based on `X` in `NS`. `knnsearch` uses the *k*d-tree to find nearest neighbors. For information on these search methods, see "*k*-Nearest Neighbor Search and Radius Search" on page 13-12.

`NS = createns(X,'Name',Value)` accepts one or more optional name/value pairs. Specify *`Name`* inside single quotes. Specify `NSMethod` to determine which type of object to create. The object's properties save the information when you specify other arguments. For more information on the objects' properties, see `ExhaustiveSearcher` and `KDTreeSearcher`.

Input Arguments

Name-Value Pair Arguments

`NSMethod`

Nearest neighbors search method, used to define the type of object created. Value is either:

- `'kdtree'` — Create a `KDTreeSearcher` object. If you do not specify `NSMethod`, this is the default value when the number of columns of `X` is less than 10, `X` is not sparse, and the distance measure is one of the following measures:
  - `'euclidean'` (default)
  - `'cityblock'`

- 'minkowski'
- 'chebychev'

- 'exhaustive' — Create an ExhaustiveSearcher object. If you do not specify NSMethod, this is the default value when the default criteria for 'kdtree' do not apply.

Distance

A string or a function handle specifying the default distance metric used when you call the knnsearch method to find nearest neighbors for future query points. If you specify a distance metric but not an NSMethod, this input determines the type of object createns creates, according to the default values described in NSMethod.

For both KDTreeSearcher and ExhaustiveSearcher objects, the following options apply:

- 'euclidean' (default) — Euclidean distance.
- 'cityblock' — City block distance.
- 'chebychev' — Chebychev distance (maximum coordinate difference).
- 'minkowski' — Minkowski distance.

The following options apply only to ExhaustiveSearcher objects:

- 'seuclidean' — Standardized Euclidean distance. Each coordinate difference between rows in X and the query matrix is scaled by dividing by the corresponding element of the standard deviation computed from X, S=nanstd(X). To specify another value for S, use the Scale argument.
- 'mahalanobis' — Mahalanobis distance, which is computed using a positive definite covariance matrix C. The default value of C is the sample covariance matrix of X, as computed by nancov(X). To change the value of C, use the Cov parameter.

- `'cosine'` — One minus the cosine of the included angle between observations (treated as vectors).
- `'correlation'` — One minus the sample linear correlation between observations (treated as sequences of values).
- `'spearman'` — One minus the sample Spearman's rank correlation between observations (treated as sequences of values).
- `'hamming'` — Hamming distance, which is percentage of coordinates that differ.
- `'jaccard'` — One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.
- custom distance function — A distance function specified using `@` (for example, `@distfun`). A distance function must be of the form `function D2 = distfun(ZI, ZJ)`, taking as arguments a 1-by-n vector `ZI` containing a single row from `X` or from the query points `Y`, and an $m2$-by-n matrix `ZJ` containing multiple rows of `X` or `Y`, and returning an $m2$-by-1 vector of distances $d2$, whose jth element is the distance between the observations `ZI` and `ZJ(j,:)`.

`P`

A positive scalar, p, indicating the exponent of the Minkowski distance. This parameter is only valid when `Distance` is `'minkowski'`. Default is 2.

`Cov`

A positive definite matrix indicating the covariance matrix when computing the Mahalanobis distance. This parameter is only valid when `Distance` is `'mahalanobis'`. Default is `nancov(X)`.

`Scale`

A vector `S` with the length equal to the number of columns in `X`. Each coordinate of `X` and each query point is scaled by the corresponding element of `S` when computing the standardized

Euclidean distance. This parameter is only valid when `Distance` is `'seuclidean'`. Default is `nanstd(X)`.

`BucketSize`

A positive integer, indicating the maximum number of data points in each leaf node of the *k*d-tree. This argument is only meaningful when using the *k*d-tree search method. Default is 50.

Examples

Create a *k*d-tree with a Minkowski distance metric and a `P` value of 5:

```
load fisheriris
x = meas(:,3:4);
% Since x has only two columns and the Distance is Minkowski,
% createns creates a KDTreeSearcher object by default:
knnobj = createns(x,'Distance','minkowski','P',5)

knnobj =

  KDTreeSearcher

  Properties:
       BucketSize: 50
                X: [150x2 double]
         Distance: 'minkowski'
    DistParameter: 5
```

See Also

`ExhaustiveSearcher.knnsearch` | `KDTreeSearcher.knnsearch` | `ExhaustiveSearcher` | `KDTreeSearcher`

How To

- "*k*-Nearest Neighbor Search and Radius Search" on page 13-12

Purpose

Cross-tabulation

Syntax

```
table = crosstab(x1,x2)
table = crosstab(x1,x2,...,xn)
[table,chi2,p] = crosstab(x1,...,xn)
[table,chi2,p,labels] = crosstab(x1,...,xn)
```

Description

`table = crosstab(x1,x2)` returns a cross-tabulation `table` of two vectors of the same length `x1` and `x2`. `table` is *m*-by-*n*, where *m* is the number of distinct values in `x1` and *n* is the number of distinct values in `x2`.

`x1` and `x2` are grouping variables, as described in "Grouped Data" on page 2-34. `crosstab` uses `grp2idx` to assign a positive integer to each distinct value. `table(i,j)` is a count of indices where `grp2idx(x1)` is `i` and `grp2idx(x2)` is `j`. The numerical order of `grp2idx(x1)` and `grp2idx(x2)` order rows and columns of `table`, respectively.

`table = crosstab(x1,x2,...,xn)` returns a multi-dimensional `table` where `table(i,j,...,n)` is a count of indices where `grp2idx(x1)` is `i`, `grp2idx(x2)` is `j`, `grp2idx(x3)` is `k`, and so on.

`[table,chi2,p] = crosstab(x1,...,xn)` also returns the chi-square statistic `chi2` and its *p* value `p` for a test that `table` is independent in each dimension. The null hypothesis is that the proportion in any entry of `table` is the product of the proportions in each dimension.

`[table,chi2,p,labels] = crosstab(x1,...,xn)` also returns a cell array `labels` with one column for each input argument. The entries in the first column are labels for the rows of `table`, the entries in the second column are labels for the columns, and so on, for a multi-dimensional `table`.

Examples

Example 1

Cross-tabulate two vectors with three and four distinct values, respectively:

```
x = [1 1 2 3 1]; y = [1 2 5 3 1];
```

```
table = crosstab(x,y)
table =
     2     1     0     0
     0     0     0     1
     0     0     1     0
```

Example 2

Generate two independent vectors, each containing 50 discrete uniform random numbers in the range `1:3`:

```
x1 = unidrnd(3,50,1);
x2 = unidrnd(3,50,1);
[table,chi2,p] = crosstab(x1,x2)
table =
     1     6     7
     5     5     2
    11     7     6
chi2 =
    7.5449
p =
    0.1097
```

At the 95% confidence level, the p value fails to reject the null hypothesis that `table` is independent in each dimension.

Example 3

The file `carbig.mat` contains measurements of large model cars during the years 1970-1982:

```
load carbig
[table,chi2,p,labels] = crosstab(cyl4,when,org)
table(:,:,1) =
    82    75    25
    12    22    38
table(:,:,2) =
     0     4     3
    23    26    17
table(:,:,3) =
```

```
     3     3     4
    12    25    32

chi2 =
  207.7689

p =
     0

label =
    'Other'    'Early'    'USA'
    'Four'     'Mid'      'Europe'
         []    'Late'     'Japan'
```

`table` and `label` together show that the number of four-cylinder cars made in the USA during the late period of the data was `table(2,3,1)` or 38 cars.

See Also

`grp2idx` | `tabulate`

How To

- "Grouped Data" on page 2-34

crossval

Purpose

Loss estimate using cross-validation

Syntax

```
vals = crossval(fun,X)
vals = crossval(fun,X,Y,...)
mse = crossval('mse',X,y,'Predfun',predfun)
mcr = crossval('mcr',X,y,'Predfun',predfun)
val = crossval(criterion,X1,X2,...,y,'Predfun',predfun)
vals = crossval(...,'name',value)
```

Description

`vals = crossval(fun,X)` performs 10-fold cross-validation for the function `fun`, applied to the data in `X`.

`fun` is a function handle to a function with two inputs, the training subset of `X`, `XTRAIN`, and the test subset of `X`, `XTEST`, as follows:

```
testval = fun(XTRAIN,XTEST)
```

Each time it is called, `fun` should use `XTRAIN` to fit a model, then return some criterion `testval` computed on `XTEST` using that fitted model.

`X` can be a column vector or a matrix. Rows of `X` correspond to observations; columns correspond to variables or features. Each row of `vals` contains the result of applying `fun` to one test set. If `testval` is a non-scalar value, `crossval` converts it to a row vector using linear indexing and stored in one row of `vals`.

`vals = crossval(fun,X,Y,...)` is used when data are stored in separate variables `X`, `Y`, ... All variables (column vectors, matrices, or arrays) must have the same number of rows. `fun` is called with the training subsets of `X`, `Y`, ... , followed by the test subsets of `X`, `Y`, ... , as follows:

```
testvals = fun(XTRAIN,YTRAIN,...,XTEST,YTEST,...)
```

`mse = crossval('mse',X,y,'Predfun',predfun)` returns `mse`, a scalar containing a 10-fold cross-validation estimate of mean-squared error for the function `predfun`. `X` can be a column vector, matrix, or array of predictors. `y` is a column vector of response values. `X` and `y` must have the same number of rows.

`predfun` is a function handle called with the training subset of `X`, the training subset of `y`, and the test subset of `X` as follows:

```
yfit = predfun(XTRAIN,ytrain,XTEST)
```

Each time it is called, `predfun` should use `XTRAIN` and `ytrain` to fit a regression model and then return fitted values in a column vector `yfit`. Each row of `yfit` contains the predicted values for the corresponding row of `XTEST`. `crossval` computes the squared errors between `yfit` and the corresponding response test set, and returns the overall mean across all test sets.

`mcr = crossval('mcr',X,y,'Predfun',predfun)` returns `mcr`, a scalar containing a 10-fold cross-validation estimate of misclassification rate (the proportion of misclassified samples) for the function `predfun`. The matrix `X` contains predictor values and the vector `y` contains class labels. `predfun` should use `XTRAIN` and `YTRAIN` to fit a classification model and return `yfit` as the predicted class labels for `XTEST`. `crossval` computes the number of misclassifications between `yfit` and the corresponding response test set, and returns the overall misclassification rate across all test sets.

`val = crossval(`*`criterion`*`,X1,X2,...,y,'Predfun',predfun)`, where *`criterion`* is `'mse'` or `'mcr'`, returns a cross-validation estimate of mean-squared error (for a regression model) or misclassification rate (for a classification model) with predictor values in `X1`, `X2`, ... and, respectively, response values or class labels in `y`. `X1`, `X2`, ... and `y` must have the same number of rows. `predfun` is a function handle called with the training subsets of `X1`, `X2`, ..., the training subset of `y`, and the test subsets of `X1`, `X2`, ..., as follows:

```
yfit=predfun(X1TRAIN,X2TRAIN,...,ytrain,X1TEST,X2TEST,...)
```

`yfit` should be a column vector containing the fitted values.

`vals = crossval(...,'`*`name`*`',`*`value`*`)` specifies one or more optional parameter name/value pairs from the following table. Specify *`name`* inside single quotes.

Name	Value
holdout	A scalar specifying the ratio or the number of observations p for holdout cross-validation. When 0 < p < 1, approximately p*n observations for the test set are randomly selected. When p is an integer, p observations for the test set are randomly selected.
kfold	A scalar specifying the number of folds k for k-fold cross-validation.
leaveout	Specifies leave-one-out cross-validation. The value must be 1.
mcreps	A positive integer specifying the number of Monte-Carlo repetitions for validation. Ifthe first input of crossval is 'mse' or 'mcr', crossval returns the mean of mean-squared error or misclassification rate across all of the Monte-Carlo repetitions. Otherwise, crossval concatenates the values vals from all of the Monte-Carlo repetitions along the first dimension.
partition	An object c of the cvpartition class, specifying the cross-validation type and partition.
stratify	A column vector group specifying groups for stratification. Both training and test sets have roughly the same class proportions as in group. NaNs or empty strings in group are treated as missing values, and the corresponding rows of the data are ignored.
options	A structure that specifies whether to run in parallel, and specifies the random stream or streams. Create the options structure with statset. Option fields:

Name	Value
	• `UseParallel` — Set to `'always'` to compute in parallel. Default is `'never'`. • `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. Default is `'never'`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. • `Streams` — A `RandStream` object or cell array consisting of one such object. If you do not specify `Streams`, `crossval` uses the default stream. For more information on using parallel computing, see Chapter 17, "Parallel Statistics".

Only one of `kfold`, `holdout`, `leaveout`, or `partition` can be specified, and `partition` cannot be specified with `stratify`. If both `partition` and `mcreps` are specified, the first Monte-Carlo repetition uses the partition information in the `cvpartition` object, and the `repartition` method is called to generate new partitions for each of the remaining repetitions. If no cross-validation type is specified, the default is 10-fold cross-validation.

Note When using cross-validation with classification algorithms, stratification is preferred. Otherwise, some test sets may not include observations from all classes.

Examples

Example 1

Compute mean-squared error for regression using 10-fold cross-validation:

```
load('fisheriris');
y = meas(:,1);
X = [ones(size(y,1),1),meas(:,2:4)];

regf=@(XTRAIN,ytrain,XTEST)(XTEST*regress(ytrain,XTRAIN));

cvMse = crossval('mse',X,y,'predfun',regf)
cvMse =
    0.1015
```

Example 2

Compute misclassification rate using stratified 10-fold cross-validation:

```
load('fisheriris');
y = species;
X = meas;
cp = cvpartition(y,'k',10); % Stratified cross-validation

classf = @(XTRAIN, ytrain,XTEST)(classify(XTEST,XTRAIN,...
ytrain));

cvMCR = crossval('mcr',X,y,'predfun',classf,'partition',cp)
cvMCR =
    0.0200
```

Example 3

Compute the confusion matrix using stratified 10-fold cross-validation:

```
load('fisheriris');
y = species;
X = meas;
order = unique(y); % Order of the group labels
cp = cvpartition(y,'k',10); % Stratified cross-validation

f = @(xtr,ytr,xte,yte)confusionmat(yte,...
classify(xte,xtr,ytr),'order',order);
```

```
cfMat = crossval(f,X,y,'partition',cp);
cfMat = reshape(sum(cfMat),3,3)
cfMat =
    50     0     0
     0    48     2
     0     1    49
```

`cfMat` is the summation of 10 confusion matrices from 10 test sets.

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*. New York: Springer, 2001.

See Also

`cvpartition`

How To

- "Grouped Data" on page 2-34

ClassificationDiscriminant.crossval

Purpose

Cross-validated discriminant analysis classifier

Syntax

```
cvmodel = crossval(obj)
cvmodel = crossval(obj,Name,Value)
```

Description

`cvmodel = crossval(obj)` creates a partitioned model from `obj`, a fitted discriminant analysis classifier. By default, `crossval` uses 10-fold cross validation on the training data to create `cvmodel`.

`cvmodel = crossval(obj,Name,Value)` creates a partitioned model with additional options specified by one or more `Name,Value` pair arguments.

Tips

- Assess the predictive performance of `obj` on cross-validated data using the "kfold" methods and properties of `cvmodel`, such as `kfoldLoss`.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `ClassificationDiscriminant.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`cvpartition`

Object of class `cvpartition`, created by the `cvpartition` function. `crossval` splits the data into subsets with `cvpartition`.

Use only one of these options at a time: `'cvpartition'`, `'holdout'`, `'kfold'`, or `'leaveout'`.

Default: `[]`

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. Use only one of these options at a time: `'cvpartition'`, `'holdout'`, `'kfold'`, or `'leaveout'`.

`kfold`

Number of folds to use in a cross-validated classifier, a positive integer.

Use only one of these options at a time: `'cvpartition'`, `'holdout'`, `'kfold'`, or `'leaveout'`.

Default: 10

`leaveout`

Set to `'on'` for leave-one-out cross validation.

Use only one of these options at a time: `'cvpartition'`, `'holdout'`, `'kfold'`, or `'leaveout'`.

Examples

Create a classification model for the Fisher iris data, and then create a cross-validation model. Evaluate the quality the model using `kfoldLoss`.

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species);
cvmodel = crossval(obj);
L = kfoldLoss(cvmodel)

L =
    0.0200
```

Alternatives

You can create a cross-validation classifier directly from the data, instead of creating a discriminant analysis classifier followed by a cross-validation classifier. To do so, include one of these options in

`ClassificationDiscriminant.fit`: `'crossval'`, `'cvpartition'`, `'holdout'`, `'kfold'`, or `'leaveout'`.

See Also

`ClassificationDiscriminant.fit` | `crossval` | `kfoldEdge` | `kfoldfun` | `kfoldLoss` | `kfoldMargin` | `kfoldPredict`

How To

- “Discriminant Analysis” on page 12-3

Purpose

Cross validate ensemble

Syntax

```
cvens = crossval(ens)
cvens = crossval(ens,Name,Value)
```

Description

`cvens = crossval(ens)` creates a cross-validated ensemble from `ens`, a classification ensemble. Default is 10-fold cross validation.

`cvens = crossval(ens,Name,Value)` creates a cross-validated ensemble with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`cvpartition`

A partition of class `cvpartition`. Sets the partition for cross validation.

Use no more than one of the name-value pairs `cvpartition`, `holdout`, `kfold`, or `leaveout`.

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`kfold`

Number of folds for cross validation, a numeric positive scalar.

Use no more than one of the name-value pairs `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`leaveout`

If `'on'`, use leave-one-out cross validation.

Use no more than one of the name-value pairs `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`nprint`

Printout frequency, a positive integer scalar. Use this parameter to observe the training of cross-validation folds.

Default: `'off'`, meaning no printout

Output Arguments

`cvens`

A cross-validated classification ensemble of class `ClassificationPartitionedEnsemble`.

Alternatives

You can create a cross-validation ensemble directly from the data, instead of creating an ensemble followed by a cross-validation ensemble. To do so, include one of these five options in `fitensemble`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Examples

Create a cross-validated classification model for the Fisher iris data, and assess its quality using the `kfoldLoss` method.

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
cvens = crossval(ens);
L = kfoldLoss(cvens)

L =
    0.0467
```

See Also

`ClassificationPartitionedEnsemble` | `cvpartition`

How To

- Chapter 13, “Nonparametric Supervised Learning”

ClassificationTree.crossval

Purpose

Cross-validated decision tree

Syntax

```
cvmodel = crossval(model)
cvmodel = crossval(model,Name,Value)
```

Description

`cvmodel = crossval(model)` creates a partitioned model from `model`, a fitted classification tree. By default, `crossval` uses 10-fold cross validation on the training data to create `cvmodel`.

`cvmodel = crossval(model,Name,Value)` creates a partitioned model with additional options specified by one or more `Name,Value` pair arguments.

Tips

- Assess the predictive performance of `model` on cross-validated data using the "kfold" methods and properties of `cvmodel`, such as `kfoldLoss`.

Input Arguments

`model`

A classification model, produced using `ClassificationTree.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`cvpartition`

Object of class `cvpartition`, created by the `cvpartition` function. `crossval` splits the data into subsets with `cvpartition`.

Use only one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: `[]`

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`kfold`

Number of folds to use in a cross-validated tree, a positive integer.

Use only one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: 10

`leaveout`

Set to `'on'` for leave-one-out cross validation.

Output Arguments

`cvmodel`

A partitioned model of class `ClassificationPartitionedModel`.

Examples

Create a classification model for the ionosphere data, then create a cross-validation model. Evaluate the quality the model using `kfoldLoss`.

```
load ionosphere
tree = ClassificationTree.fit(X,Y);
cvmodel = crossval(tree);
L = kfoldLoss(cvmodel)

L =
    0.1168
```

Alternatives

You can create a cross-validation tree directly from the data, instead of creating a decision tree followed by a cross-validation tree. To do so, include one of these five options in `ClassificationTree.fit`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

See Also `ClassificationTree.fit | crossval`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Cross validate ensemble

Syntax

```
cvens = crossval(ens)
cvens = crossval(ens,Name,Value)
```

Description

`cvens = crossval(ens)` creates a cross-validated ensemble from `ens`, a regression ensemble. Default is 10-fold cross validation.

`cvens = crossval(ens,Name,Value)` creates a cross-validated ensemble with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`cvpartition`

A partition of class `cvpartition`. Sets the partition for cross validation.

Use no more than one of the name-value pairs `cvpartition`, `holdout`, `kfold`, and `leaveout`.

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`kfold`

Number of folds for cross validation, a numeric positive scalar.

Use no more than one of the name-value pairs `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`leaveout`

If `'on'`, use leave-one-out cross-validation.

Use no more than one of the name-value pairs `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`nprint`

Printout frequency, a positive integer scalar. Use this parameter to observe the training of cross-validation folds.

Default: `'off'`, meaning no printout

Output Arguments

`cvens`

A cross-validated classification ensemble of class `RegressionPartitionedEnsemble`.

Alternatives

You can create a cross-validation ensemble directly from the data, instead of creating an ensemble followed by a cross-validation ensemble. To do so, include one of these five options in `fitensemble`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Examples

Create a cross-validated classification model for the `carsmall` data, and assess its quality using the `kfoldLoss` method:

```
X = [Acceleration Displacement Horsepower Weight];
rens = fitensemble(X,MPG,'LSBoost',100,'Tree');
cvens = crossval(rens);
L = kfoldLoss(cvens)

L =
   21.9868
```

See Also

`RegressionPartitionedEnsemble` | `cvpartition`

How To

- Chapter 13, "Nonparametric Supervised Learning"

RegressionTree.crossval

Purpose

Cross-validated decision tree

Syntax

```
cvmodel = crossval(model)
cvmodel = crossval(model,Name,Value)
```

Description

`cvmodel = crossval(model)` creates a partitioned model from `model`, a fitted regression tree. By default, `crossval` uses 10-fold cross validation on the training data to create `cvmodel`.

`cvmodel = crossval(model,Name,Value)` creates a partitioned model with additional options specified by one or more `Name,Value` pair arguments.

Tips

- Assess the predictive performance of `model` on cross-validated data using the "kfold" methods and properties of `cvmodel`, such as `kfoldLoss`.

Input Arguments

`model`

A regression model, produced using `RegressionTree.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`cvpartition`

Object of class `cvpartition`, created by the `cvpartition` function. `crossval` splits the data into subsets with `cvpartition`.

Use only one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: `[]`

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`kfold`

Number of folds to use in a cross-validated tree, a positive integer.

Use only one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: 10

`leaveout`

Set to `'on'` for leave-one-out cross-validation.

Output Arguments

`cvmodel`

A partitioned model of class `RegressionPartitionedModel`.

Examples

Create a regression model of the `carsmall` data, and assess its accuracy with `kfoldLoss`:

```
load carsmall
X = [Acceleration Displacement Horsepower Weight];
tree = RegressionTree.fit(X,MPG);
cvtree = crossval(tree);
L = kfoldLoss(cvtree)

L =
   25.2432
```

Alternatives

You can create a cross-validation tree directly from the data, instead of creating a decision tree followed by a cross-validation tree. To do so, include one of these five options in `RegressionTree.fit`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

See Also `RegressionTree.fit | crossval`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Transpose categorical matrix

Syntax

```
B = ctranspose(A)
```

Description

`B = ctranspose(A)` returns the transpose of the 2-D categorical matrix `A`. Note that `ctranspose` is identical to `transpose` for categorical arrays.

See Also

`transpose` | `permute`

classregtree.cutcategories

Purpose

Cut categories

Syntax

```
C = cutcategories(t)
C = cutcategories(t,nodes)
```

Description

`C = cutcategories(t)` returns an n-by-2 cell array `C` of the categories used at branches in the decision tree `t`, where n is the number of nodes. For each branch node `i` based on a categorical predictor variable `x`, the left child is chosen if `x` is among the categories listed in `C{i,1}`, and the right child is chosen if `x` is among those listed in `C{i,2}`. Both columns of `C` are empty for branch nodes based on continuous predictors and for leaf nodes.

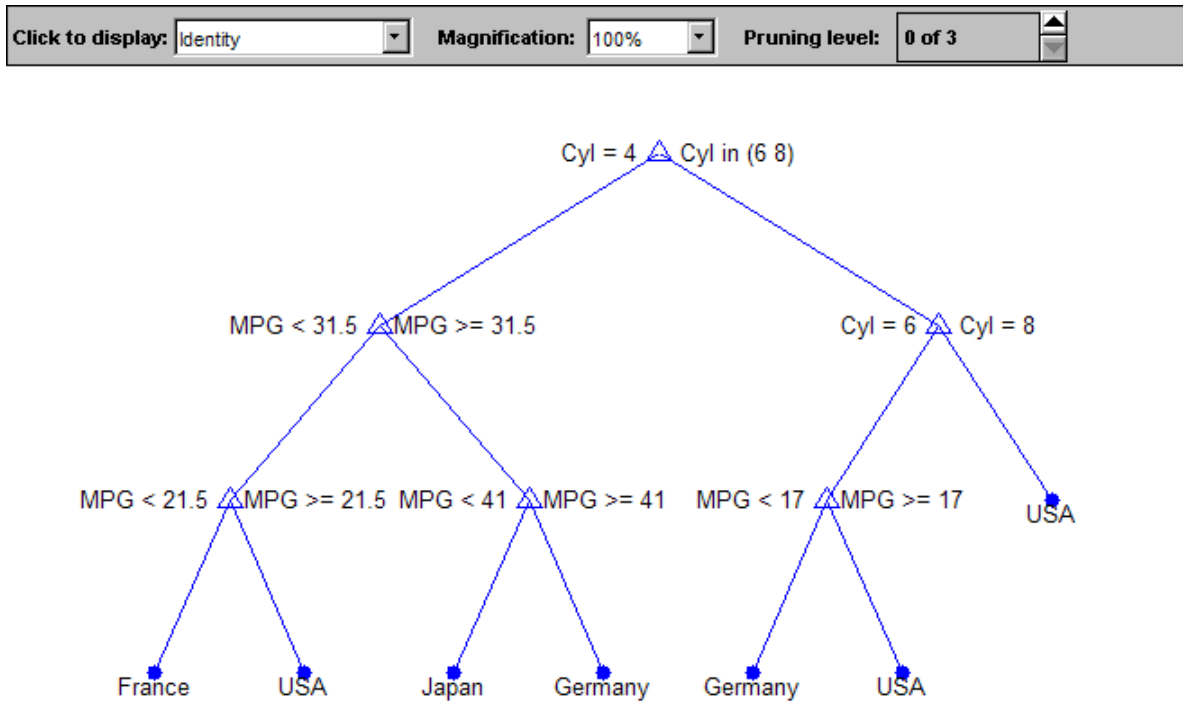
`C = cutcategories(t,nodes)` takes a vector `nodes` of node numbers and returns the categories for the specified nodes.

Examples

Create a classification tree for car data:

```
load carsmall

t = classregtree([MPG Cylinders],Origin,...
                 'names',{'MPG' 'Cyl'},'cat',2)
t =
Decision tree for classification
 1  if Cyl=4 then node 2 elseif Cyl in {6 8} then node 3 else USA
 2  if MPG<31.5 then node 4 elseif MPG>=31.5 then node 5 else USA
 3  if Cyl=6 then node 6 elseif Cyl=8 then node 7 else USA
 4  if MPG<21.5 then node 8 elseif MPG>=21.5 then node 9 else USA
 5  if MPG<41 then node 10 elseif MPG>=41 then node 11 else Japan
 6  if MPG<17 then node 12 elseif MPG>=17 then node 13 else USA
 7  class = USA
 8  class = France
 9  class = USA
10  class = Japan
11  class = Germany
12  class = Germany
13  class = USA
```

```
view(t)
```




```
C = cutcategories(t)
C =
    [4]    [1x2 double]
     []               []
    [6]    [         8]
     []               []
     []               []
     []               []
     []               []
     []               []
```

```
     []              []
     []              []
     []              []
     []              []
     []              []
C{1,2}
ans =
     6     8
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `cutpoint` | `cuttype` | `cutvar`

Purpose

Decision tree cut point values

Syntax

```
v = cutpoint(t)
v = cutpoint(t,nodes)
```

Description

`v = cutpoint(t)` returns an n-element vector `v` of the values used as cut points in the decision tree `t`, where n is the number of nodes. For each branch node `i` based on a continuous predictor variable `x`, the left child is chosen if `x < v(i)` and the right child is chosen if `x >= v(i)`. `v` is `NaN` for branch nodes based on categorical predictors and for leaf nodes.

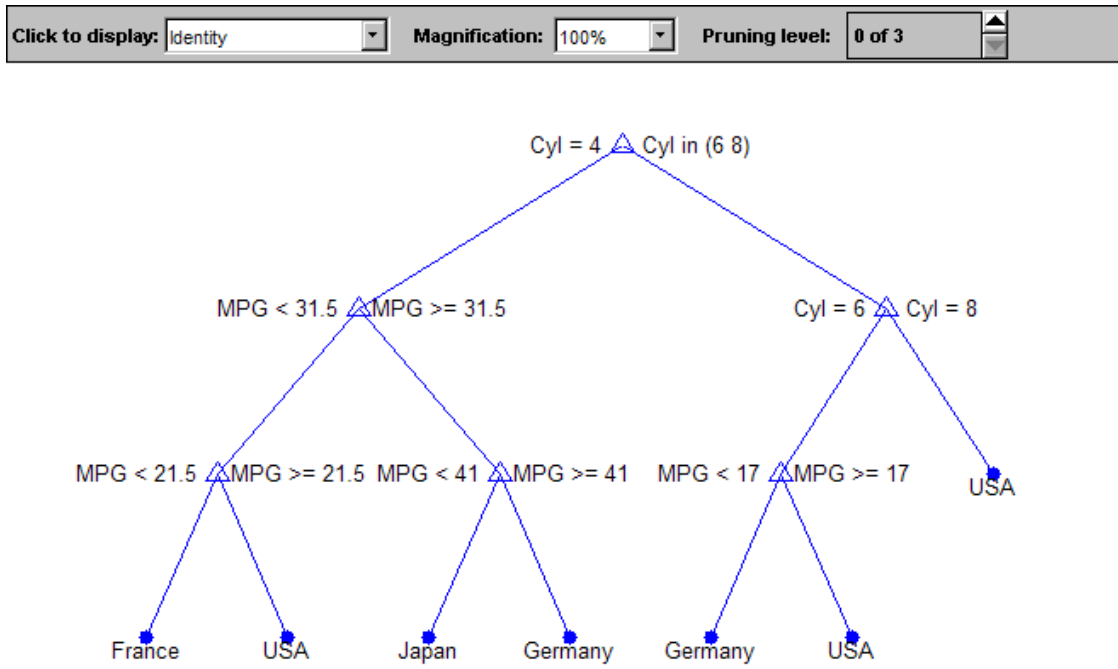
`v = cutpoint(t,nodes)` takes a vector `nodes` of node numbers and returns the cut points for the specified nodes.

Examples

Create a classification tree for car data:

```
load carsmall

t = classregtree([MPG Cylinders],Origin,...
                 'names',{'MPG' 'Cyl'},'cat',2)
t =
Decision tree for classification
 1  if Cyl=4 then node 2 elseif Cyl in {6 8} then node 3 else USA
 2  if MPG<31.5 then node 4 elseif MPG>=31.5 then node 5 else USA
 3  if Cyl=6 then node 6 elseif Cyl=8 then node 7 else USA
 4  if MPG<21.5 then node 8 elseif MPG>=21.5 then node 9 else USA
 5  if MPG<41 then node 10 elseif MPG>=41 then node 11 else Japan
 6  if MPG<17 then node 12 elseif MPG>=17 then node 13 else USA
 7  class = USA
 8  class = France
 9  class = USA
10  class = Japan
11  class = Germany
12  class = Germany
13  class = USA
```

```
view(t)
```




```
v = cutpoint(t)
v =
       NaN
   31.5000
       NaN
   21.5000
   41.0000
   17.0000
       NaN
       NaN
       NaN
       NaN
```

```
    NaN
    NaN
    NaN
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `cutcategories` | `cuttype` | `cutvar`

classregtree.cuttype

Purpose

Cut types

Syntax

```
c = cuttype(t)
c = cuttype(t,nodes)
```

Description

`c = cuttype(t)` returns an n-element cell array `c` indicating the type of cut at each node in the tree `t`, where n is the number of nodes. For each node `i`, `c{i}` is:

- `'continuous'` — If the cut is defined in the form `x < v` for a variable `x` and cut point `v`.
- `'categorical'` — If the cut is defined by whether a variable `x` takes a value in a set of categories.
- `''` — If `i` is a leaf node.

`cutvar` returns the cut points for `'continuous'` cuts, and `cutcategories` returns the set of categories.

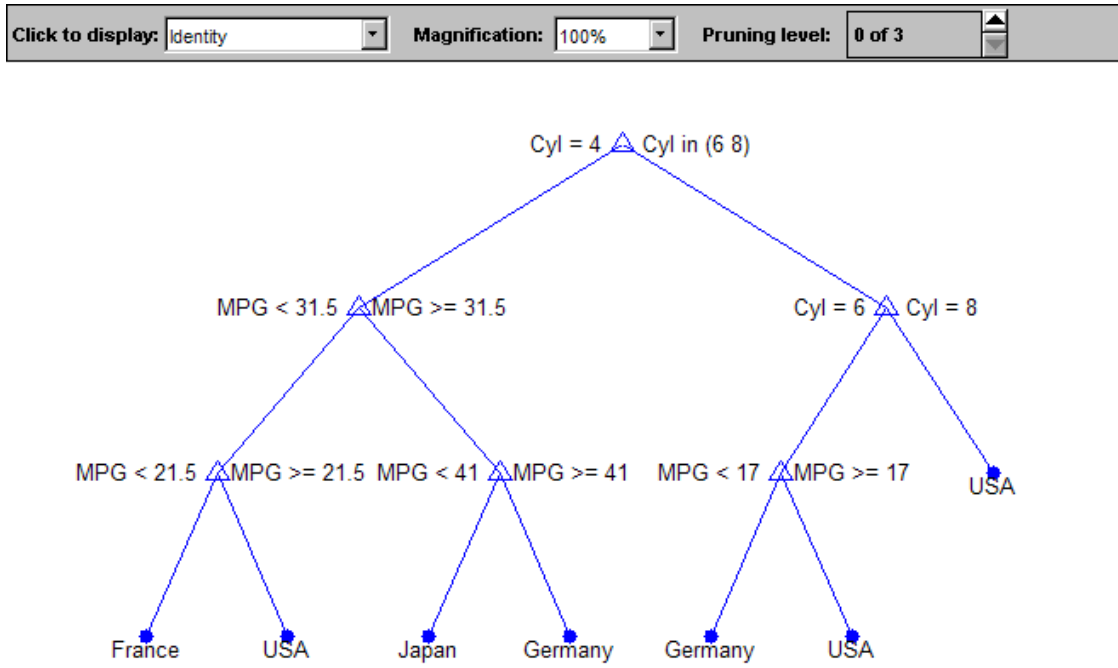
`c = cuttype(t,nodes)` takes a vector `nodes` of node numbers and returns the cut types for the specified nodes.

Examples

Create a classification tree for car data:

```
load carsmall

t = classregtree([MPG Cylinders],Origin,...
                 'names',{'MPG' 'Cyl'},'cat',2)
t =
Decision tree for classification
 1  if Cyl=4 then node 2 elseif Cyl in {6 8} then node 3 else USA
 2  if MPG<31.5 then node 4 elseif MPG>=31.5 then node 5 else USA
 3  if Cyl=6 then node 6 elseif Cyl=8 then node 7 else USA
 4  if MPG<21.5 then node 8 elseif MPG>=21.5 then node 9 else USA
 5  if MPG<41 then node 10 elseif MPG>=41 then node 11 else Japan
 6  if MPG<17 then node 12 elseif MPG>=17 then node 13 else USA
 7  class = USA
```

```
 8  class = France
 9  class = USA
10  class = Japan
11  class = Germany
12  class = Germany
13  class = USA
view(t)
```




```
c = cuttype(t)
c =
    'categorical'
    'continuous'
    'categorical'
    'continuous'
```

```
'continuous'
'continuous'
''
''
''
''
''
''
''
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes` | `cutvar` | `cutcategories`

Purpose

Cut variable names

Syntax

```
v = cutvar(t)
v = cutvar(t,nodes)
[v,num] = cutvar(...)
```

Description

`v = cutvar(t)` returns an *n*-element cell array `v` of the names of the variables used for branching in each node of the tree `t`, where *n* is the number of nodes. These variables are sometimes known as *cut variables*. For leaf nodes, `v` contains an empty string.

`v = cutvar(t,nodes)` takes a vector `nodes` of node numbers and returns the cut variables for the specified nodes.

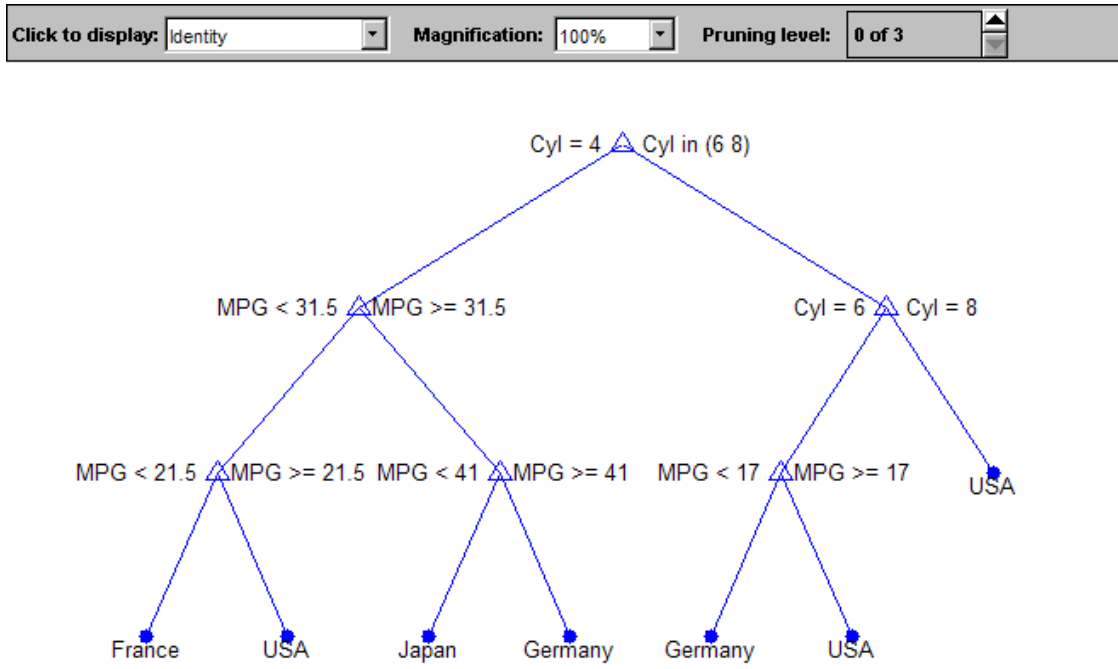
`[v,num] = cutvar(...)` also returns a vector `num` containing the number of each variable.

Examples

Create a classification tree for car data:

```
load carsmall

t = classregtree([MPG Cylinders],Origin,...
                 'names',{'MPG' 'Cyl'},'cat',2)
t =
Decision tree for classification
 1  if Cyl=4 then node 2 elseif Cyl in {6 8} then node 3 else USA
 2  if MPG<31.5 then node 4 elseif MPG>=31.5 then node 5 else USA
 3  if Cyl=6 then node 6 elseif Cyl=8 then node 7 else USA
 4  if MPG<21.5 then node 8 elseif MPG>=21.5 then node 9 else USA
 5  if MPG<41 then node 10 elseif MPG>=41 then node 11 else Japan
 6  if MPG<17 then node 12 elseif MPG>=17 then node 13 else USA
 7  class = USA
 8  class = France
 9  class = USA
10  class = Japan
11  class = Germany
12  class = Germany
13  class = USA
```

```
view(t)
```




```
[v,num] = cutvar(t)
v =
    'Cyl'
    'MPG'
    'Cyl'
    'MPG'
    'MPG'
    'MPG'
    ''
    ''
    ''
```

```
    ''
    ''
    ''
    ''
num =
     2
     1
     2
     1
     1
     1
     0
     0
     0
     0
     0
     0
     0
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes` | `children`

ClassificationTree.cvLoss

Purpose

Classification error by cross validation

Syntax

```
E = cvLoss(tree)
[E,SE] = cvLoss(tree)
[E,SE,Nleaf] = cvLoss(tree)
[E,SE,Nleaf,BestLevel] = cvLoss(tree)
[E,...] = cvLoss(tree,Name,Value)
```

Description

`E = cvLoss(tree)` returns the cross-validated classification error (loss) for `tree`, a classification tree.

`[E,SE] = cvLoss(tree)` returns the standard error of `E`.

`[E,SE,Nleaf] = cvLoss(tree)` returns the number of leaves of `tree`.

`[E,SE,Nleaf,BestLevel] = cvLoss(tree)` returns the optimal pruning level for `tree`.

`[E,...] = cvLoss(tree,Name,Value)` cross validates with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`tree`

A classification tree produced by `ClassificationTree.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`subtrees`

Vector of pruning levels, with `0` representing the full, unpruned tree. `tree` must include a pruning sequence as created either by `ClassificationTree.fit` with `'prune'` set to `'on'`, or by the `prune` method. The returned `E`, `SE`, and `Nleaf` are vectors of

the same length as `subtrees`; `BestLevel` is a scalar. If you set `subtrees` to `'all'`, `cvLoss` uses the entire pruning sequence.

Default: `0`

`treesize`

One of the following strings:

- `'se'` — `cvLoss` uses the smallest tree whose cost is within one standard error of the minimum cost.
- `'min'` — `cvLoss` uses the minimal cost tree.

Default: `'se'`

`kfold`

Number of cross-validation samples, a positive integer.

Default: `10`

Output Arguments

`E`

The cross-validation classification error (loss). A vector or scalar depending on the setting of the `subtrees` name-value pair.

`SE`

The standard error of `E`. A vector or scalar depending on the setting of the `subtrees` name-value pair.

`Nleaf`

Number of leaf nodes in `tree`. Leaf nodes are terminal nodes, which give classifications, not splits. A vector or scalar depending on the setting of the `subtrees` name-value pair.

`BestLevel`

By default, a scalar representing the largest pruning level that achieves a value of `E` within `SE` of the minimum error. If you set `treesize` to `'min'`, `BestLevel` is the smallest value in `subtrees`.

Examples

Compute the cross-validation error for the default classification tree for the `ionosphere` data:

```
load ionosphere
tree = ClassificationTree.fit(X,Y);
[E,SE,Nleaf,BestLevel] = cvLoss(tree)

E =
    0.1282

SE =
    0.0178

Nleaf =
    19

BestLevel =
     0
```

Find the best level by using the `subtrees` name-value pair:

```
[~,~,~,BestLevel] = cvLoss(tree,'subtrees','all')

BestLevel =
    6
```

Alternatives

You can construct a cross-validated tree model with `crossval`, and call `kfoldLoss` instead of `cvLoss`. The alternative can save time if you are going to examine the cross-validated tree more than once.

However, unlike `cvLoss`, `kfoldLoss` does not return `SE`,`Nleaf`, or `BestLevel`. `kfoldLoss` also does not allow you to examine any error other than classification error.

See Also

`ClassificationTree.fit` | `crossval` | `loss` | `kfoldLoss`

How To

- Chapter 13, "Nonparametric Supervised Learning"

RegressionTree.cvLoss

Purpose

Regression error by cross validation

Syntax

```
E = cvLoss(tree)
[E,SE] = cvLoss(tree)
[E,SE,Nleaf] = cvLoss(tree)
[E,SE,Nleaf,BestLevel] = cvLoss(tree)
[E,...] = cvLoss(tree,Name,Value)
```

Description

`E = cvLoss(tree)` returns the cross-validated regression error (loss) for `tree`, a regression tree.

`[E,SE] = cvLoss(tree)` returns the standard error of `E`.

`[E,SE,Nleaf] = cvLoss(tree)` returns the number of leaves (terminal nodes) in `tree`.

`[E,SE,Nleaf,BestLevel] = cvLoss(tree)` returns the optimal pruning level for `tree`.

`[E,...] = cvLoss(tree,Name,Value)` cross validates with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`tree`

A regression tree produced by `RegressionTree.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`subtrees`

Vector of pruning levels, with `0` representing the full, unpruned tree. `tree` must include a pruning sequence as created either by `ClassificationTree.fit` with `'prune'` set to `'on'`, or by

the `prune` method. The returned `E`, `SE`, and `Nleaf` are vectors of the same length as `subtrees`; `BestLevel` is a scalar. If you set `subtrees` to `'all'`, `cvLoss` uses the entire pruning sequence.

Default: `0`

`treesize`

One of the following strings:

- `'se'` — `cvLoss` uses the smallest tree whose cost is within one standard error of the minimum cost.
- `'min'` — `cvLoss` uses the minimal cost tree.

Default: `'se'`

`kfold`

Number of cross-validation samples, a positive integer.

Default: `10`

Output Arguments

`E`

The cross-validation mean squared error (loss). A vector or scalar depending on the setting of the `subtrees` name-value pair.

`SE`

The standard error of `E`. A vector or scalar depending on the setting of the `subtrees` name-value pair.

`Nleaf`

Number of leaf nodes in `tree`. Leaf nodes are terminal nodes, which give responses, not splits. A vector or scalar depending on the setting of the `subtrees` name-value pair.

`BestLevel`

By default, a scalar representing the largest pruning level that achieves a value of `E` within `SE` of the minimum error. If you set `treesize` to `'min'`, `BestLevel` is the smallest value in `subtrees`.

Examples

Compute the cross-validation error for the default classification tree for the `carsmall` data:

```
load carsmall
X = [Displacement Horsepower Weight];
tree = RegressionTree.fit(X,MPG);
[E,SE,Nleaf,BestLevel] = cvLoss(tree)

E =
   30.7558

SE =
    6.0651

Nleaf =
    19

BestLevel =
     0
```

Find the best level by using the `subtrees` name-value pair:

```
[~,~,~,BestLevel] = cvLoss(tree,'subtrees','all')

BestLevel =
    15
```

Alternatives

You can construct a cross-validated tree model with `crossval`, and call `kfoldLoss` instead of `cvLoss`. The alternative can save time if you are going to examine the cross-validated tree more than once.

However, unlike `cvLoss`, `kfoldLoss` does not return `SE`,`Nleaf`, or `BestLevel`.

See Also

`crossval` | `kfoldLoss` | `RegressionTree.fit` | `loss`

How To

- Chapter 13, "Nonparametric Supervised Learning"

cvpartition

Purpose

Data partitions for cross-validation

Description

An object of the `cvpartition` class defines a random partition on a set of data of a specified size. Use this partition to define test and training sets for validating a statistical model using cross-validation.

Construction

cvpartition	Create cross-validation partition for data

Methods

disp	Display `cvpartition` object
display	Display `cvpartition` object
repartition	Repartition data for cross-validation
test	Test indices for cross-validation
training	Training indices for cross-validation

Properties

N	Number of observations (including observations with missing `group` values)
NumTestSets	Number of test sets
TestSize	Size of each test set
TrainSize	Size of each training set
Type	Type of partition

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

Examples

Use a 10-fold stratified cross-validation to compute the misclassification error for `classify` on iris data.

```
load('fisheriris');
CVO = cvpartition(species,'k',10);
err = zeros(CVO.NumTestSets,1);
for i = 1:CVO.NumTestSets
    trIdx = CVO.training(i);
    teIdx = CVO.test(i);
    ytest = classify(meas(teIdx,:),meas(trIdx,:),...
   species(trIdx,:));
    err(i) = sum(~strcmp(ytest,species(teIdx)));
end
cvErr = sum(err)/sum(CVO.TestSize);
```

See Also

`crossval`

How To

- “Grouped Data” on page 2-34

cvpartition

Purpose

Create cross-validation partition for data

Syntax

```
c = cvpartition(n,'kfold',k)
c = cvpartition(group,'kfold',k)
c = cvpartition(n,'holdout',p)
c = cvpartition(group,'holdout',p)
c = cvpartition(n,'leaveout')
c = cvpartition(n,'resubstitution')
```

Description

`c = cvpartition(n,'kfold',k)` constructs an object `c` of the `cvpartition` class defining a random partition for `k`-fold cross-validation on `n` observations. The partition divides the observations into `k` disjoint subsamples (or *folds*), chosen randomly but with roughly equal size. The default value of `k` is `10`.

`c = cvpartition(group,'kfold',k)` creates a random partition for a stratified `k`-fold cross-validation. `group` is a numeric vector, categorical array, string array, or cell array of strings indicating the class of each observation (see "Grouped Data" on page 2-34). Each subsample has roughly equal size and roughly the same class proportions as in `group`. `cvpartition` treats `NaN`s or empty strings in `group` as missing values.

`c = cvpartition(n,'holdout',p)` creates a random partition for holdout validation on `n` observations. This partition divides the observations into a training set and a test (or *holdout*) set. The parameter `p` must be a scalar. When `0 < p < 1`, `cvpartition` randomly selects approximately `p*n` observations for the test set. When `p` is an integer, `cvpartition` randomly selects `p` observations for the test set. The default value of `p` is `1/10`.

`c = cvpartition(group,'holdout',p)` randomly partitions observations into a training set and a test set with stratification, using the class information in `group`; that is, both training and test sets have roughly the same class proportions as in `group`.

`c = cvpartition(n,'leaveout')` creates a random partition for leave-one-out cross-validation on `n` observations. Leave-one-out is a special case of `'kfold'`, in which the number of folds equals the number of observations.

`c = cvpartition(n,'resubstitution')` creates an object `c` that does not partition the data. Both the training set and the test set contain all of the original `n` observations.

Examples

Use stratified 10-fold cross-validation to compute misclassification rate:

```
load fisheriris;
y = species;
c = cvpartition(y,'k',10);

fun = @(xT,yT,xt,yt)(sum(~strcmp(yt,classify(xt,xT,yT))));

rate = sum(crossval(fun,meas,y,'partition',c))...
           /sum(c.TestSize)
rate =
    0.0200
```

See Also

`crossval` | `repartition`

How To

- Grouped Data

RegressionEnsemble.cvshrink

Purpose

Cross validate shrinking (pruning) ensemble

Syntax

```
vals = cvshrink(ens)
[vals,nlearn] = cvshrink(ens)
[vals,nlearn] = cvshrink(ens,Name,Value)
```

Description

`vals = cvshrink(ens)` returns an `L`-by-`T` matrix with cross-validated values of the mean squared error. `L` is the number of `lambda` values in the `ens.Regularization` structure. `T` is the number of `threshold` values on weak learner weights. If `ens` does not have a `Regularization` property filled in by the `regularize` method, pass a `lambda` name-value pair.

`[vals,nlearn] = cvshrink(ens)` returns an `L`-by-`T` matrix of the mean number of learners in the cross-validated ensemble.

`[vals,nlearn] = cvshrink(ens,Name,Value)` cross validates with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A regression ensemble, created with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`cvpartition`

A partition created with `cvpartition` to use in a cross-validated tree. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`kfold`

Number of folds to use in a cross-validated tree, a positive integer. If you do not supply a cross-validation method, `cvshrink` uses 10-fold cross validation. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: `10`

`lambda`

Vector of nonnegative regularization parameter values for lasso. If empty, `cvshrink` does not perform cross validation.

Default: `[]`

`leaveout`

Use leave-one-out cross validation by setting to `'on'`. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`threshold`

Numeric vector with lower cutoffs on weights for weak learners. `cvshrink` discards learners with weights below `threshold` in its cross-validation calculation.

Default: `0`

Output Arguments

`vals`

`L`-by-`T` matrix with cross-validated values of the mean squared error. `L` is the number of values of the regularization parameter

'lambda', and T is the number of 'threshold' values on weak learner weights.

nlearn

L-by-T matrix with cross-validated values of the mean number of learners in the cross-validated ensemble.L is the number of values of the regularization parameter 'lambda', and T is the number of 'threshold' values on weak learner weights.

Examples

Create a regression ensemble for predicting mileage from the carsmall data. Cross validate the ensemble for three values each of lambda and threshold.

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'bag',100,'Tree',...
    'type','regression');
[vals nlearn] = cvshrink(ens,'lambda',[.01 .1 1],...
    'threshold',[0 .01 .1])

vals =
   20.0949   19.9007  131.6316
   20.0924   19.8431  128.0989
   19.9759   19.7987  119.5574

nlearn =
   13.3000   11.6000    3.5000
   13.2000   11.5000    3.6000
   13.4000   11.4000    3.9000
```

Clearly, setting a threshold of 0.1 leads to unacceptable errors, while a threshold of 0.01 gives similar errors to a threshold of 0. The mean number of learners with a threshold of 0.1 is about 11.5, whereas the mean number is about 13.2 when the threshold is 0.

See Also

regularize | shrink

How To

- Chapter 13, “Nonparametric Supervised Learning”

datasample

Purpose

Randomly sample from data, with or without replacement

Syntax

```
y = datasample(data,k)
y = datasample(data,k,dim)
[y,idx] = datasample(data,k,...)
[y,...] = datasample(s,data,k,...)
[y,...] = datasample(data,k,Name,Value)
[y,...] = datasample(data,k,dim,Name,Value)
```

Description

`y = datasample(data,k)` returns `k` observations sampled uniformly at random, with replacement, from the data in `data`.

`y = datasample(data,k,dim)` returns a sample taken along dimension `dim` of `data`.

`[y,idx] = datasample(data,k,...)` returns an index vector indicating which values `datasample` sampled from `data`.

`[y,...] = datasample(s,data,k,...)` uses the random number stream `s` to generate random numbers.

`[y,...] = datasample(data,k,Name,Value)` or `[y,...] = datasample(data,k,dim,Name,Value)` samples with additional options specified by one or more `Name,Value` pair arguments.

Tips

- To sample random integers with replacement from a range, use `randi`.
- To sample random integers without replacement, use `randperm` or `datasample`.
- To randomly sample from data, with or without replacement, use `datasample`.

Input Arguments

`data`

Vector, matrix, *N*-dimensional array, or dataset array representing the data from which to sample. By default, `datasample` regards the rows of a `data` matrix, or the first

nonsingleton dimension of a `data` array, as data elements. Change this behavior with the `dim` argument.

`k`

Positive integer, the number of samples.

`dim`

Integer specifying the dimension on which to take samples. For example, if `data` is a matrix and `dim` is `2`, `y` contains a selection of columns in `data`. If `data` is a dataset array and `dim` is `2`, `y` contains a selection of variables in `data`. Use `dim` to ensure sampling along a specific dimension regardless of whether `data` is a vector, matrix or *N*-dimensional array.

Default: `1`

`s`

Random number stream. Create `s` using `rng` or `RandStream`.

Default: The global random number stream

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`Replace`

Select the sample with replacement if `Replace` is `true`, or without replacement if `Replace` is `false`. If `Replace` is `false`, `k` must not be larger than the number of data elements in `data`.

Default: `true`

`Weights`

Vector with the same number of elements as data elements in `data`, and with nonnegative elements. Sample with probability proportional to the elements of `Weights`.

Default: `ones(datasize,1)`, where `datasize` is the number of data elements in `data`

Output Arguments

`y`

- If `data` is a vector, `y` is a vector containing `k` elements selected from `data`.
- If `data` is a matrix, `y` is a matrix containing `k` rows selected from `data`. Or, if `dim = 2`, `y` is a matrix containing `k` columns selected from `data`
- If `data` is an *N*-dimensional array, `datasample` samples along its first non-singleton dimension. Or, if you give a `dim` name-value pair, `datasample` samples along the dimension `dim`.

When the sample is taken with replacement (default), `y` can contain repeated observations from `data`. Set the `Replace` name-value pair to `false` to sample without replacement.

`idx`

Vector of indices indicating which elements `datasample` chose from `data` to create `y`. For example:

- If `data` is a vector, `y = data(idx)`.
- If `data` is a matrix, `y = data(idx,:)`.

Examples

Draw five unique values from the integers `1:10`.

```
y = datasample(1:10,5,'Replace',false)

y =
     6     3     7     8     5
```

Generate a random sequence of the characters ACGT, with replacement, according to specified probabilities.

```
seq = datasample('ACGT',48,'Weights',[0.15 0.35 0.35 0.15])

seq =
CTTCGACTGTGAGTGGGCGCGACAAGGCTACCGGCCCGGGCGGCACTC
```

Select a random subset of columns from a data matrix.

```
X = randn(10,1000);
Y = datasample(X,5,2,'Replace',false)

Y =
    0.7007    0.3382    2.1298   -0.1891    0.5026
    0.6520   -0.6693   -0.1961   -0.9915    1.9107
    0.1785    0.6640    2.3247   -1.1735   -1.0020
    1.6760    2.6102   -0.8902   -0.7735    1.8676
   -0.3251   -0.6415   -0.2572   -0.1629   -1.0523
    0.1011    0.9323   -1.3088   -0.4477    0.8036
   -0.5767   -0.5778   -0.8556    0.8672   -0.0727
   -0.0615   -0.9084    0.9020   -0.4185   -1.9520
    0.7256   -1.1228    0.7558    1.2691    2.4997
   -1.2273    0.5754   -0.8755   -0.8224   -1.2066
```

Resample observations from a dataset array to create a bootstrap replicate dataset.

```
load hospital
y = datasample(hospital,size(hospital,1));
```

Use the second output to sample “in parallel" from two data vectors.

```
x1 = randn(100,1);
x2 = randn(100,1);
[y1,idx] = datasample(x1,10);
y2 = x2(idx);
```

Algorithms

`datasample` uses `randperm`, `rand`, or `randi` to generate random values. Therefore, `datasample` changes the state of the MATLAB global random number generator. Control the random number generator using `rng`.

For selecting weighted samples without replacement, `datasample` uses the algorithm of Wong and Easton [1].

References

[1] Wong, C. K. and M. C. Easton. *An Efficient Method for Weighted Sampling Without Replacement.* SIAM Journal of Computing 9(1), pp. 111–113, 1980.

Alternatives

You can use `randi` or `randperm` to generate indices for random sampling with or without replacement, respectively. However, `datasample` can be more convenient because it samples directly from your data. `datasample` also allows weighted sampling.

See Also

`rand` | `randi` | `randperm` | `RandStream` | `rng`

Purpose

Arrays for statistical data

Description

Dataset arrays are used to collect heterogeneous data and metadata including variable and observation names into a single container variable. Dataset arrays are suitable for storing column-oriented or tabular data that are often stored as columns in a text file or in a spreadsheet, and can accommodate variables of different types, sizes, units, etc.

Dataset arrays can contain different kinds of variables, including numeric, logical, character, categorical, and cell. However, a dataset array is a different class than the variables that it contains. For example, even a dataset array that contains only variables that are double arrays cannot be operated on as if it were itself a double array. However, using dot subscripting, you can operate on variable in a dataset array as if it were a workspace variable.

You can subscript dataset arrays using parentheses much like ordinary numeric arrays, but in addition to numeric and logical indices, you can use variable and observation names as indices.

Construction

Use the `dataset` constructor to create a dataset array from variables in the MATLAB workspace. You can also create a dataset array by reading data from a text or spreadsheet file. You can access each variable in a dataset array much like fields in a structure, using dot subscripting. See the following section for a list of operations available for dataset arrays.

dataset	Construct dataset array

Methods

cat	Concatenate dataset arrays
cellstr	Create cell array of strings from dataset array
datasetfun	Apply function to dataset array variables

disp	Display dataset array
display	Display dataset array
double	Convert dataset variables to double array
end	Last index in indexing expression for dataset array
export	Write dataset array to file
get	Access dataset array properties
grpstats	Summary statistics by group for dataset arrays
horzcat	Horizontal concatenation for dataset arrays
isempty	True for empty dataset array
join	Merge observations
length	Length of dataset array
ndims	Number of dimensions of dataset array
numel	Number of elements in dataset array
replacedata	Replace dataset variables
set	Set and display properties
single	Convert dataset variables to single array
size	Size of dataset array
sortrows	Sort rows of dataset array
stack	Stack data from multiple variables into single variable

subsasgn	Subscripted assignment to dataset array
subsref	Subscripted reference for dataset array
summary	Print summary of dataset array
unique	Unique observations in dataset array
unstack	Unstack data from single variable into multiple variables
vertcat	Vertical concatenation for dataset arrays

Properties

A dataset array `D` has properties that store metadata (information about your data). Access or assign to a property using `P = D.Properties.PropName` or `D.Properties.PropName = P`, where `PropName` is one of the following:

Description	String describing data set
DimNames	Two-element cell array of strings giving names of dimensions of data set
ObsNames	Cell array of nonempty, distinct strings giving names of observations in data set
Units	Units of variables in data set
UserData	Variable containing additional information associated with data set

VarDescription	Cell array of strings giving descriptions of variables in data set
VarNames	Cell array giving names of variables in data set

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

Examples

Load a dataset array from a .mat file and create some simple subsets:

```
load hospital
h1 = hospital(1:10,:)
h2 = hospital(:,{'LastName' 'Age' 'Sex' 'Smoker'})

% Access and modify metadata
hospital.Properties.Description
hospital.Properties.VarNames{4} = 'Wgt'

% Create a new dataset variable from an existing one
hospital.AtRisk = hospital.Smoker | (hospital.Age > 40)

% Use individual variables to explore the data
boxplot(hospital.Age,hospital.Sex)
h3 = hospital(hospital.Age<30,...
   {'LastName' 'Age' 'Sex' 'Smoker'})

% Sort the observations based on two variables
h4 = sortrows(hospital,{'Sex','Age'})
```

See Also

`genvarname` | `tdfread` | `textscan` | `xlsread`

How To

- “Dataset Arrays” on page 2-23

Purpose

Construct dataset array

Syntax

```
A = dataset(varspec,'ParamName',Value)
A = dataset('File',filename,'ParamName',Value)
A = dataset('XLSFile',filename,'ParamName',Value)
A = dataset('XPTFile',xptfilename,'ParamName',Value)
```

Description

`A = dataset(varspec,'ParamName',Value)` creates dataset array `A` using one or more of the following workspace variable input methods and one or more optional name/value pairs (see Parameter Name/Value Pairs):

- *VAR* — a workspace variable. `dataset` uses the workspace name for the variable name in `A`. Variables can be arrays of any size, but all variables must have the same number of rows. `VAR` may also be an expression. In this case, `dataset` creates a default name automatically.
- {*VAR*,*name*} — a workspace variable, *VAR* and a variable name. `dataset` uses *name* as the variable name.
- {*VAR*,*name_1*,...,*name_m*} — an m-columned workspace variable, *VAR* . `dataset` uses the names *name_1*, ..., *name_m* as variable names. You must include a name for every column in `VAR`. Each column becomes a separate variable in `A`.

You can combine these input methods to include as many variables and names as needed. Names must be valid, unique MATLAB identifier strings. For example input combinations, see Examples. For optional name/value pairs see Inputs.

Note Dataset arrays may contain built-in types or array objects as variables. Array objects must implement each of the following:

- Standard MATLAB parenthesis indexing of the form `var(i,...)`, where `i` is a numeric or logical vector corresponding to rows of the variable
- A `size` method with a `dim` argument
- A `vertcat` method

`A = dataset('File',filename,'ParamName',Value)` creates dataset array `A` from column-oriented data in the text file specified by the string `filename`. Variables in `A` are of type `double` if data in the corresponding column of the file, following the column header, are entirely numeric; otherwise the variables in `A` are cell arrays of strings. `dataset` converts empty fields to either `NaN` (for a numeric variable) or the empty string (for a string-valued variable). `dataset` ignores insignificant white space in the file. You cannot specify both a file and workspace variables as input. See Name/Value Pairs for more information.

`A = dataset('XLSFile',filename,'ParamName',Value)` creates dataset array `A` from column-oriented data in the Excel® spreadsheet specified by the string `filename`. Variables in `A` are of type `double` if data in the corresponding column of the spreadsheet, following the column header, are entirely numeric; otherwise the variables in `A` are cell arrays of strings. See Name/Value Pairs for more information.

`A = dataset('XPTFile',xptfilename,'ParamName',Value)` creates a dataset array from a SAS® XPORT format file. Variable names from the XPORT format file are preserved. Numeric data types in the XPORT format file are preserved but all other data types are converted to cell arrays of strings. The XPORT format allows for 28 missing data types. `dataset` represents these in the file by an upper case letter, `'.'` or `'_'`. `dataset` converts all missing data to `NaN` values in `A`. However, if you

need the specific missing types you can use the `xptread` function to recover the information. See Name/Value Pairs for more information.

Parameter Name/Value Pairs

Specify one or more of the following name/value pairs when constructing a dataset:

`VarNames`

A cell array `{name_1,...,name_m}` naming the `m` variables in `A` with the specified variable names. Names must be valid, unique MATLAB identifier strings. The number of names must equal the number of variables in `A`. You cannot use the `VarNames` parameter if you provide names for individual variables using `{VAR,name}` pairs. To specify `VarNames` when using a file as input, set `ReadVarNames` to `false`.

`ObsNames`

A cell array `{name_1,...,name_n}` naming the `n` observations in `A` with the specified observation names. The names need not be valid MATLAB identifier strings, but must be unique. The number of names must equal the number of observations (rows) in `A`. To specify `ObsNames` when using a file as input, set `ReadObsNames` to `false`.

Name/value pairs available when using text files as inputs:

`Delimiter`

A string indicating the character separating columns in the file. Values are

- `'\t'` (tab, the default when no `format` is specified)
- `' '` (space, the default when a `format` is specified)
- `','` (comma)
- `';'` (semicolon)
- `'|'` (bar)

`Format`

A format string, as accepted by `textscan`. `dataset` reads the file using `textscan`, and creates variables in `A` according to the conversion specifiers in the format string. You may also provide any name/value pairs accepted by `textscan`. Using the `Format` parameter is much faster for large files. If `ReadObsNames` is `true`, the `format` string should include a format specifier for the first column of the file.

`HeaderLines`

Numeric value indicating the number of lines to skip at the beginning of a file.

Default: `0`

`TreatAsEmpty`

Specifies strings to treat as the empty string in a numeric column. Values may be a character string or a cell array of strings. The parameter applies only to numeric columns in the file; `dataset` does not accept numeric literals such as `'-99'`.

Name/value pairs available when using text files or Excel spreadsheets as inputs:

`ReadVarNames`

A logical value indicating whether (`true`) or not (`false`) to read variable names from the first row of the file. The default is `true`. If `ReadVarNames` is `true`, variable names in the column headers of the file or range (if using an Excel spreadsheet) cannot be empty.

`ReadObsNames`

A logical value indicating whether (`true`) or not (`false`) to read observation names from the first column of the file or range (if using an Excel spreadsheet). The default is `false`. If `ReadObsNames` and `ReadVarNames` are both `true`, `dataset` saves

the header of the first column in the file or range as the name of the first dimension in `A.Properties.DimNames`.

When reading from an `XPT` format file, the `ReadObsNames` parameter name/value pair determines whether or not to try to use the first variable in the file as observation names. Specify as a logical value (default `false`). If the contents of the first variable are not valid observation names then `dataset` reads the variable into a variable of the dataset array and does not set the observation names.

Name/value pairs available when using Excel spreadsheets as input:

`Sheet`

A positive scalar value of type `double` indicating the sheet number, or a quoted string indicating the sheet name.

`Range`

A string of the form `'C1:C2'` where `C1` and `C2` are the names of cells at opposing corners of a rectangular region to be read, as for `xlsread`. By default, the rectangular region extends to the right-most column containing data. If the spreadsheet contains empty columns between columns of data, or if the spreadsheet contains figures or other non-tabular information, specify a range that contains only data.

Examples

Create a dataset array from workspace variables, including observation names:

```
load cereal
cereal = dataset(Calories,Protein,Fat,Sodium,Fiber,Carbo,...
   Sugars,'ObsNames',Name)
cereal.Properties.VarDescription = Variables(4:10,2);
```

Create a dataset array from a single, multi-columned workspace variable, designating variable names for each column:

```
load cities
categories = cellstr(categories);
cities = dataset({ratings,categories{:}},...
   'ObsNames',cellstr(names))
```

Load data from a text or spreadsheet file

```
patients = dataset('File','hospital.dat',...
   'Delimiter',',','ReadObsNames',true)
patients2 = dataset('XLSFile','hospital.xls',...
   'ReadObsNames',true)
```

---

1. Load patient data from the CSV file `hospital.dat` and store the information in a `dataset` array with observation names given by the first column in the data (patient identification):

   ```
   patients = dataset('file','hospital.dat', ...
                'format','%s%s%s%f%f%f%f%f%f%f%f', ...
                'Delimiter',',','ReadObsNames',true);
   ```

   You can also load the data without specifying a format string. `dataset` will automatically create `dataset` variables that are either `double` arrays or cell arrays of strings, depending on the contents of the file:

   ```
   patients = dataset('file','hospital.dat',...
                      'delimiter',',',...
                      'ReadObsNames',true);
   ```

2. Make the {0,1}-valued variable `smoke` nominal, and change the labels to `'No'` and `'Yes'`:

```
patients.smoke = nominal(patients.smoke,{'No','Yes'});
```

3 Add new levels to `smoke` as placeholders for more detailed histories of smokers:

```
patients.smoke = addlevels(patients.smoke,...
                 {'0-5 Years','5-10 Years','LongTerm'});
```

4 Assuming the nonsmokers have never smoked, relabel the `'No'` level:

```
patients.smoke = setlabels(patients.smoke,'Never','No');
```

5 Drop the undifferentiated `'Yes'` level from `smoke`:

```
patients.smoke = droplevels(patients.smoke,'Yes');

Warning: OLDLEVELS contains categorical levels that
were present in A, caused some array elements to have
undefined levels.
```

Note that smokers now have an undefined level.

6 Set each smoker to one of the new levels, by observation name:

```
patients.smoke('YPL-320') = '5-10 Years';
```

See Also

`tdfread` | `textscan` | `xlsread`

dataset.datasetfun

Purpose

Apply function to dataset array variables

Syntax

```
b = datasetfun(fun,A)
[b,c,...] = datasetfun(fun,A)
[b,...] = datasetfun(fun,A,...,'UniformOutput',false)
[b,...] = datasetfun(fun,A,...,'DatasetOutput',true)
[b,...] = datasetfun(fun,A,...,'DataVars',vars)
[b,...] = datasetfun(fun,A,...,'ObsNames',obsnames)
[b,...] = datasetfun(fun,A,...,'ErrorHandler',efun)
```

Description

`b = datasetfun(fun,A)` applies the function specified by `fun` to each variable of the dataset array `A`, and returns the results in the vector `b`. The *i*th element of `b` is equal to `fun` applied to the *i*th dataset variable of `A`. `fun` is a function handle to a function that takes one input argument and returns a scalar value. `fun` must return values of the same class each time it is called, and `datasetfun` concatenates them into the vector `b`. The outputs from `fun` must be one of the following types: numeric, logical, character, structure, or cell.

To apply functions that return results that are nonscalar or of different sizes and types, use the `'UniformOutput'` or `'DatasetOutput'` parameters described below.

Do not rely on the order in which `datasetfun` computes the elements of `b`, which is unspecified.

If `fun` is bound to more than one built-in function or file, (that is, if it represents a set of overloaded functions), `datasetfun` follows MATLAB dispatching rules in calling the function. (See "Determining Which Function Gets Called".)

`[b,c,...] = datasetfun(fun,A)`, where `fun` is a function handle to a function that returns multiple outputs, returns vectors `b`, `c`, ..., each corresponding to one of the output arguments of `fun`. `datasetfun` calls `fun` each time with as many outputs as there are in the call to `datasetfun`. `fun` may return output arguments having different classes, but the class of each output must be the same each time `fun` is called.

`[b,...] = datasetfun(fun,A,...,'UniformOutput',false)` allows you to specify a function `fun` that returns values of different sizes or types. `datasetfun` returns a cell array (or multiple cell arrays), where the *i*th cell contains the value of `fun` applied to the *i*th dataset variable of `A`. Setting `'UniformOutput'` to `true` is equivalent to the default behavior.

`[b,...] = datasetfun(fun,A,...,'DatasetOutput',true)` specifies that the output(s) of `fun` are returned as variables in a dataset array (or multiple dataset arrays). `fun` must return values with the same number of rows each time it is called, but it may return values of any type. The variables in the output dataset array(s) have the same names as the variables in the input. Setting `'DatasetOutput'` to `false` (the default) specifies that the type of the output(s) from `datasetfun` is determined by `'UniformOutput'`.

`[b,...] = datasetfun(fun,A,...,'DataVars',vars)` allows you to apply `fun` only to the dataset variables in `A` specified by `vars`. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

`[b,...] = datasetfun(fun,A,...,'ObsNames',obsnames)` specifies observation names for the dataset output when `'DatasetOutput'` is `true`.

`[b,...] = datasetfun(fun,A,...,'ErrorHandler',efun)`, where `efun` is a function handle, specifies the MATLAB function to call if the call to `fun` fails. The error-handling function is called with the following input arguments:

- A structure with the fields `identifier`, `message`, and `index`, respectively containing the identifier of the error that occurred, the text of the error message, and the linear index into the input array(s) at which the error occurred
- The set of input arguments at which the call to the function failed

The error-handling function should either re-throw an error, or return the same number of outputs as `fun`. These outputs are then returned as

the outputs of `datasetfun`. If `'UniformOutput'` is true, the outputs of the error handler must also be scalars of the same type as the outputs of `fun`. For example, the following code could be saved in a file as the error-handling function:

```
function [A,B] = errorFunc(S,varargin)

warning(S.identifier,S.message);
A = NaN;
B = NaN;
```

If an error-handling function is not specified, the error from the call to `fun` is rethrown.

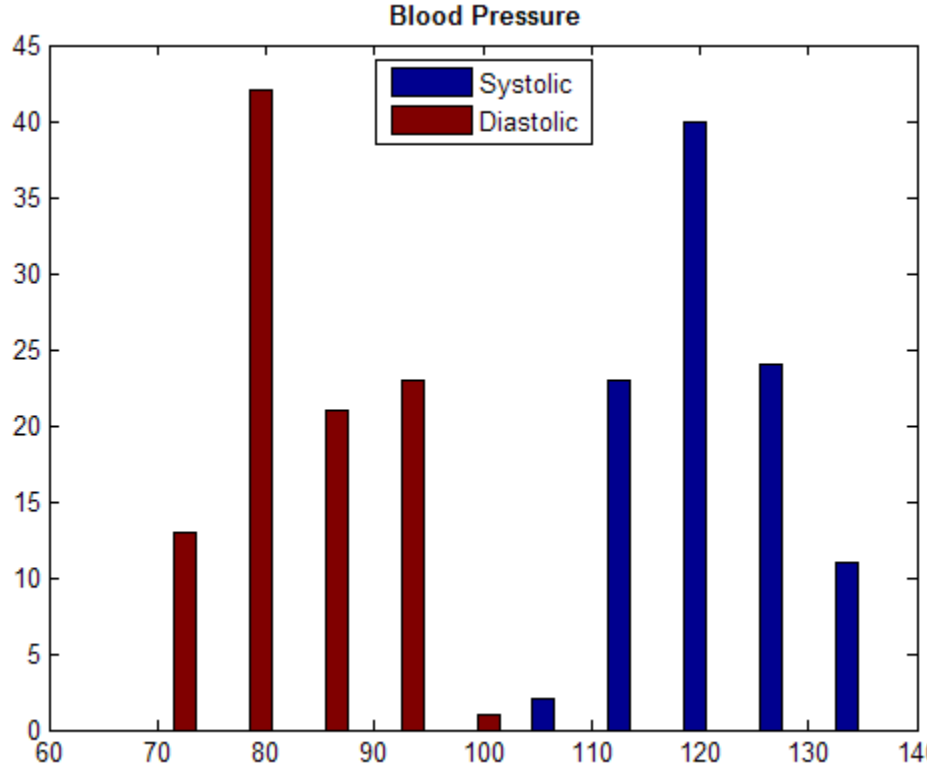
Examples

Compute statistics on selected variables in the `hospital` dataset array:

```
load hospital

stats = ...
     datasetfun(@mean,hospital,...
                'DataVars',{'Weight','BloodPressure'},...
                'UniformOutput',false)
stats =
    [154]    [1x2 double]
stats{2}
ans =
  122.7800   82.9600
```

Display the blood pressure variable:

```
datasetfun(@hist,hospital,...
           'DataVars','BloodPressure',...
           'UniformOutput',false);
title('{\bf Blood Pressure}')
legend('Systolic','Diastolic','Location','N')
```



See Also `grpstats`

daugment

Purpose

D-optimal augmentation

Syntax

```
dCE2 = daugment(dCE,mruns)
[dCE2,X] = daugment(dCE,mruns)
[dCE2,X] = daugment(dCE,mruns,model)
[dCE2,X] = daugment(...,param1,val1,param2,val2,...)
```

Description

`dCE2 = daugment(dCE,mruns)` uses a coordinate-exchange algorithm to *D*-optimally add `mruns` runs to an existing experimental design `dCE` for a linear additive model.

`[dCE2,X] = daugment(dCE,mruns)` also returns the design matrix `X` associated with the augmented design.

`[dCE2,X] = daugment(dCE,mruns,model)` uses the linear regression model specified in *`model`*. *`model`* is one of the following strings:

- `'linear'` — Constant and linear terms. This is the default.
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms
- `'purequadratic'` — Constant, linear, and squared terms

The order of the columns of `X` for a full quadratic model with n terms is:

1. The constant term
2. The linear terms in order 1, 2, ..., n
3. The interaction terms in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n–1, n)
4. The squared terms in order 1, 2, ..., n

Other models use a subset of these terms, in the same order.

Alternatively, *`model`* can be a matrix specifying polynomial terms of arbitrary order. In this case, *`model`* should have one column for each factor and one row for each term in the model. The entries in any row

of *model* are powers for the factors in the columns. For example, if a model has factors X1, X2, and X3, then a row [0 1 2] in *model* specifies the term (X1.^0).*(X2.^1).*(X3.^2). A row of all zeros in *model* specifies a constant term, which can be omitted.

[dCE2,X] = daugment(...,*param1*,*val1*,*param2*,*val2*,...) specifies additional parameter/value pairs for the design. Valid parameters and their values are listed in the following table.

Parameter	Value
'bounds'	Lower and upper bounds for each factor, specified as a 2-by-nfactors matrix, where nfactors is the number of factors. Alternatively, this value can be a cell array containing nfactors elements, each element specifying the vector of allowable values for the corresponding factor.
'categorical'	Indices of categorical predictors.
'display'	Either 'on' or 'off' to control display of the iteration counter. The default is 'on'.
'excludefun'	Handle to a function that excludes undesirable runs. If the function is *f*, it must support the syntax $b = f(S)$, where S is a matrix of treatments with nfactors columns, where nfactors is the number of factors, and b is a vector of Boolean values with the same number of rows as S. $b(i)$ is true if the ith row S should be excluded.
'init'	Initial design as an mruns-by-nfactors matrix, where nfactors is the number of factors. The default is a randomly selected set of points.
'levels'	Vector of number of levels for each factor.
'maxiter'	Maximum number of iterations. The default is 10.

Parameter	Value
'options'	The value is a structure that contains options specifying whether to compute multiple tries in parallel, and specifying how to use random numbers when generating the starting points for the tries. Create the options structure with statset. Applicable statset parameters are: • 'UseParallel' — If 'always' and if a matlabpool of the Parallel Computing Toolbox is open, compute in parallel. If the Parallel Computing Toolbox is not installed, or a matlabpool is not open, computation occurs in serial mode. Default is 'never', meaning serial computation. • UseSubstreams — Set to 'always' to compute in parallel in a reproducible fashion. Default is 'never'. To compute reproducibly, set Streams to a type allowing substreams: 'mlfg6331_64' or 'mrg32k3a'. • Streams — A RandStream object or cell array of such objects. If you do not specify Streams, daugment uses the default stream or streams. If you choose to specify Streams, use a single object except in the case - You have an open MATLAB pool - UseParallel is 'always' - UseSubstreams is 'never' In that case, use a cell array the same size as the MATLAB pool.

Parameter	Value
	For more information on using parallel computing, see Chapter 17, "Parallel Statistics".
'tries'	Number of times to try to generate a design from a new starting point. The algorithm uses random points for each try, except possibly the first. The default is 1.

Note The daugment function augments an existing design using a coordinate-exchange algorithm; the 'start' parameter of the candexch function provides the same functionality using a row-exchange algorithm.

Examples

The following eight-run design is adequate for estimating main effects in a four-factor model:

```
dCEmain = cordexch(4,8)
dCEmain =
     1    -1    -1     1
    -1    -1     1     1
    -1     1    -1     1
     1     1     1    -1
     1     1     1     1
    -1     1    -1    -1
     1    -1    -1    -1
    -1    -1     1    -1
```

To estimate the six interaction terms in the model, augment the design with eight additional runs:

```
dCEinteraction = daugment(dCEmain,8,'interaction')
dCEinteraction =
     1    -1    -1     1
```

```
    -1    -1     1     1
    -1     1    -1     1
     1     1     1    -1
     1     1     1     1
    -1     1    -1    -1
     1    -1    -1    -1
    -1    -1     1    -1
    -1     1     1     1
    -1    -1    -1    -1
     1    -1     1    -1
     1     1    -1     1
    -1     1     1    -1
     1     1    -1    -1
     1    -1     1     1
     1     1     1    -1
```

The augmented design is full factorial, with the original eight runs in the first eight rows.

See Also

`dcovary` | `cordexch` | `candexch`

Purpose

D-optimal design with fixed covariates

Syntax

```
dCV = dcovary(nfactors,fixed)
[dCV,X] = dcovary(nfactors,fixed)
[dCV,X] = dcovary(nfactors,fixed,model)
[dCV,X] = daugment(...,param1,val1,param2,val2,...)
```

Description

`dCV = dcovary(nfactors,fixed)` uses a coordinate-exchange algorithm to generate a *D*-optimal design for a linear additive model with `nfactors` factors, subject to the constraint that the model include the fixed covariate factors in `fixed`. The number of runs in the design is the number of rows in `fixed`. The design `dCV` augments `fixed` with initial columns for treatments of the model terms.

`[dCV,X] = dcovary(nfactors,fixed)` also returns the design matrix `X` associated with the design.

`[dCV,X] = dcovary(nfactors,fixed,model)` uses the linear regression model specified in *`model`*. *`model`* is one of the following strings:

- `'linear'` — Constant and linear terms. This is the default.
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms
- `'purequadratic'` — Constant, linear, and squared terms

The order of the columns of `X` for a full quadratic model with n terms is:

1. The constant term
2. The linear terms in order 1, 2, ..., n
3. The interaction terms in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n–1, n)
4. The squared terms in order 1, 2, ..., n

Other models use a subset of these terms, in the same order.

Alternatively, *model* can be a matrix specifying polynomial terms of arbitrary order. In this case, *model* should have one column for each factor and one row for each term in the model. The entries in any row of *model* are powers for the factors in the columns. For example, if a model has factors X1, X2, and X3, then a row [0 1 2] in *model* specifies the term (X1.^0).*(X2.^1).*(X3.^2). A row of all zeros in *model* specifies a constant term, which can be omitted.

[dCV,X] = daugment(...,*param1*,*val1*,*param2*,*val2*,...) specifies additional parameter/value pairs for the design. Valid parameters and their values are listed in the following table.

Parameter	Value
'bounds'	Lower and upper bounds for each factor, specified as a 2-by-nfactors matrix. Alternatively, this value can be a cell array containing nfactors elements, each element specifying the vector of allowable values for the corresponding factor.
'categorical'	Indices of categorical predictors.
'display'	Either 'on' or 'off' to control display of the iteration counter. The default is 'on'.
'excludefun'	Handle to a function that excludes undesirable runs. If the function is *f*, it must support the syntax $b = f(S)$, where S is a matrix of treatments with nfactors columns and b is a vector of Boolean values with the same number of rows as S. $b(i)$ is true if the ith row S should be excluded.
'init'	Initial design as an mruns-by-nfactors matrix. The default is a randomly selected set of points.
'levels'	Vector of number of levels for each factor.
'maxiter'	Maximum number of iterations. The default is 10.

Parameter	Value
`'options'`	The value is a structure that contains options specifying whether to compute multiple tries in parallel, and specifying how to use random numbers when generating the starting points for the tries. Create the options structure with `statset`. Applicable `statset` parameters are: • `'UseParallel'` — If `'always'` and if a `matlabpool` of the Parallel Computing Toolbox is open, compute in parallel. If the Parallel Computing Toolbox is not installed, or a `matlabpool` is not open, computation occurs in serial mode. Default is `'never'`, meaning serial computation. • `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. Default is `'never'`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. • `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `dcovary` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case - You have an open MATLAB pool - `UseParallel` is `'always'` - `UseSubstreams` is `'never'` In that case, use a cell array the same size as the MATLAB pool.

Parameter	Value
	For more information on using parallel computing, see Chapter 17, “Parallel Statistics”.
`'tries'`	Number of times to try to generate a design from a new starting point. The algorithm uses random points for each try, except possibly the first. The default is `1`.

Examples

Example 1

Suppose you want a design to estimate the parameters in a three-factor linear additive model, with eight runs that necessarily occur at different times. If the process experiences temporal linear drift, you may want to include the run time as a variable in the model. Produce the design as follows:

```
time = linspace(-1,1,8)';
[dCV1,X] = dcovary(3,time,'linear')
dCV1 =
   -1.0000    1.0000    1.0000   -1.0000
    1.0000   -1.0000   -1.0000   -0.7143
   -1.0000   -1.0000   -1.0000   -0.4286
    1.0000   -1.0000    1.0000   -0.1429
    1.0000    1.0000   -1.0000    0.1429
   -1.0000    1.0000   -1.0000    0.4286
    1.0000    1.0000    1.0000    0.7143
   -1.0000   -1.0000    1.0000    1.0000
X =
    1.0000   -1.0000    1.0000    1.0000   -1.0000
    1.0000    1.0000   -1.0000   -1.0000   -0.7143
    1.0000   -1.0000   -1.0000   -1.0000   -0.4286
    1.0000    1.0000   -1.0000    1.0000   -0.1429
    1.0000    1.0000    1.0000   -1.0000    0.1429
    1.0000   -1.0000    1.0000   -1.0000    0.4286
    1.0000    1.0000    1.0000    1.0000    0.7143
```

```
    1.0000   -1.0000   -1.0000    1.0000    1.0000
```

The column vector `time` is a fixed factor, normalized to values between ±1. The number of rows in the fixed factor specifies the number of runs in the design. The resulting design `dCV` gives factor settings for the three controlled model factors at each time.

Example 2

The following example uses the `dummyvar` function to block an eight-run experiment into 4 blocks of size 2 for estimating a linear additive model with two factors:

```
fixed = dummyvar([1 1 2 2 3 3 4 4]);
dCV2 = dcovary(2,fixed(:,1:3),'linear')
dCV2 =
   1   1   1   0   0
  -1  -1   1   0   0
  -1   1   0   1   0
   1  -1   0   1   0
   1   1   0   0   1
  -1  -1   0   0   1
  -1   1   0   0   0
   1  -1   0   0   0
```

The first two columns of `dCV2` contain the settings for the two factors; the last three columns are dummy variable codings for the four blocks.

See Also

`daugment` | `cordexch` | `dummyvar`

TreeBagger.DefaultYfit property

Purpose

Default value returned by `predict` and `oobPredict`

Description

The `DefaultYfit` property controls what predicted value `TreeBagger` returns when no prediction is possible, for example when the `oobPredict` method needs to predict for an observation that is in-bag for all trees in the ensemble.

For classification, you can set this property to either `''` or `'MostPopular'`. If you choose `'MostPopular'` (default), the property value becomes the name of the most probable class in the training data.

For regression, you can set this property to any numeric scalar. The default is the mean of the response for the training data.

If you set this property to `''` for classification or `NaN` for regression, `TreeBagger` excludes the in-bag observations from computation of the out-of-bagerror and margin.

See Also

`oobPredict` | `Predict` | `OOBIndices`

Purpose

Delete handle object

Syntax

```
delete(h)
```

Description

`delete(h)` deletes the handle object `h`, where `h` is a scalar handle. The `delete` method deletes a handle object but does not clear the handle from the workspace. A deleted handle is no longer valid.

See Also

`clear` | `isvalid` | `qrandstream`

TreeBagger.DeltaCritDecisionSplit property

Purpose

Split criterion contributions for each predictor

Description

The `DeltaCritDecisionSplit` property is a numeric array of size 1-by-`Nvars` of changes in the split criterion summed over splits on each variable, averaged across the entire ensemble of grown trees.

See Also

`classregtree.varimportance`

Purpose

Dendrogram plot

Syntax

```
H = dendrogram(Z)
H = dendrogram(Z,p)
[H,T] = dendrogram(...)
[H,T,perm] = dendrogram(...)
[...] = dendrogram(...,'colorthreshold',t)
[...] = dendrogram(...,'orientation','orient')
[...] = dendrogram(...,'labels',S)
```

Description

`H = dendrogram(Z)` generates a dendrogram plot of the hierarchical, binary cluster tree represented by `Z`. `Z` is an (`m`-1)-by-3 matrix, generated by the `linkage` function, where `m` is the number of objects in the original data set. The output, `H`, is a vector of handles to the lines in the dendrogram.

A dendrogram consists of many U-shaped lines connecting objects in a hierarchical tree. The height of each U represents the distance between the two objects being connected. If there were 30 or fewer data points in the original dataset, each leaf in the dendrogram corresponds to one data point. If there were more than 30 data points, the complete tree can look crowded, and `dendrogram` collapses lower branches as necessary, so that some leaves in the plot correspond to more than one data point.

`H = dendrogram(Z,p)` generates a dendrogram with no more than `p` leaf nodes, by collapsing lower branches of the tree. To display the complete tree, set `p = 0`.

`[H,T] = dendrogram(...)` generates a dendrogram and returns `T`, a vector of length `m` that contains the leaf node number for each object in the original data set. `T` is useful when `p` is less than the total number of objects, so some leaf nodes in the display correspond to multiple objects. For example, to find out which objects are contained in leaf node `k` of the dendrogram, use `find(T==k)`. When there are fewer than `p` objects in the original data, all objects are displayed in the dendrogram. In this case, `T` is the identity map, i.e., `T = (1:m)'`, where each node contains only a single object.

`[H,T,perm] = dendrogram(...)` generates a dendrogram and returns the permutation vector of the node labels of the leaves of the dendrogram. `perm` is ordered from left to right on a horizontal dendrogram and bottom to top for a vertical dendrogram.

`[...] = dendrogram(...,'colorthreshold',t)` assigns a unique color to each group of nodes in the dendrogram where the linkage is less than the threshold `t`. `t` is a value in the interval `[0,max(Z(:,3))]`. Setting `t` to the string `'default'` is the same as t = .7(`max(Z(:,3))`). `0` is the same as not specifying `'colorthreshold'`. The value `max(Z(:,3))` treats the entire tree as one group and colors it all one color.

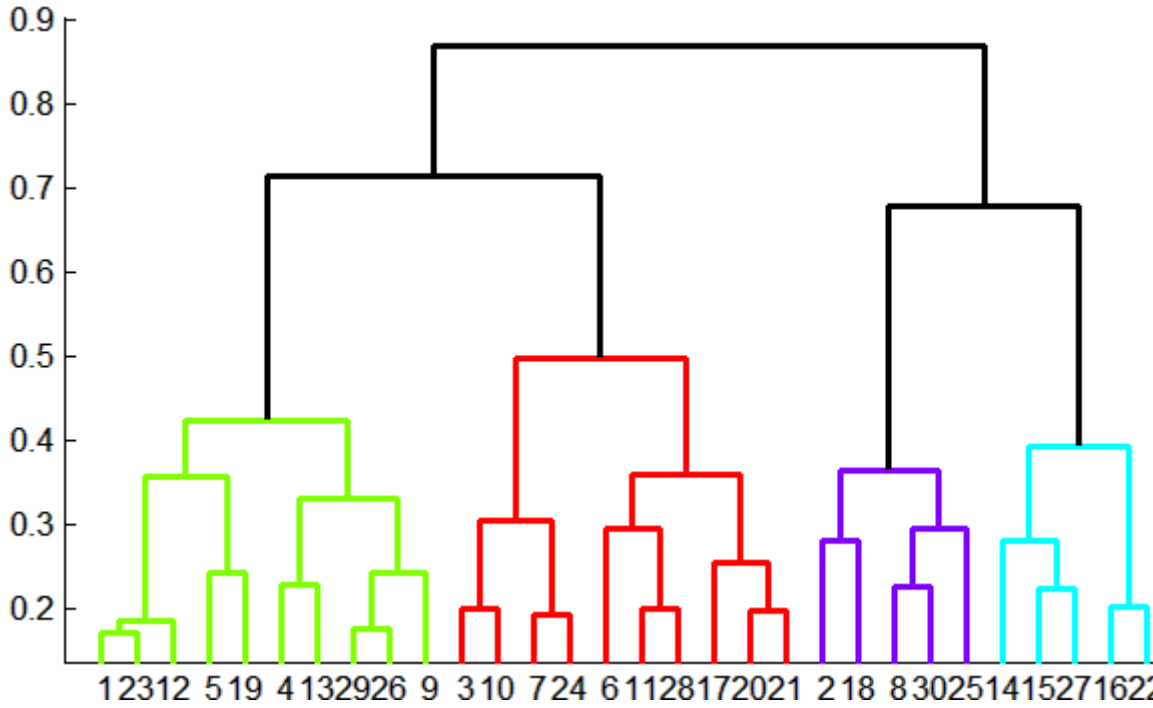
`[...] = dendrogram(...,'orientation','orient')` orients the dendrogram within the figure window. Acceptable values for '*orient*' are:

Value	Description
`'top'`	Top to bottom (default)
`'bottom'`	Bottom to top
`'left'`	Left to right
`'right'`	Right to left

`[...] = dendrogram(...,'labels',S)` accepts a character array or cell array of strings `S` with one label for each observation. Any leaves in the tree containing a single observation are labeled with that observation's label.

Examples

```
X = rand(100,2);
Y = pdist(X,'cityblock');
Z = linkage(Y,'average');
[H,T] = dendrogram(Z,'colorthreshold','default');
set(H,'LineWidth',2)
```




```
find(T==20)
ans =
    20
    49
    62
    65
    73
    96
```

This output indicates that leaf node 20 in the dendrogram contains the original data points 20, 49, 62, 65, 73, and 96.

See Also

`cluster` | `clusterdata` | `cophenet` | `inconsistent` | `linkage` | `silhouette`

dataset.Description property

Purpose

String describing data set

Description

`Description` is a string describing the data set. The default is an empty string.

Purpose

Interactive distribution fitting

Syntax

```
dfittool
dfittool(y)
dfittool(y,cens)
dfittool(y,cens,freq)
dfittool(y,cens,freq,dsname)
```

Description

`dfittool` opens a graphical user interface for displaying fit distributions to data. To fit distributions to your data and display them over plots of the empirical distributions, you can import data from the workspace.

`dfittool(y)` displays the Distribution Fitting Tool and creates a data set with data specified by the vector `y`.

`dfittool(y,cens)` uses the vector `cens` to specify whether the observation `y(j)` is censored, `(cens(j)==1)` and/or observed, exactly `(cens(j)==0)`. If `cens` is omitted or empty, no `y` values are censored.

`dfittool(y,cens,freq)` uses the vector `freq` to specify the frequency of each element of `y`. If `freq` is omitted or empty, all `y` values have a frequency of 1.

`dfittool(y,cens,freq,dsname)` creates a data set with the name `dsname` using the data vector `y`, censoring indicator `cens`, and frequency vector `freq`.

For more information, see "Modeling Data Using the Distribution Fitting Tool" on page 5-11.

See Also

`mle` | `randtool` | `disttool`

qrandset.Dimensions property

Purpose

Number of dimensions

Description

Number of dimensions in the point set. The `Dimensions` property of a point set contains a positive integer that indicates the number of dimensions for which the points have values. For example, a point set with `Dimensions=5` produces points that each have five values.

Set this property by specifying the number of dimensions when constructing a new point set. After construction, you cannot change the value. The default number of dimensions is 2.

Purpose

Two-element cell array of strings giving names of dimensions of data set

Description

A two-element cell array of strings giving the names of the two dimensions of the data set. The default is `{'Observations' 'Variables'}`.

categorical.disp

Purpose

Display categorical array

Syntax

```
disp(A)
```

Description

`disp(A)` prints the categorical array `A` without printing the array name. In all other ways it's the same as leaving the semicolon off an expression, except that empty arrays don't display.

See Also

`categorical` | `display`

Purpose

Display `classregtree` object

Syntax

```
display(t)
```

Description

`display(t)` prints the `classregtree` object `t`.

See Also

`classregtree` | `view`

cvpartition.disp

Purpose Display `cvpartition` object

Syntax `disp(c)`

Description `disp(c)` prints the `cvpartition` object `c`.

See Also `cvpartition`

Purpose

Display dataset array

Syntax

```
disp(ds)
```

Description

`disp(ds)` prints the dataset array `ds`, including variable names and observation names (if present), without printing the dataset name. In all other ways it's the same as leaving the semicolon off an expression.

For numeric or categorical variables that are 2-D and have three or fewer columns, `disp` prints the actual data using either short g, long g, or bank format, depending on the current command line setting. Otherwise, `disp` prints the size and type of each dataset element.

For character variables that are 2-D and 10 or fewer characters wide, `disp` prints quoted strings. Otherwise, `disp` prints the size and type of each dataset element.

For cell variables that are 2-D and have three or fewer columns, `disp` prints the contents of each cell (or its size and type if too large). Otherwise, `disp` prints the size of each dataset element.

For time series variables, `disp` prints columns for both the time and the data. If the variable is 2-D and has three or fewer columns, `disp` prints the actual data Otherwise, `disp` prints the size and type of each dataset element.

For other types of variables, `disp` prints the size and type of each dataset element.

See Also

`dataset` | `display` | `format`

gmdistribution.disp

Purpose

Display Gaussian mixture distribution object

Syntax

```
disp(obj)
```

Description

`disp(obj)` prints a text representation of the `gmdistribution` object, `obj`, without printing the object name. In all other ways it's the same as leaving the semicolon off an expression.

See Also

`gmdistribution` | `display`

Purpose

Display `NaiveBayes` classifier object

Syntax

```
disp(nb)
```

Description

`disp(nb)` prints a text representation of the `NaiveBayes` object `nb`, without printing the object name. In all other ways it's the same as leaving the semicolon off an expression.

See Also

`NaiveBayes` | `display`

piecewisedistribution.disp

Purpose

Display piecewisedistribution object

Syntax

```
disp(A)
```

Description

`disp(A)` prints a text representation of the piecewisedistribution object `A`, without printing the object name. In all other ways it's the same as leaving the semicolon off an expression.

See Also

`piecewisedistribution`

Purpose

Display qrandset object

Syntax

```
disp(p)
```

Description

`disp(p)` displays the properties of the quasi-random point set `s`, without printing the variable name. `disp` prints out the number of dimensions and points in the point-set, and follows this with the list of all property values for the object.

See Also

`qrandset`

qrandstream.disp

Purpose

Display `qrandstream` object

Syntax

```
disp(q)
```

Description

`disp(q)` displays the quasi-random stream `q`, without printing the variable name. `disp` prints the type and number of dimensions in the stream, and follows it with the list of point set properties.

See Also

`qrandstream`

Purpose

Display categorical array

Syntax

```
display(A)
```

Description

`display(A)` prints the categorical array A. `categorical` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`categorical` | `disp`

classregtree.display

Purpose

Display `classregtree` object

Syntax

```
display(t)
display(A)
```

Description

`display(t)` prints the `classregtree` object `t`. `classregtree` calls`display` when a you do not use a semicolon to terminate a statement.

`display(A)` prints the categorical array A. `categorical` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`classregtree` | `eval` | `prune` | `test`

Purpose

Display `cvpartition` object

Syntax

```
display(c)
```

Description

`display(c)` prints the `cvpartition` object `c`. `cvpartition` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`cvpartition`

dataset.display

Purpose

Display dataset array

Syntax

```
display(ds)
```

Description

`display(ds)` prints the dataset array `ds`, including variable names and observation names (if present). `dataset` calls`display` when a you do not use a semicolon to terminate a statement

For numeric or categorical variables that are 2-D and have three or fewer columns, `display` prints the actual data. Otherwise, `display` prints the size and type of each dataset element.

For character variables that are 2-D and 10 or fewer characters wide, `display` prints quoted strings. Otherwise, `display` prints the size and type of each dataset element.

For cell variables that are 2-D and have three or fewer columns, `display` prints the contents of each cell (or its size and type if too large). Otherwise, `display` prints the size of each dataset element.

For time series variables, `display` prints columns for both the time and the data. If the variable is 2-D and has three or fewer columns, `display` prints the actual data. Otherwise, `display` prints the size and type of each dataset element.

For other types of variables, `display` prints the size and type of each dataset element.

See Also

`dataset` | `display` | `format`

Purpose

Display Gaussian mixture distribution object

Syntax

```
display(obj)
```

Description

`display(obj)` prints a text representation of the `gmdistribution` object `obj`. `gmdistribution` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`gmdistribution` | `disp`

NaiveBayes.display

Purpose

Display `NaiveBayes` classifier object

Syntax

```
display(nb)
```

Description

`display(nb)` prints a text representation of the `NaiveBayes` object `nb`. `NaiveBayes` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`NaiveBayes` | `display`

Purpose

Display piecewisedistribution object

Syntax

```
display(A)
```

Description

`display(A)` prints a text representation of the piecewisedistribution object `A`, without printing the object name. `piecewisedistribution` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`piecewisedistribution`

ProbDist.DistName property

Purpose

Read-only string containing probability distribution name of ProbDist object

Description

`DistName` is a read-only property of the `ProbDist` class. `DistName` is a string containing the type of distribution used to create the object.

Values

Possible values are:

- `'kernel'`
- `'beta'`
- `'binomial'`
- `'birnbaumsaunders'`
- `'exponential'`
- `'extreme value'`
- `'gamma'`
- `'generalized extreme value'`
- `'generalized pareto'`
- `'inversegaussian'`
- `'logistic'`
- `'loglogistic'`
- `'lognormal'`
- `'nakagami'`
- `'negative binomial'`
- `'normal'`
- `'poisson'`
- `'rayleigh'`
- `'rician'`

- `'tlocationscale'`
- `'weibull'`

Use this information to view and compare the type of distribution used to create distribution objects.

NaiveBayes.Dist property

Purpose

Distribution names

Description

The `Dist` property is a string or a 1-by-`NDims` cell array of strings indicating the types of distributions for all the features. If all the features use the same type of distribution, `Dist` is a single string. Otherwise `Dist(j)` indicates the distribution type used for the `j`th feature.

The valid strings for this property are the following:

`'normal'`	Normal distribution.
`'kernel'`	Kernel smoothing density estimate.
`'mvmn'`	Multivariate multinomial distribution.
`'mn'`	Multinomial bag-of-tokens model.

Purpose

Type of distribution

Description

The string `'gaussian mixture distribution'`.

disttool

Purpose

Interactive density and distribution plots

Syntax

```
disttool
```

Description

`disttool` is a graphical interface for exploring the effects of changing parameters on the plot of a cdf or pdf.

See Also

`randtool` | `dfittool`

Purpose

Convert categorical array to double array

Syntax

```
B = double(A)
```

Description

`B = double(A)` converts the categorical array `A` to a double array. Each element of `B` contains the internal categorical level code for the corresponding element of `A`.

See Also

`single`

dataset.double

Purpose

Convert dataset variables to double array

Syntax

```
b = double(A)
b = double(a,vars)
```

Description

`b = double(A)` returns the contents of the dataset `A`, converted to one double array. The classes of the variables in the dataset must support the conversion.

`b = double(a,vars)` returns the contents of the dataset variables specified by `vars`. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

See Also

`dataset` | `single` | `replacedata`

Purpose

Drop levels

Syntax

```
B = droplevels(A)
B = droplevels(A,oldlevels)
```

Description

`B = droplevels(A)` removes unused levels from the categorical array `A`. `B` is a categorical array with the same size and values as `A`, but with a list of potential levels that includes only those present in some element of `A`.

`B = droplevels(A,oldlevels)` removes specified levels from the categorical array `A`. `oldlevels` is a cell array of strings or a 2-D character matrix specifying the levels to be removed.

`droplevels` removes levels, but does not remove elements. Elements of `B` that correspond to elements of `A` having levels in `oldlevels` all have an undefined level.

Examples

Example 1

Drop unused age levels from the data in `hospital.mat`:

```
load hospital
edges = 0:10:100;
labels = strcat(num2str((0:10:90)','%d'),{'s'});
AgeGroup = ordinal(hospital.Age,labels,[],edges);
AgeGroup = droplevels(AgeGroup);
getlabels(AgeGroup)
ans =
    '20s'    '30s'    '40s'    '50s'
```

Example 2

1. Load patient data from the CSV file `hospital.dat` and store the information in a dataset array with observation names given by the first column in the data (patient identification):

```
patients = dataset('file','hospital.dat',...
                   'delimiter',',',...
```

```
                                'ReadObsNames',true);
```

2. Make the {0,1}-valued variable `smoke` nominal, and change the labels to `'No'` and `'Yes'`:

```
patients.smoke = nominal(patients.smoke,{'No','Yes'});
```

3. Add new levels to `smoke` as placeholders for more detailed histories of smokers:

```
patients.smoke = addlevels(patients.smoke,...
                 {'0-5 Years','5-10 Years','LongTerm'});
```

4. Assuming the nonsmokers have never smoked, relabel the `'No'` level:

```
patients.smoke = setlabels(patients.smoke,'Never','No');
```

5. Drop the undifferentiated `'Yes'` level from `smoke`:

```
patients.smoke = droplevels(patients.smoke,'Yes');

Warning: OLDLEVELS contains categorical levels that
were present in A, caused some array elements to have
undefined levels.
```

   Note that smokers now have an undefined level.

6. Set each smoker to one of the new levels, by observation name:

```
patients.smoke('YPL-320') = '5-10 Years';
```

See Also

`addlevels` | `getlabels` | `islevel` | `mergelevels` | `reorderlevels`

Purpose

Create dummy variables

Syntax

```
D = dummyvar(group)
```

Description

`D = dummyvar(group)` returns a matrix `D` containing zeros and ones, whose columns are dummy variables for the grouping variable `group`. Columns of `group` represent categorical predictor variables, with values indicating categorical levels. Rows of `group` represent observations across variables.

`group` can be a numeric vector or categorical column vector representing levels within a single variable, a cell array containing one or more grouping variables, or a numeric matrix or cell array of categorical column vectors representing levels within multiple variables. If `group` is a numeric vector or matrix, values in any column must be positive integers in the range from `1` to the number of levels for the corresponding variable. In this case, `dummyvars` treats each column as a separate numeric grouping variable. With multiple grouping variables, the sets of dummy variable columns are in the same order as the grouping variables in `group`.

The order of the dummy variable columns in `D` matches the order of the groups defined by `group`. When `group` is a categorical vector, the groups and their order match the output of the `getlabels(group)` method. When `group` is a numeric vector, `dummyvar` assumes that the groups and their order are `1:max(group)`. In this respect, `dummyvars` treats a numeric grouping variable differently than `grp2idx`.

If `group` is n-by-p, `D` is n-by-S, where S is the sum of the number of levels in each of the columns of `group`. The number of levels s in any column of `group` is the maximum positive integer in the column or the number of categorical levels. Levels are considered distinct if they appear in different columns of `group`, even if they have the same value. Columns of `D` are, from left to right, dummy variables created from the first column of `group`, followed by dummy variables created from the second column of `group`, etc.

`dummyvar` treats `NaN` values or undefined categorical levels in `group` as missing data and returns `NaN` values in `D`.

Dummy variables are used in regression analysis and ANOVA to indicate values of categorical predictors.

Note If a column of 1s is introduced in the matrix `D`, the resulting matrix `X = [ones(size(D,1),1) D]` will be rank deficient. The matrix `D` itself will be rank deficient if `group` has multiple columns. This is because dummy variables produced from any column of `group` always sum to a column of 1s. Regression and ANOVA calculations often address this issue by eliminating one dummy variable (implicitly setting the coefficients for dropped columns to zero) from each group of dummy variables produced by a column of `group`.

Examples

Suppose you are studying the effects of two machines and three operators on a process. Use `group` to organize predictor data on machine-operator combinations:

```
machine = [1 1 1 1 2 2 2 2]';
operator = [1 2 3 1 2 3 1 2]';
group = [machine operator]
group =
     1     1
     1     2
     1     3
     1     1
     2     2
     2     3
     2     1
     2     2
```

Use `dummyvar` to create dummy variables for a regression or ANOVA calculation:

```
D = dummyvar(group)
D =
     1     0     1     0     0
```

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

The first two columns of `D` represent observations of machine `1` and machine `2`, respectively; the remaining columns represent observations of the three operators.

See Also

`regress` | `anova1`

How To

- "Grouped Data" on page 2-34

Purpose

Durbin-Watson test

Syntax

```
[P,DW] = dwtest(R,X)
[...] = dwtest(R,X,method)
[...] = dwtest(R,X,method,tail)
```

Description

`[P,DW] = dwtest(R,X)` performs a Durbin-Watson test on the vector `R` of residuals from a linear regression, where `X` is the design matrix from that linear regression. `P` is the computed `p` value for the test, and `DW` is the Durbin-Watson statistic. The Durbin-Watson test is used to test if the residuals are uncorrelated, against the alternative that there is autocorrelation among them. Small values of `P` indicate that the residuals are correlated.

`[...] = dwtest(R,X,method)` specifies the method to be used in computing the `p` value. *`method`* can be either of the following:

- `'exact'` — Calculates an exact `p` value using the PAN algorithm (the default if the sample size is less than 400).
- `'approximate'` — Calculates the `p` value using a normal approximation (the default if the sample size is 400 or larger).

`[...] = dwtest(R,X,method,tail)` performs the test against one of the following alternative hypotheses, specified by *`tail`*:

Tail	Alternative Hypothesis
`'both'`	Serial correlation is not 0.
`'right'`	Serial correlation is greater than 0 (right-tailed test).
`'left'`	Serial correlation is less than 0 (left-tailed test).

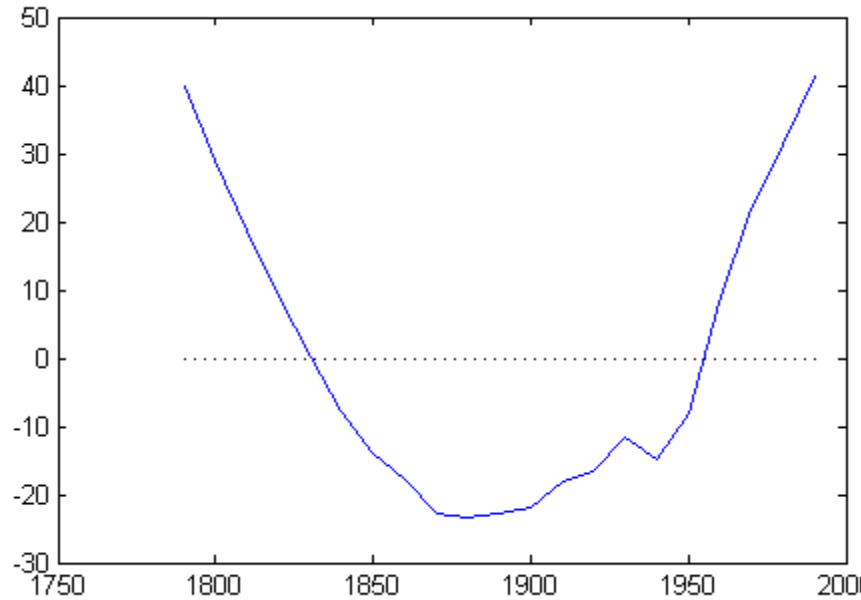
Examples

Fit a straight line to the census data, plot the residuals, and note their autocorrelation:

```
load census
n = length(cdate);
```

```
X = [ones(n,1),cdate];
[b,bint,r1] = regress(pop,X);
p1 = dwtest(r1,X)
plot(cdate,r1,'b-',cdate,zeros(n,1),'k:')

p1 =
     0
```

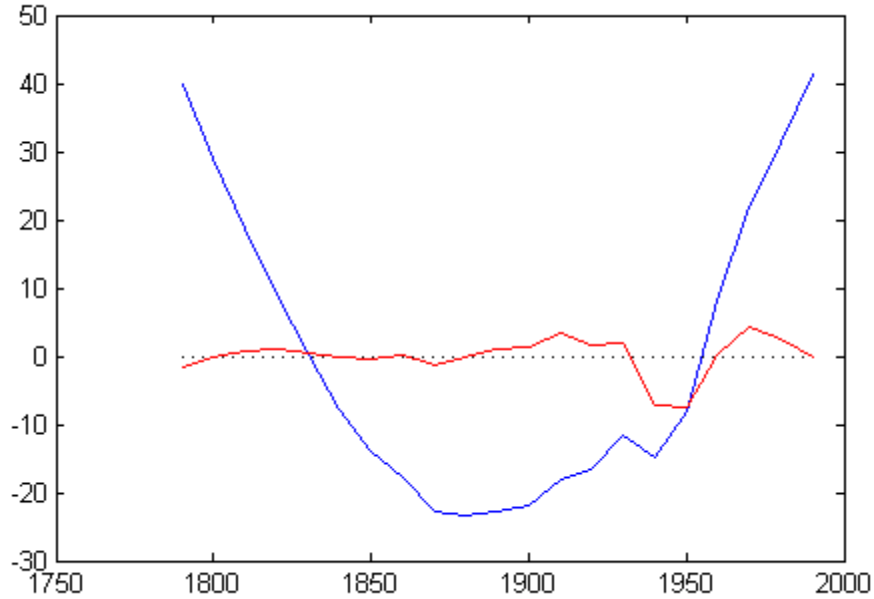
The test strongly rejects the hypothesis of no correlation in the residuals.



Adding a squared term gives less correlation in the residuals, but the resulting `p` value is still significantly small:

```
X = [ones(n,1),cdate,cdate.^2];
[b,bint,r2] = regress(pop,X);
p2 = dwtest(r2,X)
```

```
line(cdate,r2,'color','r')

p2 =
    0.0041
```



See Also

`regress`

Purpose

Empirical cumulative distribution function

Syntax

```
[f,x] = ecdf(y)
[f,x,flo,fup] = ecdf(y)
ecdf(...)
ecdf(ax,...)
[...] = ecdf(y,param1,val1,param2,val2,...)
```

Description

`[f,x] = ecdf(y)` calculates the Kaplan-Meier estimate of the cumulative distribution function (cdf), also known as the empirical cdf. `y` is a vector of data values. `f` is a vector of values of the empirical cdf evaluated at `x`.

`[f,x,flo,fup] = ecdf(y)` also returns lower and upper confidence bounds for the cdf. These bounds are calculated using Greenwood's formula, and are not simultaneous confidence bounds.

`ecdf(...)` without output arguments produces a plot of the empirical cdf.

`ecdf(ax,...)` plots into axes `ax` instead of `gca`.

`[...] = ecdf(y,param1,val1,param2,val2,...)` specifies additional parameter/value pairs chosen from the following:

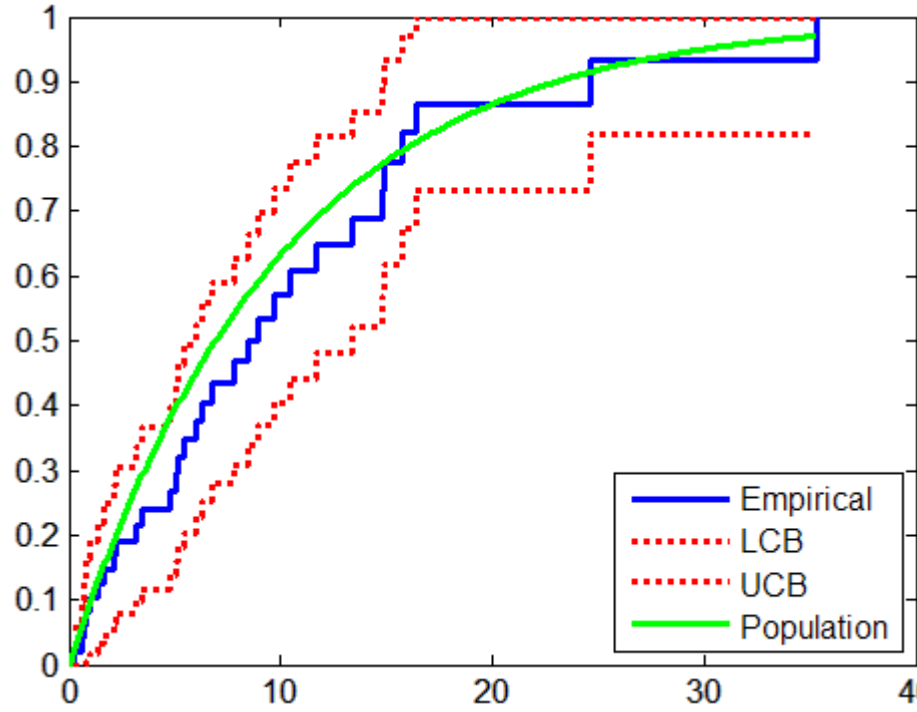
Parameter	Value
`'censoring'`	Boolean vector of the same size as `x`. Elements are `1` for observations that are right-censored and `0` for observations that are observed exactly. Default is all observations observed exactly.
`'frequency'`	Vector of the same size as `x` containing nonnegative integer counts. The `j`th element of this vector gives the number of times the `j`th element of `x` was observed. Default is `1` observation per element of `x`.
`'alpha'`	Value between `0` and `1` for a confidence level of `100(1-alpha)`%. Default is `alpha=0.05` for 95% confidence.

Parameter	Value
'function'	Type of function returned as the f output argument, chosen from 'cdf' (default), 'survivor', or 'cumulative hazard'.
'bounds'	Either 'on' to include bounds, or 'off' (the default) to omit them. Used only for plotting.

Examples

Generate random failure times and random censoring times, and compare the empirical cdf with the known true cdf:

```
y = exprnd(10,50,1); % Random failure times exponential(10)
d = exprnd(20,50,1); % Drop-out times exponential(20)
t = min(y,d); % Observe the minimum of these times
censored = (y>d); % Observe whether the subject failed

% Calculate and plot empirical cdf and confidence bounds
[f,x,flo,fup] = ecdf(t,'censoring',censored);
stairs(x,f,'LineWidth',2)
hold on
stairs(x,flo,'r:','LineWidth',2)
stairs(x,fup,'r:','LineWidth',2)

% Superimpose a plot of the known population cdf
xx = 0:.1:max(t);
yy = 1-exp(-xx/10);
plot(xx,yy,'g-','LineWidth',2)
legend('Empirical','LCB','UCB','Population',...
       'Location','SE')
hold off
```



References

[1] Cox, D. R., and D. Oakes. *Analysis of Survival Data*. London: Chapman & Hall, 1984.

See Also

`cdfplot` | `ecdfhist`

ecdfhist

Purpose

Empirical cumulative distribution function histogram

Syntax

```
n = ecdfhist(f,x)
n = ecdfhist(f,x,m)
n = ecdfhist(f,x,c)
[n,c] = ecdfhist(...)
ecdfhist(...)
```

Description

`n = ecdfhist(f,x)` takes a vector `f` of empirical cumulative distribution function (cdf) values and a vector `x` of evaluation points, and returns a vector `n` containing the heights of histogram bars for 10 equally spaced bins. The function computes the bar heights from the increases in the empirical cdf, and normalizes them so that the area of the histogram is equal to 1. In contrast, `hist` produces bars whose heights represent bin counts.

`n = ecdfhist(f,x,m)`, where `m` is a scalar, uses `m` bins.

`n = ecdfhist(f,x,c)`, where `c` is a vector, uses bins with centers specified by `c`.

`[n,c] = ecdfhist(...)` also returns the position of the bin centers in `c`.

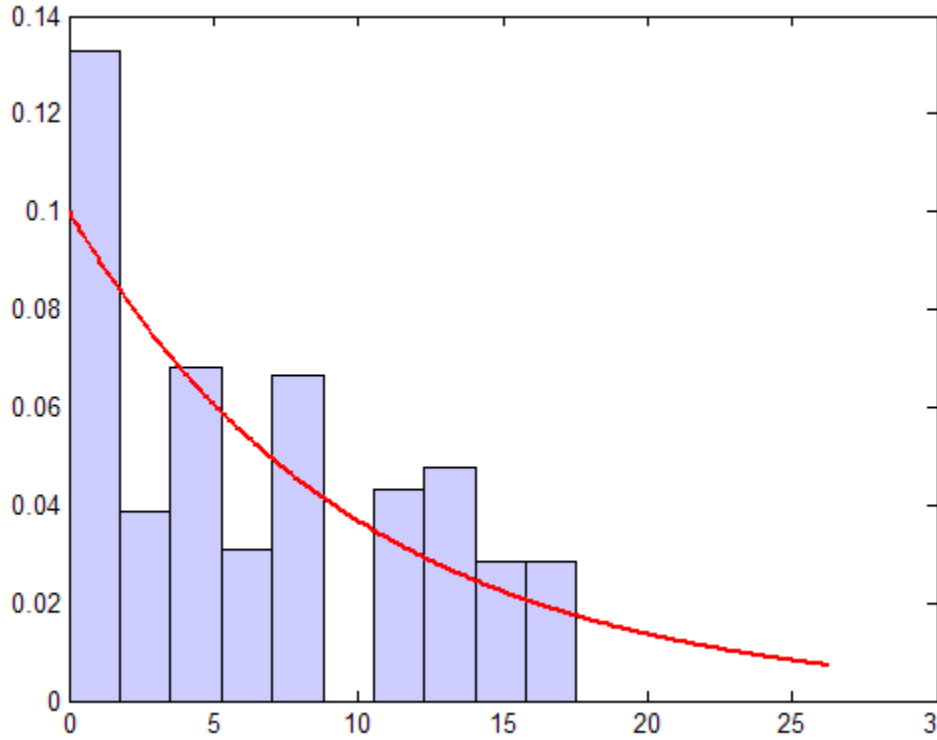
`ecdfhist(...)` without output arguments produces a histogram bar plot of the results.

Examples

The following code generates random failure times and random censoring times, and compares the empirical pdf with the known true pdf.

```
y = exprnd(10,50,1); % Random failure times
d = exprnd(20,50,1); % Drop-out times
t = min(y,d);        % Observe the minimum of these times
censored = (y>d);    % Observe whether the subject failed

% Calculate the empirical cdf and plot a histogram from it
[f,x] = ecdf(t,'censoring',censored);
ecdfhist(f,x)
```

```
set(get(gca,'Children'),'FaceColor',[.8 .8 1])
hold on

% Superimpose a plot of the known population pdf
xx = 0:.1:max(t);
yy = exp(-xx/10)/10;
plot(xx,yy,'r-','LineWidth',2)
hold off
```



See Also

ecdf | hist | histc

CompactClassificationDiscriminant.edge

Purpose

Classification edge

Syntax

```
E = edge(obj,X,Y)
E = edge(obj,X,Y,Name,Value)
```

Description

`E = edge(obj,X,Y)` returns the classification edge for `obj` with data `X` and classification `Y`.

`E = edge(obj,X,Y,Name,Value)` computes the edge with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`obj`

Discriminant analysis classifier of class `ClassificationDiscriminant` or `CompactClassificationDiscriminant`, typically constructed with `ClassificationDiscriminant.fit`.

`X`

Matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `obj`.

`Y`

Class labels, with the same data type as exists in `obj`. The number of elements of `Y` must equal the number of rows of `X`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`weights`

Observation weights, a numeric vector of length `size(X,1)`. If you supply weights, `edge` computes the weighted classification edge.

Default: `ones(size(X,1))`

Output Arguments

`E`

Edge, a scalar representing the weighted average value of the margin.

Definitions

Edge

The *edge* is the weighted mean value of the classification *margin*. The weights are the class probabilities in `obj.Prior`. If you supply weights in the `weights` name-value pair, those weights are normalized to sum to the prior probabilities in the respective classes, and are then used to compute the weighted average.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `X`. A high value of margin indicates a more reliable prediction than a low value.

Score (discriminant analysis)

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see "Posterior Probability" on page 12-7.

Examples

Compute the classification edge and margin for the Fisher iris data, trained on its first two columns of data, and view the last 10 entries:

```
load fisheriris
X = meas(:,1:2);
obj = ClassificationDiscriminant.fit(X,species);
E = edge(obj,X,species)

E =
    0.4980
```

```
M = margin(obj,X,species);
M(end-10:end)

ans =
    0.6551
    0.4838
    0.6551
   -0.5127
    0.5659
    0.4611
    0.4949
    0.1024
    0.2787
   -0.1439
   -0.4444
```

The classifier trained on all the data is better:

```
obj = ClassificationDiscriminant.fit(meas,species);
E = edge(obj,meas,species)

E =
    0.9454

M = margin(obj,meas,species);
M(end-10:end)

ans =
    0.9983
    1.0000
    0.9991
    0.9978
    1.0000
    1.0000
    0.9999
    0.9882
```

```
    0.9937
    1.0000
    0.9649
```

See Also

`ClassificationDiscriminant` | `loss` | `margin` | `predict`

How To

- “Discriminant Analysis” on page 12-3

CompactClassificationEnsemble.edge

Purpose

Classification edge

Syntax

```
E = edge(ens,X,Y)
E = edge(ens,X,Y,Name,Value)
```

Description

`E = edge(ens,X,Y)` returns the classification edge for `ens` with data `X` and classification `Y`.

`E = edge(ens,X,Y,Name,Value)` computes the edge with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A classification ensemble constructed with `fitensemble`, or a compact classification ensemble constructed with `compact`.

`X`

A matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `ens`.

`Y`

Class labels, with the same data type as exists in `ens`. The number of elements of `Y` must equal the number of rows of `X`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `ens.NTrained`. `edge` uses only these learners for calculating loss.

Default: `1:NTrained`

`mode`

String representing the meaning of the output `E`:

- `'ensemble'` — `E` is a scalar value, the edge for the entire ensemble.
- `'individual'` — `E` is a vector with one element per trained learner.
- `'cumulative'` — `E` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

`UseObsForLearner`

A logical matrix of size `N`-by-`T`, where:

- `N` is the number of rows of `X`.
- `T` is the number of weak learners in `ens`.

When `UseObsForLearner(i,j)` is `true`, learner `j` is used in predicting the class of row `i` of `X`.

Default: `true(N,T)`

`weights`

Observation weights, a numeric vector of length `size(X,1)`. If you supply weights, `edge` computes weighted classification edge.

Default: `ones(size(X,1))`

Output Arguments

`E`

The classification edge, a vector or scalar depending on the setting of the `mode` name-value pair. Classification edge is weighted average classification margin.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `X`.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in `ens.Prior`. If you supply weights in the `weights` name-value pair, those weights are used instead of class probabilities.

Examples

Make a boosted ensemble classifier for the `ionosphere` data, and find the classification edge for the last few rows:

```
load ionosphere
ens = fitensemble(X,Y,'AdaboostM1',100,'Tree');
E = edge(ens,X(end-10:end,:),Y(end-10:end))

E =
    8.3310
```

See Also

`margin` | `edge`

How To

- Chapter 13, “Nonparametric Supervised Learning”

CompactClassificationTree.edge

Purpose

Classification edge

Syntax

```
E = edge(tree,X,Y)
E = edge(tree,X,Y,Name,Value)
```

Description

`E = edge(tree,X,Y)` returns the classification edge for `tree` with data `X` and classification `Y`.

`E = edge(tree,X,Y,Name,Value)` computes the edge with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`tree`

A classification tree created by `ClassificationTree.fit`, or a compact classification tree created by `compact`.

`X`

A matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `tree`.

`Y`

Class labels, with the same data type as exists in `tree`. The number of elements of `Y` must equal the number of rows of `X`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`weights`

Observation weights, a numeric vector of length `size(X,1)`. If you supply weights, `edge` computes weighted classification edge.

Default: `ones(size(X,1))`

Output Arguments

`E`

The edge, a scalar representing the weighted average value of the margin.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as the matrix `X`.

Score (tree)

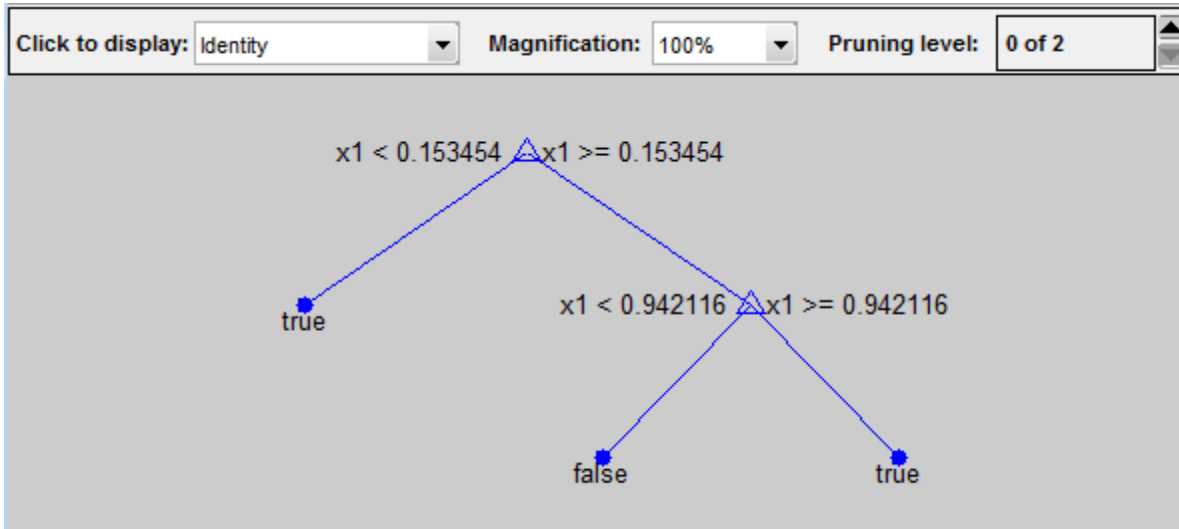
For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

1

Generate 100 random points and classify them:

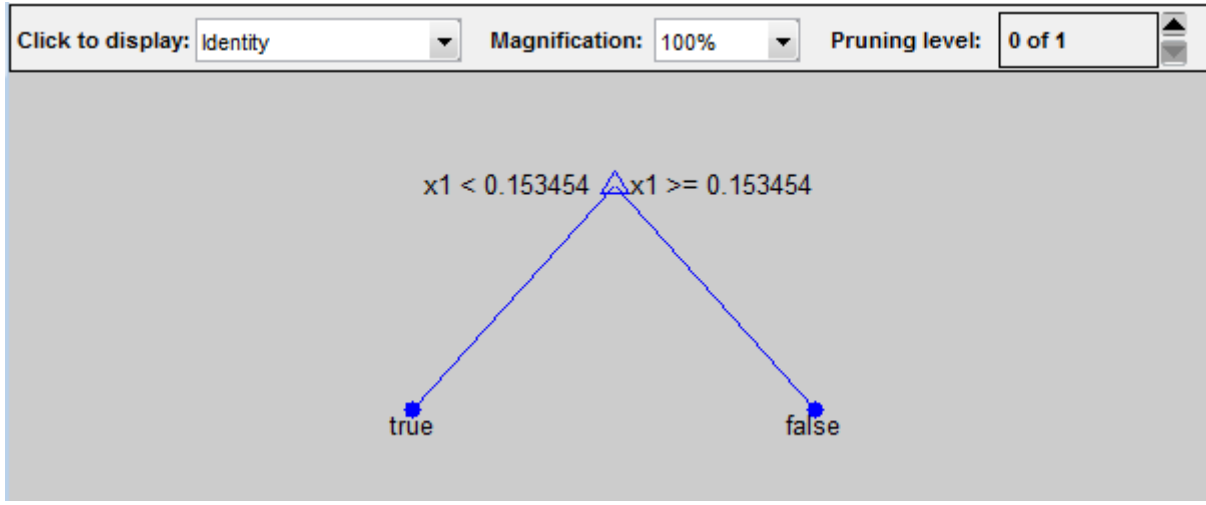
```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = ClassificationTree.fit(X,Y);
view(tree,'mode','graph')
```



2

Prune the tree:

```
tree1 = prune(tree,'level',1);
view(tree1,'mode','graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

3

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]

ans =
    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
```

```
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the rightmost column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in `tree.Prior`. If you supply weights in the `weights` name-value pair, those weights are normalized to sum to the prior probabilities in the respective classes, and are then used to compute the weighted average.

Examples

Compute the classification margin and edge for the Fisher iris data, trained on its first two columns of data, and view the last 10 entries:

```
load fisheriris
X = meas(:,1:2);
tree = ClassificationTree.fit(X,species);
E = edge(tree,X,species)

E =
    0.6299

M = margin(tree,X,species);
M(end-10:end)

ans =
    0.1111
    0.1111
    0.1111
   -0.2857
```

```
    0.6364
    0.6364
    0.1111
    0.7500
    1.0000
    0.6364
    0.2000
```

The classification tree trained on all the data is better:

```
tree = ClassificationTree.fit(meas,species);
E = edge(tree,meas,species)

E =
    0.9384

M = margin(tree,meas,species);
M(end-10:end)

ans =
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
```

See Also

`margin` | `loss` | `predict`

How To

- Chapter 13, "Nonparametric Supervised Learning"

categorical.end

Purpose

Last index in indexing expression for categorical array

Syntax

```
end(A,k,n)
```

Description

`end(A,k,n)` indexes expressions involving the categorical array `A` when `end` is part of the `k`-th index out of `n` indices. For example, the expression `A(end-1,:)` calls `A`'s `end` method with `end(A,1,2)`.

See Also

`single`

Purpose

Last index in indexing expression for dataset array

Syntax

```
end(A,k,n)
```

Description

`end(A,k,n)` is called for indexing expressions involving the dataset `A` when `end` is part of the `k`-th index out of `n` indices. For example, the expression `A(end-1,:)` calls `A`'s `end` method with `end(A,1,2)`.

See Also

`size`

qrandset.end

Purpose

Last index in indexing expression for point set

Syntax

```
end(p,k,n)
```

Description

`end(p,k,n)` is called for indexing expressions involving the point set `p` when `end` is part of the `k`-th index out of `n` indices. For example, the expression `p(end-1,:)` calls `p`'s `end` method with `end(p,1,2)`.

See Also

`qrandset`

Purpose

Extreme value cumulative distribution function

Syntax

```
P = evcdf(X,mu,sigma)
[P,PLO,PUP] = evcdf(X,mu,sigma,pcov,alpha)
```

Description

`P = evcdf(X,mu,sigma)` computes the cumulative distribution function (cdf) for the type 1 extreme value distribution, with location parameter `mu` and scale parameter `sigma`, at each of the values in `X`. `X`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The default values for `mu` and `sigma` are `0` and `1`, respectively.

`[P,PLO,PUP] = evcdf(X,mu,sigma,pcov,alpha)` produces confidence bounds for `P` when the input parameters `mu` and `sigma` are estimates. `pcov` is a 2-by-2 covariance matrix of the estimated parameters. `alpha` has a default value of `0.05`, and specifies `100(1 - alpha)`% confidence bounds. `PLO` and `PUP` are arrays of the same size as `P`, containing the lower and upper confidence bounds.

The function `evcdf` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\frac{X - \hat{\mu}}{\hat{\sigma}}$$

and then transforming those bounds to the scale of the output `P`. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `X`. See "Extreme Value Distribution" on page B-19 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

See Also `cdf` | `evpdf` | `evinv` | `evstat` | `evfit` | `evlike` | `evrnd`

How To

- "Extreme Value Distribution" on page B-19

Purpose

Extreme value parameter estimates

Syntax

```
parmhat = evfit(data)
[parmhat,parmci] = evfit(data)
[parmhat,parmci] = evfit(data,alpha)
[...] = evfit(data,alpha,censoring)
[...] = evfit(data,alpha,censoring,freq)
[...] = evfit(data,alpha,censoring,freq,options)
```

Description

`parmhat = evfit(data)` returns maximum likelihood estimates of the parameters of the type 1 extreme value distribution given the data in the vector `data`. `parmhat(1)` is the location parameter, , and `parmhat(2)` is the scale parameter, σ.

`[parmhat,parmci] = evfit(data)` returns 95% confidence intervals for the parameter estimates on the and σ parameters in the 2-by-2 matrix `parmci`. The first column of the matrix of the extreme value fit contains the lower and upper confidence bounds for the parameter , and the second column contains the confidence bounds for the parameter σ.

`[parmhat,parmci] = evfit(data,alpha)` returns 100(1 - `alpha`)% confidence intervals for the parameter estimates, where `alpha` is a value in the range `[0 1]` specifying the width of the confidence intervals. By default, `alpha` is `0.05`, which corresponds to 95% confidence intervals.

`[...] = evfit(data,alpha,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is `1` for observations that are right-censored and `0` for observations that are observed exactly.

`[...] = evfit(data,alpha,censoring,freq)` accepts a frequency vector, `freq` of the same size as `data`. Typically, `freq` contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `alpha`, `censoring`, or `freq` to use their default values.

`[...] = evfit(data,alpha,censoring,freq,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood

estimates. You can create `options` using the function `statset`. Enter `statset('evfit')` to see the names and default values of the parameters that `evfit` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `X`. See "Extreme Value Distribution" on page B-19 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

See Also

`mle` | `evlike` | `evpdf` | `evcdf` | `evinv` | `evstat` | `evrnd`

How To

- "Extreme Value Distribution" on page B-19

Purpose

Extreme value inverse cumulative distribution function

Syntax

```
X = evinv(P,mu,sigma)
[X,XLO,XUP] = evinv(P,mu,sigma,pcov,alpha)
```

Description

`X = evinv(P,mu,sigma)` returns the inverse cumulative distribution function (cdf) for a type 1 extreme value distribution with location parameter `mu` and scale parameter `sigma`, evaluated at the values in `P`. `P`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The default values for `mu` and `sigma` are `0` and `1`, respectively.

`[X,XLO,XUP] = evinv(P,mu,sigma,pcov,alpha)` produces confidence bounds for `X` when the input parameters `mu` and `sigma` are estimates. `pcov` is the covariance matrix of the estimated parameters. `alpha` is a scalar that specifies 100(1 – `alpha`)% confidence bounds for the estimated parameters, and has a default value of 0.05. `XLO` and `XUP` are arrays of the same size as `X` containing the lower and upper confidence bounds.

The function `evinv` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\hat{\mu} + \hat{\sigma} q$$

where q is the `P`th quantile from an extreme value distribution with parameters $\mu = 0$ and $\sigma = 1$. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `X`. See “Extreme Value Distribution” on page B-19 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

See Also

icdf | evcdf | evpdf | evstat | evfit | evlike | evrnd

Purpose

Test handle equality

Syntax

```
h1 == h2
tf = eq(h1, h2)
```

Description

`h1 == h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise equality result. If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = eq(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `ge` | `gt` | `le` | `lt` | `ne`

CompactTreeBagger.error

Purpose

Error (misclassification probability or MSE)

Syntax

```
err = error(B,X,Y)
err = error(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`err = error(B,X,Y)` computes the misclassification probability (for classification trees) or mean squared error (MSE, for regression trees) for each tree, for predictors `X` given true response `Y`. For classification, `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. For regression, `Y` must be a numeric vector. `err` is a vector with one error measure for each of the `NTrees` trees in the ensemble `B`.

`err = error(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how the method computes errors. If set to `'cumulative'` (default), `error` computes cumulative errors and `err` is a vector of length `NTrees`, where the first element gives error from `trees(1)`, second element gives error from`trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `err` is a vector of length `NTrees`, where each element is an error from each tree in the ensemble. If set to `'ensemble'`, `err` is a scalar showing the cumulative error for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element gives error from `trees(1)`, the second element gives error from `trees(1:2)` etc.

`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. The method uses these weights to combine output from the specified trees by taking a weighted average instead of the simple non-weighted majority vote. You cannot use this argument in the `'individual'` mode.
`'useifort'`	Logical matrix of size `Nobs`-by-`NTrees` indicating which trees should be used to make predictions for each observation. By default the method uses all trees for all observations.

See Also

`TreeBagger.error`

TreeBagger.error

Purpose

Error (misclassification probability or MSE)

Syntax

```
err = error(B,X,Y)
err = error(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`err = error(B,X,Y)` computes the misclassification probability for classification trees or mean squared error (MSE) for regression trees for each tree, for predictors `X` given true response `Y`. For classification, `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. For regression, `Y` must be a numeric vector. `err` is a vector with one error measure for each of the `NTrees` trees in the ensemble `B`.

`err = error(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how the method computes errors. If set to `'cumulative'` (default), `error` computes cumulative errors and `err` is a vector of length `NTrees`, where the first element gives error from `trees(1)`, second element gives error from`trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `err` is a vector of length `NTrees`, where each element is an error from each tree in the ensemble. If set to `'ensemble'`, `err` is a scalar showing the cumulative error for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element gives error from `trees(1)`, the second element gives error from `trees(1:2)` etc.

`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. The method uses these weights to combine output from the specified trees by taking a weighted average instead of the simple non-weighted majority vote. You cannot use this argument in the `'individual'` mode.
`'useifort'`	Logical matrix of size `Nobs`-by-`NTrees` indicating which trees should be used to make predictions for each observation. By default the method uses all trees for all observations.

See Also

`CompactTreeBagger.error`

classregtree.eval

Purpose

Predicted responses

Syntax

```
yfit = eval(t,X)
yfit = eval(t,X,s)
[yfit,nodes] = eval(...)
[yfit,nodes,cnums] = eval(...)
[...] = t(X)
[...] = t(X,s)
```

Description

`yfit = eval(t,X)` takes a classification or regression tree `t` and a matrix `X` of predictors, and produces a vector `yfit` of predicted response values. For a regression tree, `yfit(i)` is the fitted response value for a point having the predictor values `X(i,:)`. For a classification tree, `yfit(i)` is the class into which the tree assigns the point with data `X(i,:)`.

`yfit = eval(t,X,s)` takes an additional vector `s` of pruning levels, with 0 representing the full, unpruned tree. `t` must include a pruning sequence as created by `classregtree` or by `prune`. If `s` has k elements and `X` has n rows, the output `yfit` is an n-by-k matrix, with the `j`th column containing the fitted values produced by the `s(j)` subtree. `s` must be sorted in ascending order.

To compute fitted values for a tree that is not part of the optimal pruning sequence, first use `prune` to prune the tree.

`[yfit,nodes] = eval(...)` also returns a vector `nodes` the same size as `yfit` containing the node number assigned to each row of `X`. Use `view` to display the node numbers for any node you select.

`[yfit,nodes,cnums] = eval(...)` is valid only for classification trees. It returns a vector `cnum` containing the predicted class numbers.

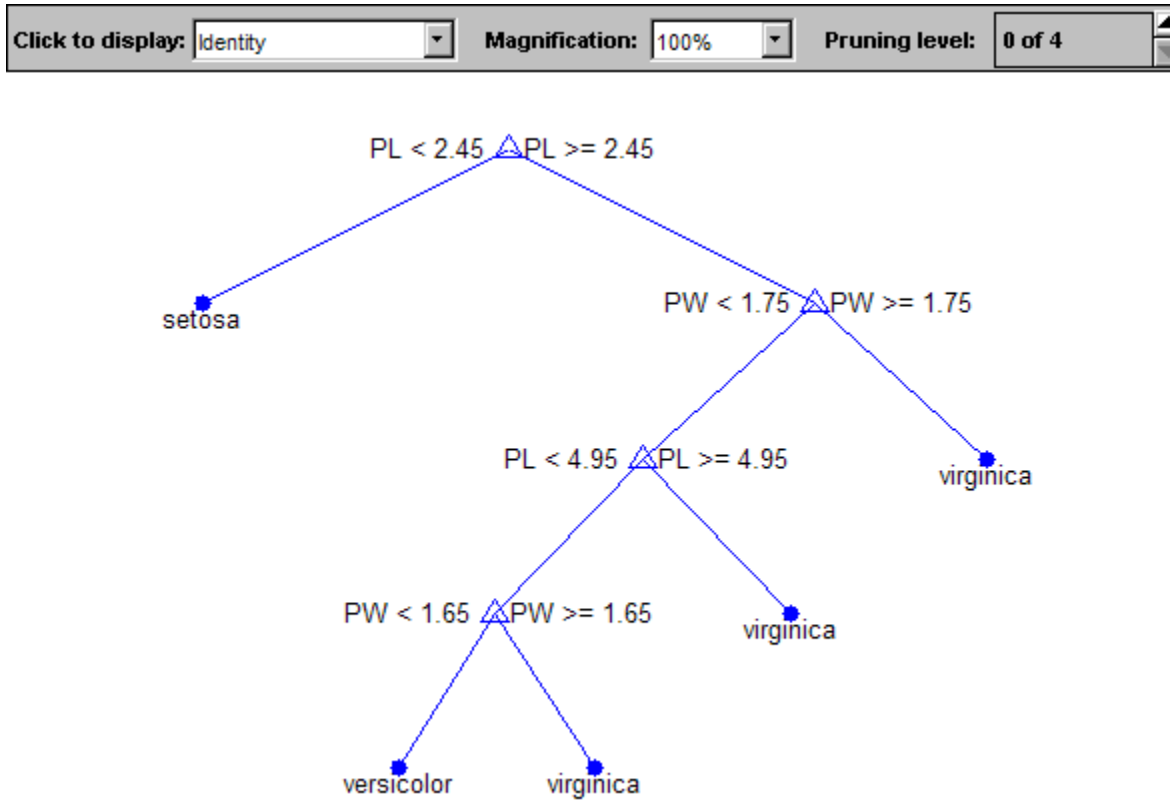
`NaN` values in `X` are treated as missing. If `eval` encounters a missing value when it attempts to evaluate the split rule at a branch node, it cannot determine whether to proceed to the left or right child node. Instead, it sets the corresponding fitted value equal to the fitted value assigned to the branch node.

`[...] = t(X)` or `[...] = t(X,s)` also invoke `eval`.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```



Find assigned class names:

```
sfit = eval(t,meas);
```

Compute that proportion is correctly classified:

```
pct = mean(strcmp(sfit,species))
pct =
    0.9800
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `prune` | `test` | `view`

evlike

Purpose

Extreme value negative log-likelihood

Syntax

```
nlogL = evlike(params,data)
[nlogL,AVAR] = evlike(params,data)
[...] = evlike(params,data,censoring)
[...] = evlike(params,data,censoring,freq)
```

Description

`nlogL = evlike(params,data)` returns the negative of the log-likelihood for the type 1 extreme value distribution. `params(1)` is the tail location parameter, `mu`, and `params(2)` is the scale parameter, `sigma`. `nlogL` is a scalar.

`[nlogL,AVAR] = evlike(params,data)` returns the inverse of Fisher's information matrix, `AVAR`. If the input parameter values in `params` are the maximum likelihood estimates, the diagonal elements of `AVAR` are their asymptotic variances. `AVAR` is based on the observed Fisher's information, not the expected information.

`[...] = evlike(params,data,censoring)` accepts a Boolean vector of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = evlike(params,data,censoring,freq)` accepts a frequency vector of the same size as `data`. `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `censoring` to use its default value.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `data`. See "Extreme Value Distribution" on page B-19 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

See Also

`evfit` | `evpdf` | `evcdf` | `evinv` | `evstat` | `evrnd`

How To

- "Extreme Value Distribution" on page B-19

Purpose

Extreme value probability density function

Syntax

```
Y = evpdf(X,mu,sigma)
```

Description

`Y = evpdf(X,mu,sigma)` returns the pdf of the type 1 extreme value distribution with location parameter `mu` and scale parameter `sigma`, evaluated at the values in `X`. `X`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The default values for `mu` and `sigma` are `0` and `1`, respectively.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `X`. See "Extreme Value Distribution" on page B-19 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

See Also

`pdf` | `evcdf` | `evinv` | `evstat` | `evfit` | `evlike` | `evrnd`

How To

- "Extreme Value Distribution" on page B-19

evrnd

Purpose

Extreme value random numbers

Syntax

```
R = evrnd(mu,sigma)
R = evrnd(mu,sigma,m,n,...)
R = evrnd(mu,sigma,[m,n,...])
```

Description

`R = evrnd(mu,sigma)` generates random numbers from the extreme value distribution with parameters specified by location parameter `mu` and scale parameter `sigma`. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of R. A scalar input for `mu` or `sigma` is expanded to a constant array with the same dimensions as the other input.

`R = evrnd(mu,sigma,m,n,...)` or `R = evrnd(mu,sigma,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the extreme value distribution with parameters `mu` and `sigma`. `mu` and `sigma` can each be scalars or arrays of the same size as `R`.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `R`. See "Extreme Value Distribution" on page B-19 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

See Also

`random` | `evpdf` | `evcdf` | `evinv` | `evstat` | `evfit` | `evlike`

How To

- "Extreme Value Distribution" on page B-19

Purpose

Extreme value mean and variance

Syntax

```
[M,V] = evstat(mu,sigma)
```

Description

`[M,V] = evstat(mu,sigma)` returns the mean of and variance for the type 1 extreme value distribution with location parameter `mu` and scale parameter `sigma`. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other input. The default values for `mu` and `sigma` are `0` and `1`, respectively.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima. See "Extreme Value Distribution" on page B-19 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

See Also

`evpdf` | `evcdf` | `evinv` | `evfit` | `evlike` | `evrnd`

How To

- "Extreme Value Distribution" on page B-19

expcdf

Purpose

Exponential cumulative distribution function

Syntax

```
P = expcdf(X,mu)
[P,PLO,PUP] = expcdf(X,mu,pcov,alpha)
```

Description

`P = expcdf(X,mu)` computes the exponential cdf at each of the values in `X` using the corresponding mean parameter `mu`. `X` and `mu` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `mu` must be positive.

The exponential cdf is

$$p = F(x \mid u) = \int_0^x \frac{1}{\mu} e^{\frac{-t}{\mu}} dt = 1 - e^{\frac{-x}{\mu}}$$

The result, p, is the probability that a single observation from an exponential distribution will fall in the interval [0 x].

`[P,PLO,PUP] = expcdf(X,mu,pcov,alpha)` produces confidence bounds for `P` when the input mean parameter `mu` is an estimate. `pcov` is the variance of the estimated `mu`. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is 0.05. `PLO` and `PUP` are arrays of the same size as `P` containing the lower and upper confidence bounds. The bounds are based on a normal approximation for the distribution of the log of the estimate of `mu`. If you estimate `mu` from a set of data, you can get a more accurate set of bounds by applying `expfit` to the data to get a confidence interval for `mu`, and then evaluating `expinv` at the lower and upper endpoints of that interval.

Examples

The following code shows that the median of the exponential distribution is `*log(2)`.

```
mu = 10:10:60;
p = expcdf(log(2)*mu,mu)
p =
  0.5000  0.5000  0.5000  0.5000  0.5000  0.5000
```

What is the probability that an exponential random variable is less than or equal to the mean, μ?

```
mu = 1:6;
x = mu;
p = expcdf(x,mu)
p =
  0.6321  0.6321  0.6321  0.6321  0.6321  0.6321
```

See Also

cdf | exppdf | expinv | expstat | expfit | explike | exprnd

How To

- "Exponential Distribution" on page B-16

expfit

Purpose

Exponential parameter estimates

Syntax

```
muhat = expfit(data)
[muhat,muci] = expfit(data)
[muhat,muci] = expfit(data,alpha)
[...] = expfit(data,alpha,censoring)
[...] = expfit(data,alpha,censoring,freq)
```

Description

`muhat = expfit(data)` estimates the mean of an exponentially distributed sample `data`. Each entry of `muhat` corresponds to the data in a column of `data`.

`[muhat,muci] = expfit(data)` returns 95% confidence intervals for the mean parameter estimates in matrix `muci`. The first row of `muci` contains the lower bounds of the confidence intervals, and the second row contains the upper bounds.

`[muhat,muci] = expfit(data,alpha)` returns 100(1 - `alpha`)% confidence intervals for the parameter estimates, where `alpha` is a value in the range `[0 1]` specifying the width of the confidence intervals. By default, `alpha` is `0.05`, which corresponds to 95% confidence intervals.

`[...] = expfit(data,alpha,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly. `data` must be a vector in order to pass in the argument `censoring`.

`[...] = expfit(data,alpha,censoring,freq)` accepts a frequency vector, `freq` of the same size as `data`. Typically, `freq` contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `alpha`, `censoring`, or `freq` to use their default values.

Examples

The following estimates the mean `mu` of exponentially distributed data, and returns a 95% confidence interval for the estimate:

```
mu = 3;
data = exprnd(mu,100,1); % Simulated data
```

```
[muhat,muci] = expfit(data)
muhat =
    2.7511
muci =
    2.2826
    3.3813
```

See Also

mle | explike | exppdf | expcdf | expinv | expstat | exprnd

ExhaustiveSearcher

Superclasses

NeighborSearcher

Purpose

Nearest neighbors search using exhaustive search

Description

An `ExhaustiveSearcher` object performs *k*NN (*k*-nearest neighbor) search using exhaustive search. Search objects store information about the data used, and the distance metric and parameters. The search performance for this object, compared with the `KDTreeSearcher` object, tends to be better for larger dimensions (10 or more) and worse for smaller dimensions. For more information on search objects, see "What Are Search Objects?" on page 13-17.

Construction

`NS = ExhaustiveSearcher(X,'Name',Value)` constructs an `ExhaustiveSearcher` object based on `X`, where rows of `X` correspond to observations and columns correspond to variables, using one or more optional name/value pairs. You can then use this object to find neighbors in `X` nearest to the query points.

`NS = createns(X,'NSMethod','exhaustive','Name',Value)` creates an `ExhaustiveSearcher` object based on `X` using `createns`, where rows of `X` correspond to observations and columns correspond to variables, using one or more optional name/value pairs. You can use this object to find neighbors in `X` nearest to the query points.

Name-Value Pair Arguments

Both the `ExhaustiveSearcher` and the `createns` functions accept one or more of the following optional name/value pairs as input:

`Distance`

A string or function handle specifying the default distance metric used when you call the `knnsearch` method.

- `'euclidean'` — Euclidean distance (default).
- `'seuclidean'` — Standardized Euclidean distance. Each coordinate difference between rows in `X` and the query matrix is scaled by dividing by the corresponding element of the standard

deviation computed from `X`, `S=nanstd(X)`. To specify another value for `S`, use the `Scale` argument.

- `'cityblock'` — City block distance.
- `'chebychev'` — Chebychev distance (maximum coordinate difference).
- `'minkowski'` — Minkowski distance.
- `'mahalanobis'` — Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is `nancov(X)`. To change the value of `C`, use the `Cov` parameter.
- `'cosine'` — One minus the cosine of the included angle between observations (treated as vectors).
- `'correlation'` — One minus the sample linear correlation between observations (treated as sequences of values).
- `'spearman'` — One minus the sample Spearman's rank correlation between observations (treated as sequences of values).
- `'hamming'` — Hamming distance, percentage of coordinates that differ.
- `'jaccard'` — One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.
- custom distance function — A distance function specified using `@` (for example, `@distfun`). A distance function must be of the form `function D2 = distfun(ZI, ZJ)`, taking as arguments a 1-by-n vector `ZI` containing a single row from `X` or from the query points `Y`, an m2-by-n matrix `ZJ` containing multiple rows of `X` or `Y`, and returning an m2-by-1 vector of distances `D2`, whose jth element is the distance between the observations `ZI` and `ZJ`(j,:).

For more information on these distance metrics, see "Distance Metrics" on page 13-9.

`P`

A positive scalar indicating the exponent of Minkowski distance. This parameter is only valid when `Distance` is `'minkowski'`. Default is 2.

`Cov`

A positive definite matrix indicating the covariance matrix when computing the Mahalanobis distance. This parameter is only valid when `Distance` is `'mahalanobis'`. Default is `nancov(X)`.

`Scale`

A vector `S` with the length equal to the number of columns in `X`. Each coordinate of `X` and each query point is scaled by the corresponding element of `S` when computing the standardized Euclidean distance. This parameter is only valid when `Distance` is `'seuclidean'`. Default is `nanstd(X)`.

Properties

`X`

A matrix used to create the object

`Distance`

A string specifying a built-in distance metric or a function handle that you provide when you create the object. This property is the default distance metric used when you call the `knnsearch` method to find nearest neighbors for future query points.

`DistParameter`

Specifies the additional parameter for the chosen distance metric. The value is:

- If `'Distance'` is `'minkowski'`: A positive scalar indicating the exponent of the Minkowski distance.
- If `'Distance'` is `'mahalanobis'`: A positive definite matrix representing the covariance matrix used for computing the Mahalanobis distance.

- If 'Distance' is 'seuclidean': A vector representing the scale value of the data when computing the 'seuclidean' distance.
- Otherwise: Empty.

Methods

knnsearch	Find k-nearest neighbors using ExhaustiveSearcher object
rangesearch	Find all neighbors within specified distance using object

Examples

Create an ExhaustiveSearcher object using the constructor:

```
load fisheriris
x = meas(:,3:4);
NS = ExhaustiveSearcher(x,'distance','minkowski')

NS =

  ExhaustiveSearcher

  Properties:
                X: [150x2 double]
         Distance: 'minkowski'
    DistParameter: 2
```

Create an ExhaustiveSearcher object using createns:

```
load fisheriris
x = meas(:,3:4);
NS = createns(x,'NsMethod','exhaustive',...
          'distance','minkowski')
```

```
NS =

  ExhaustiveSearcher

  Properties:
                X: [150x2 double]
         Distance: 'minkowski'
    DistParameter: 2
```

For more in-depth examples using the `knnsearch` method, see the method reference page or see “Example: Classifying Query Data Using knnsearch” on page 13-18.

References

[1] Friedman, J. H., Bentely, J. and Finkel, R. A. (1977). *An Algorithm for Finding Best Matches in Logarithmic Expected Time*, ACM Transactions on Mathematical Software 3, 209.

See Also

`createns` | `KDTreeSearcher` | `NeighborSearcher`

How To

- “*k*-Nearest Neighbor Search and Radius Search” on page 13-12
- “Distance Metrics” on page 13-9

Purpose

Exponential inverse cumulative distribution function

Syntax

```
X = expinv(P,mu)
[X,XLO,XUP] = expinv(X,mu,pcov,alpha)
```

Description

`X = expinv(P,mu)` computes the inverse of the exponential `cdf` with parameters specified by mean parameter `mu` for the corresponding probabilities in `P`. `P` and `mu` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `mu` must be positive and the values in `P` must lie on the interval [0 1].

`[X,XLO,XUP] = expinv(X,mu,pcov,alpha)` produces confidence bounds for `X` when the input mean parameter `mu` is an estimate. `pcov` is the variance of the estimated `mu`. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is 0.05. `XLO` and `XUP` are arrays of the same size as `X` containing the lower and upper confidence bounds. The bounds are based on a normal approximation for the distribution of the log of the estimate of `mu`. If you estimate `mu` from a set of data, you can get a more accurate set of bounds by applying `expfit` to the data to get a confidence interval for `mu`, and then evaluating `expinv` at the lower and upper end points of that interval.

The inverse of the exponential cdf is

$$x = F^{-1}(p \mid \mu) = -\mu \ln(1 - p)$$

The result, x, is the value such that an observation from an exponential distribution with parameter μ will fall in the range [0 x] with probability p.

Examples

Let the lifetime of light bulbs be exponentially distributed with $\mu = 700$ hours. What is the median lifetime of a bulb?

```
expinv(0.50,700)
ans =
```

```
    485.2030
```

Suppose you buy a box of “700 hour” light bulbs. If 700 hours is the mean life of the bulbs, half of them will burn out in less than 500 hours.

See Also

`icdf` | `expcdf` | `exppdf` | `expstat` | `expfit` | `explike` | `exprnd`

How To

- “Exponential Distribution” on page B-16

Purpose

Exponential negative log-likelihood

Syntax

```
nlogL = explike(param,data)
[nlogL,avar] = explike(param,data)
[...] = explike(param,data,censoring)
[...] = explike(param,data,censoring,freq)
```

Description

`nlogL = explike(param,data)` returns the negative of the log-likelihood for the exponential distribution. `param` is the mean parameter, `mu`. `nlogL` is a scalar.

`[nlogL,avar] = explike(param,data)` returns the inverse of Fisher's information, `avar`, a scalar. If the input parameter value in `param` is the maximum likelihood estimate, `avar` is its asymptotic variance. `avar` is based on the observed Fisher's information, not the expected information.

`[...] = explike(param,data,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is `1` for observations that are right-censored and `0` for observations that are observed exactly.

`[...] = explike(param,data,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. The vector `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `censoring` to use its default value.

See Also

`expcdf` | `exppdf` | `expstat` | `expfit` | `expinv` | `exprnd`

How To

- "Exponential Distribution" on page B-16

dataset.export

Purpose

Write dataset array to file

Syntax

```
export(DS,'file',filename)
export(DS)
export(DS,'file',filename,'Delimiter',delim)
export(DS,'XLSfile',filename)
export(DS,'XPTFile',filename)
export(DS,...,'WriteVarNames',false)
export(DS,...,'WriteObsNames',false)
```

Description

`export(DS,'file',filename)` writes the dataset array `DS` to a tab-delimited text file, including variable names and observation names, if present. If the observation names exist, the name in the first column of the first line of the file is the first dimension name for the dataset (by default, `'Observations'`). `export` overwrites any existing file named `filename`.

`export(DS)` writes to a text file whose default name is the name of the dataset array `DS` appended by `'.txt'`. If `export` cannot construct the file name from the dataset array input, it writes to the file `'dataset.txt'`. `export` overwrites any existing file.

`export(DS,'file',filename,'Delimiter',delim)` writes the dataset array `DS` to a text file using the delimiter `delim`. `delim` must be one of the following:

- `' '` or `'space'`
- `'\t'` or `'tab'`
- `','` or `'comma'`
- `';'` or `'semi'`
- `'|'` or `'bar'`

`export(DS,'XLSfile',filename)` writes the dataset array `DS` to a Microsoft® Excel® spreadsheet file, including variable names and observation names (if present). You can specify the `'Sheet'` and

'Range' parameter name/value pairs, with parameter values as accepted by the xlsread function.

export(DS,'XPTFile',filename) writes the dataset array DS to a SAS XPORT format file. When writing to an XPORT format file, variables must be scalar valued. export saves observation names to a variable called obsnames, unless the WriteObsNames parameter described below is false. The XPORT format restricts the length of variable names to eight characters; longer variable names are truncated.

export(DS,...,'WriteVarNames',false) does not write the variable names to the text file. export(DS,...,'WriteVarNames',true) is the default, writing the names as column headings in the first line of the file.

export(DS,...,'WriteObsNames',false) does not write the observation names to the text file. export(DS,...,'WriteObsNames',true) is the default, writing the names as the first column of the file.

In some cases, export creates a text file that does not represent A exactly, as described below. If you use dataset to read the file back into MATLAB, the new dataset array may not have exactly the same contents as the original dataset array. Save A as a MAT-file if you need to import it again as a dataset array.

export writes out numeric variables using long g format, and categorical or character variables as unquoted strings.

For non-character variables with more than one column, export writes out multiple delimiter-separated fields on each line, and constructs suitable column headings for the first line of the file.

export writes out variables that have more than two dimensions as a single empty field in each line of the file.

For cell-valued variables, export writes out the contents of each cell only when the cell contains a single row, and writes out a single empty field otherwise.

In some cases, `export` creates a file that cannot be read back into MATLAB using `dataset`. Writing a dataset array that contains a cell-valued variable whose cell contents are not scalars results in a mismatch in the file between the number of fields on each line and the number of column headings on the first line. Writing a dataset array that contains a cell-valued variable whose cell contents are not all the same length results in a different number of fields on each line in the file. Therefore, if you might need to import a dataset array again, save it as a `.mat` file.

Examples

Move data between external text files and dataset arrays in the MATLAB workspace:

```
A = dataset('file','sat2.dat','delimiter',',')
A =
    Test                  Gender          Score
    'Verbal'              'Male'          470
    'Verbal'              'Female'        530
    'Quantitative'        'Male'          520
    'Quantitative'        'Female'        480

export(A(A.Score > 500,:),'file','HighScores.txt')

B = dataset('file','HighScores.txt','delimiter','\t')
B =
    Test                  Gender          Score
    'Verbal'              'Female'        530
    'Quantitative'        'Male'          520
```

See Also

`dataset`

Purpose

Exponential probability density function

Syntax

```
Y = exppdf(X,mu)
```

Description

`Y = exppdf(X,mu)` returns the pdf of the exponential distribution with mean parameter `mu`, evaluated at the values in `X`. `X` and `mu` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `mu` must be positive.

The exponential pdf is

$$y = f(x \mid \mu) = \frac{1}{\mu} e^{\frac{-x}{\mu}}$$

The exponential pdf is the gamma pdf with its first parameter equal to 1.

The exponential distribution is appropriate for modeling waiting times when the probability of waiting an additional period of time is independent of how long you have already waited. For example, the probability that a light bulb will burn out in its next minute of use is relatively independent of how many minutes it has already burned.

Examples

```
y = exppdf(5,1:5)
y =
  0.0067  0.0410  0.0630  0.0716  0.0736

y = exppdf(1:5,1:5)
y =
  0.3679  0.1839  0.1226  0.0920  0.0736
```

See Also

`pdf` | `expcdf` | `expinv` | `expstat` | `expfit` | `explike` | `exprnd`

How To

- "Exponential Distribution" on page B-16

exprnd

Purpose

Exponential random numbers

Syntax

```
R = exprnd(mu)
R = exprnd(mu,m,n,...)
R = exprnd(mu,[m,n,...])
```

Description

`R = exprnd(mu)` generates random numbers from the exponential distribution with mean parameter `mu`. `mu` can be a vector, a matrix, or a multidimensional array. The size of `R` is the size of `mu`.

`R = exprnd(mu,m,n,...)` or `R = exprnd(mu,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the exponential distribution with mean parameter `mu`. `mu` can be a scalar or an array of the same size as `R`.

Examples

```
n1 = exprnd(5:10)
n1 =
  7.5943  18.3400  2.7113  3.0936  0.6078  9.5841

n2 = exprnd(5:10,[1 6])
n2 =
  3.2752  1.1110  23.5530  23.4303  5.7190  3.9876

n3 = exprnd(5,2,3)
n3 =
  24.3339  13.5271  1.8788
   4.7932   4.3675  2.6468
```

See Also

`random` | `expcdf` | `exppdf` | `expstat` | `expfit` | `explike` | `expinv`

How To

- "Exponential Distribution" on page B-16

Purpose

Exponential mean and variance

Syntax

```
[m,v] = expstat(mu)
```

Description

`[m,v] = expstat(mu)` returns the mean of and variance for the exponential distribution with parameters `mu`. `mu` can be a vectors, matrix, or multidimensional array. The mean of the exponential distribution is μ, and the variance is μ^2.

Examples

```
[m,v] = expstat([1 10 100 1000])
m =
      1     10     100     1000
v =
      1     100    10000   1000000
```

See Also

`expinv` | `expcdf` | `exppdf` | `expstat` | `expfit` | `explike` | `exprnd`

How To

- "Exponential Distribution" on page B-16

factoran

Purpose

Factor analysis

Syntax

```
lambda = factoran(X,m)
[lambda,psi] = factoran(X,m)
[lambda,psi,T] = factoran(X,m)
[lambda,psi,T,stats] = factoran(X,m)
[lambda,psi,T,stats,F] = factoran(X,m)
[...] = factoran(...,param1,val1,param2,val2,...)
```

Definitions

`factoran` computes the maximum likelihood estimate (MLE) of the factor loadings matrix Λ in the factor analysis model

$$x = \mu + \Lambda f + e$$

where x is a vector of observed variables, μ is a constant vector of means, Λ is a constant d-by-m matrix of factor loadings, f is a vector of independent, standardized common factors, and e is a vector of independent specific factors. x, μ, and e are of length d. f is of length m.

Alternatively, the factor analysis model can be specified as

$$\mathrm{cov}(x) = \Lambda\Lambda^T + \Psi$$

where $\Psi = \mathrm{cov}(e)$ is a d-by-d diagonal matrix of specific variances.

Description

`lambda = factoran(X,m)` returns the maximum likelihood estimate, `lambda`, of the factor loadings matrix, in a common factor analysis model with `m` common factors. `X` is an `n`-by-`d` matrix where each row is an observation of `d` variables. The `(i,j)`th element of the `d`-by-`m` matrix `lambda` is the coefficient, or loading, of the `j`th factor for the `i`th variable. By default, `factoran` calls the function `rotatefactors` to rotate the estimated factor loadings using the `'varimax'` option.

`[lambda,psi] = factoran(X,m)` also returns maximum likelihood estimates of the specific variances as a column vector `psi` of length `d`.

`[lambda,psi,T] = factoran(X,m)` also returns the `m`-by-`m` factor loadings rotation matrix `T`.

`[lambda,psi,T,stats] = factoran(X,m)` also returns a structure `stats` containing information relating to the null hypothesis, H_0, that the number of common factors is `m`. `stats` includes the following fields:

Field	Description
`loglike`	Maximized log-likelihood value
`dfe`	Error degrees of freedom = `((d-m)^2 - (d+m))/2`
`chisq`	Approximate chi-squared statistic for the null hypothesis
`p`	Right-tail significance level for the null hypothesis

`factoran` does not compute the `chisq` and `p` fields unless `dfe` is positive and all the specific variance estimates in `psi` are positive (see "Heywood Case" on page 20-537 below). If `X` is a covariance matrix, then you must also specify the `'nobs'` parameter if you want `factoran` to compute the `chisq` and `p` fields.

`[lambda,psi,T,stats,F] = factoran(X,m)` also returns, in `F`, predictions of the common factors, known as factor scores. `F` is an `n`-by-`m` matrix where each row is a prediction of `m` common factors. If `X` is a covariance matrix, `factoran` cannot compute `F`. `factoran` rotates `F` using the same criterion as for `lambda`.

`[...] = factoran(...,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` enables you to specify optional parameter name/value pairs to control the model fit and the outputs. The following are the valid parameter/value pairs.

Parameter	Value	
`'xtype'`	Type of input in the matrix `X`. `'xtype'` can be one of:	
	`'data'`	Raw data (default)
	`'covariance'`	Positive definite covariance or correlation matrix

Parameter	Value	
'scores'	Method for predicting factor scores. 'scores' is ignored if X is not raw data.	
	'wls' 'Bartlett'	Synonyms for a weighted least-squares estimate that treats F as fixed (default)
	'regression' 'Thomson'	Synonyms for a minimum mean squared error prediction that is equivalent to a ridge regression
'start'	Starting point for the specific variances psi in the maximum likelihood optimization. Can be specified as:	
	'random'	Chooses d uniformly distributed values on the interval [0,1].
	'Rsquared'	Chooses the starting vector as a scale factor times diag(inv(corrcoef(X))) (default). For examples, see Jöreskog [2].
	Positive integer	Performs the given number of maximum likelihood fits, each initialized as with 'random'. factoran returns the fit with the highest likelihood.
	Matrix	Performs one maximum likelihood fit for each column of the specified matrix. The ith optimization is initialized with the values from the ith column. The matrix must have d rows.

Parameter	Value	
'rotate'	Method used to rotate factor loadings and scores. 'rotate' can have the same values as the 'Method' parameter of rotatefactors. See the reference page for rotatefactors for a full description of the available methods.	
	'none'	Performs no rotation.
	'equamax'	Special case of the orthomax rotation. Use the 'normalize', 'reltol', and 'maxit' parameters to control the details of the rotation.
	'orthomax'	Orthogonal rotation that maximizes a criterion based on the variance of the loadings. Use the 'coeff', 'normalize', 'reltol', and 'maxit' parameters to control the details of the rotation.
	'parsimax'	Special case of the orthomax rotation (default). Use the 'normalize', 'reltol', and 'maxit' parameters to control the details of the rotation.
	'pattern'	Performs either an oblique rotation (the default) or an orthogonal rotation to best match a specified pattern matrix. Use the 'type' parameter to choose the type of rotation. Use the 'target' parameter to specify the pattern matrix.

Parameter	Value	
	`'procrustes'`	Performs either an oblique (the default) or an orthogonal rotation to best match a specified target matrix in the least squares sense. Use the `'type'` parameter to choose the type of rotation. Use `'target'` to specify the target matrix.
	`'promax'`	Performs an oblique procrustes rotation to a target matrix determined by `factoran` as a function of an orthomax solution. Use the `'power'` parameter to specify the exponent for creating the target matrix. Because `'promax'` uses `'orthomax'` internally, you can also specify the parameters that apply to `'orthomax'`.
	`'quartimax'`	Special case of the orthomax rotation (default). Use the `'normalize'`, `'reltol'`, and `'maxit'` parameters to control the details of the rotation.
	`'varimax'`	Special case of the orthomax rotation (default). Use the `'normalize'`, `'reltol'`, and `'maxit'` parameters to control the details of the rotation.

Parameter	Value	
	Function	Function handle to rotation function of the form `[B,T] = myrotation(A,...)` where `A` is a `d`-by-`m` matrix of unrotated factor loadings, `B` is a `d`-by-`m` matrix of rotated loadings, and `T` is the corresponding `m`-by-`m` rotation matrix. Use the `factoran` parameter `'userargs'` to pass additional arguments to this rotation function. See "Example 4" on page 20-542.
`'coeff'`	Coefficient, often denoted as γ, defining the specific `'orthomax'` criterion. Must be from `0` to `1`. The value `0` corresponds to quartimax, and `1` corresponds to varimax. Default is `1`.	
`'normalize'`	Flag indicating whether the loading matrix should be row-normalized (1) or left unnormalized (0) for `'orthomax'` or `'varimax'` rotation. Default is 1.	
`'reltol'`	Relative convergence tolerance for `'orthomax'` or `'varimax'` rotation. Default is `sqrt(eps)`.	
`'maxit'`	Iteration limit for `'orthomax'` or `'varimax'` rotation. Default is `250`.	
`'target'`	Target factor loading matrix for `'procrustes'` rotation. Required for `'procrustes'` rotation. No default value.	
`'type'`	Type of `'procrustes'` rotation. Can be `'oblique'` (default) or `'orthogonal'`.	

Parameter	Value
'power'	Exponent for creating the target matrix in the 'promax' rotation. Must be ≥ 1. Default is 4.
'userargs'	Denotes the beginning of additional input values for a user-defined rotation function. factoran appends all subsequent values, in order and without processing, to the rotation function argument list, following the unrotated factor loadings matrix A. See "Example 4" on page 20-542.
'nobs'	If X is a covariance or correlation matrix, indicates the number of observations that were used in its estimation. This allows calculation of significance for the null hypothesis even when the original data are not available. There is no default. 'nobs' is ignored if X is raw data.
'delta'	Lower bound for the specific variances psi during the maximum likelihood optimization. Default is 0.005.
'optimopts'	Structure that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates. Create this structure with the function statset. Enter statset('factoran') to see the names and default values of the parameters that factoran accepts in the options structure. See the reference page for statset for more information about these options.

Tips

Observed Data Variables

The variables in the observed data matrix X must be linearly independent, i.e., cov(X) must have full rank, for maximum likelihood estimation to succeed. factoran reduces both raw data and a covariance matrix to a correlation matrix before performing the fit.

`factoran` standardizes the observed data `X` to zero mean and unit variance before estimating the loadings `lambda`. This does not affect the model fit, because MLEs in this model are invariant to scale. However, `lambda` and `psi` are returned in terms of the standardized variables, i.e., `lambda*lambda'+diag(psi)` is an estimate of the correlation matrix of the original data `X` (although not after an oblique rotation). See "Example 1" on page 20-537 and "Example 3" on page 20-539.

Heywood Case

If elements of `psi` are equal to the value of the `'delta'` parameter (i.e., they are essentially zero), the fit is known as a Heywood case, and interpretation of the resulting estimates is problematic. In particular, there can be multiple local maxima of the likelihood, each with different estimates of the loadings and the specific variances. Heywood cases can indicate overfitting (i.e., `m` is too large), but can also be the result of underfitting.

Rotation of Factor Loadings and Scores

Unless you explicitly specify no rotation using the `'rotate'` parameter, `factoran` rotates the estimated factor loadings, `lambda`, and the factor scores, `F`. The output matrix `T` is used to rotate the loadings, i.e., `lambda = lambda0*T`, where `lambda0` is the initial (unrotated) MLE of the loadings. `T` is an orthogonal matrix for orthogonal rotations, and the identity matrix for no rotation. The inverse of `T` is known as the primary axis rotation matrix, while `T` itself is related to the reference axis rotation matrix. For orthogonal rotations, the two are identical.

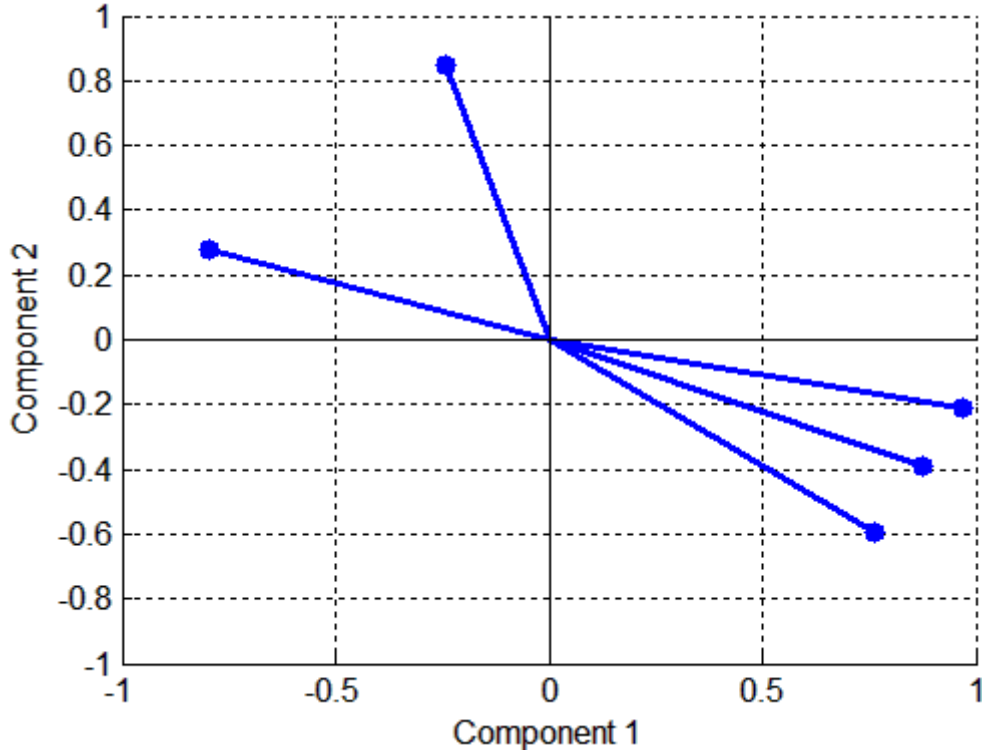
`factoran` computes factor scores that have been rotated by `inv(T')`, i.e., `F = F0 * inv(T')`, where `F0` contains the unrotated predictions. The estimated covariance of `F` is `inv(T'*T)`, which, for orthogonal or no rotation, is the identity matrix. Rotation of factor loadings and scores is an attempt to create a more easily interpretable structure in the loadings matrix after maximum likelihood estimation.

Examples

Example 1

Load the `carbig` data, and fit the default model with two factors.

```
load carbig

X = [Acceleration Displacement Horsepower MPG Weight];
X = X(all(~isnan(X),2),:);
[Lambda,Psi,T,stats,F] = factoran(X,2,...
                                  'scores','regression');
inv(T'*T) % Estimated correlation matrix of F, == eye(2)
Lambda*Lambda'+diag(Psi) % Estimated correlation matrix
Lambda*inv(T)            % Unrotate the loadings
F*T'                     % Unrotate the factor scores

biplot(Lambda,...        % Create biplot of two factors
       'LineWidth',2,...
       'MarkerSize',20)
```



Example 2

Although the estimates are the same, the use of a covariance matrix rather than raw data doesn't let you request scores or significance level:

```
[Lambda,Psi,T] = factoran(cov(X),2,'xtype','cov')
[Lambda,Psi,T] = factoran(corrcoef(X),2,'xtype','cov')
```

Example 3

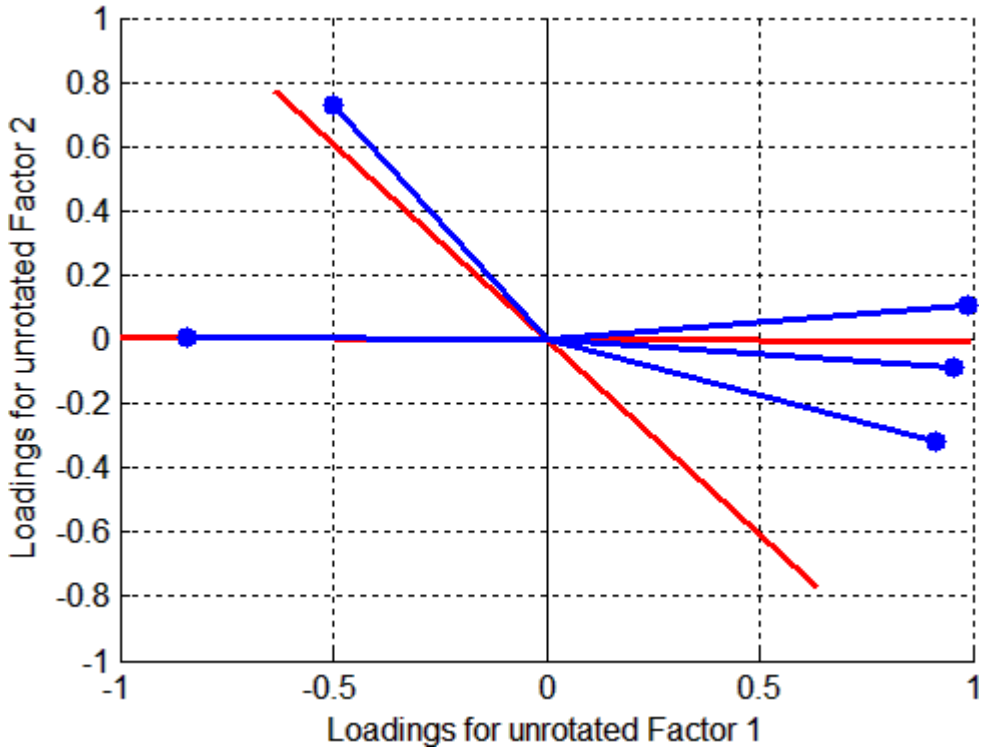
Use promax rotation:

```
[Lambda,Psi,T,stats,F] = factoran(X,2,'rotate','promax',...
                                      'powerpm',4);
```

```
inv(T'*T)                               % Est'd corr of F,
                                        % no longer eye(2)
Lambda*inv(T'*T)*Lambda'+diag(Psi)   % Est'd corr of X
```

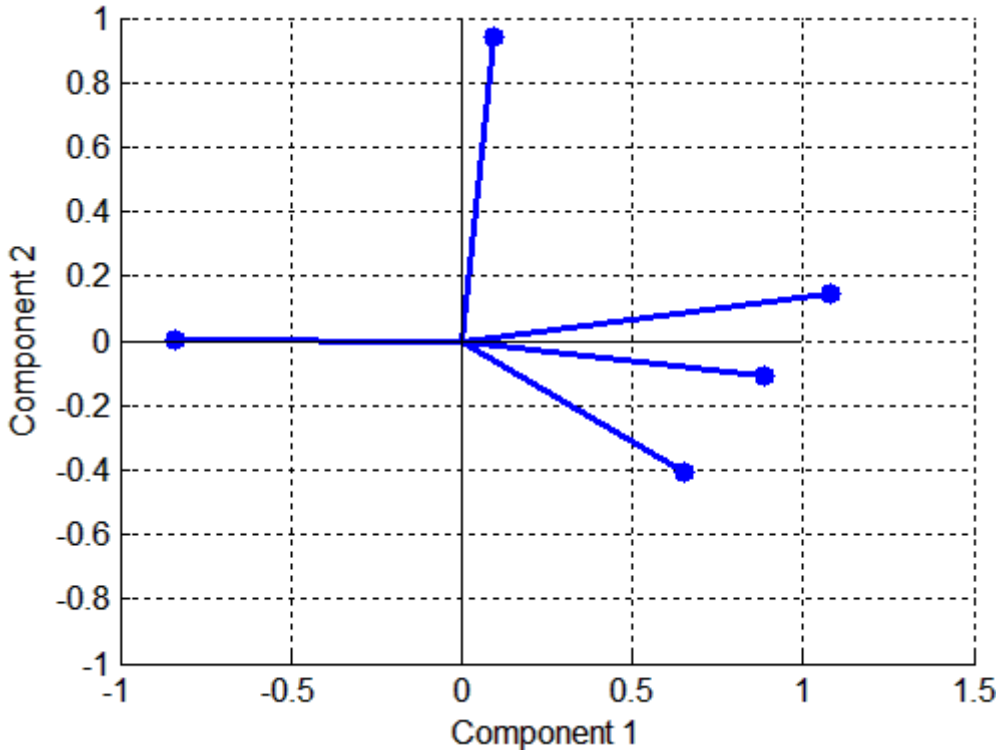
Plot the unrotated variables with oblique axes superimposed.

```
invT = inv(T)
Lambda0 = Lambda*invT

line([-invT(1,1) invT(1,1) NaN -invT(2,1) invT(2,1)], ...
     [-invT(1,2) invT(1,2) NaN -invT(2,2) invT(2,2)], ...
     'Color','r','linewidth',2)
hold on
biplot(Lambda0,...
       'LineWidth',2,...
       'MarkerSize',20)
xlabel('Loadings for unrotated Factor 1')
ylabel('Loadings for unrotated Factor 2')
```



Plot the rotated variables against the oblique axes:

```
biplot(Lambda,'LineWidth',2,'MarkerSize',20)
```



Example 4

Syntax for passing additional arguments to a user-defined rotation function:

```
[Lambda,Psi,T] = ...
     factoran(X,2,'rotate',@myrotation,'userargs',1,'two');
```

References

[1] Harman, H. H. *Modern Factor Analysis*. 3rd Ed. Chicago: University of Chicago Press, 1976.

[2] Jöreskog, K. G. "Some Contributions to Maximum Likelihood Factor Analysis." *Psychometrika*. Vol. 32, Issue 4, 1967, pp. 443–482.

[3] Lawley, D. N., and A. E. Maxwell. *Factor Analysis as a Statistical Method.* 2nd Ed. New York: American Elsevier Publishing Co., 1971.

See Also

`biplot` | `princomp` | `procrustes` | `pcacov` | `rotatefactors` | `statset`

TreeBagger.FBoot property

Purpose

Fraction of in-bag observations

Description

The `FBoot` property is the fraction of observations to be randomly selected with replacement for each bootstrap replica. The size of each replica is given by `n*FBoot`, where `n` is the number of observations in the training set. The default value is 1.

Purpose

F cumulative distribution function

Syntax

```
P = fcdf(X,V1,V2)
```

Description

`P = fcdf(X,V1,V2)` computes the F cdf at each of the values in `X` using the corresponding numerator degrees of freedom `V1` and denominator degrees of freedom `V2`. `X`, `V1`, and `V2` can be vectors, matrices, or multidimensional arrays that are all the same size. A scalar input is expanded to a constant matrix with the same dimensions as the other inputs. `V1` and `V2` parameters must contain real positive values.

The F cdf is

$$p = F(x \mid \nu_1,\nu_2) = \int_0^x \frac{\Gamma\left[\frac{(\nu_1+\nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}} \frac{t^{\frac{\nu_1-2}{2}}}{\left[1+\left(\frac{\nu_1}{\nu_2}\right)t\right]^{\frac{\nu_1+\nu_2}{2}}}\,dt$$

The result, p, is the probability that a single observation from an F distribution with parameters ν_1 and ν_2 will fall in the interval $[0\ x]$.

Examples

The following illustrates a useful mathematical identity for the F distribution:

```
nu1 = 1:5;
nu2 = 6:10;
x = 2:6;

F1 = fcdf(x,nu1,nu2)
F1 =
  0.7930  0.8854  0.9481  0.9788  0.9919

F2 = 1 - fcdf(1./x,nu2,nu1)
F2 =
  0.7930  0.8854  0.9481  0.9788  0.9919
```

See Also `cdf` | `fpdf` | `finv` | `fstat` | `frnd`

How To

- "F Distribution" on page B-25

Purpose

Two-level full factorial design

Syntax

```
dFF2 = ff2n(n)
```

Description

`dFF2 = ff2n(n)` gives factor settings `dFF2` for a two-level full factorial design with `n` factors. `dFF2` is m-by-`n`, where m is the number of treatments in the full-factorial design. Each row of `dFF2` corresponds to a single treatment. Each column contains the settings for a single factor, with values of `0` and `1` for the two levels.

Examples

```
dFF2 = ff2n(3)
dFF2 =
   0   0   0
   0   0   1
   0   1   0
   0   1   1
   1   0   0
   1   0   1
   1   1   0
   1   1   1
```

See Also

`fullfact`

TreeBagger.fillProximities

Purpose

Proximity matrix for training data

Syntax

```
B = fillProximities(B)
B = fillProximities(B,'param1',val1,'param2',val2,...
```

Description

`B = fillProximities(B)` computes a proximity matrix for the training data and stores it in the Properties field of B.

`B = fillProximities(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'trees'`	Either `'all'` or a vector of indices of the trees in the ensemble to be used in computing the proximity matrix. Default is `'all'`.
`'nprint'`	Number of training cycles (grown trees) after which `TreeBagger` displays a diagnostic message showing training progress. Default is no diagnostic messages.

See Also

`CompactTreeBagger.outlierMeasure` | `CompactTreeBagger.proximity`

Purpose

Find objects matching specified conditions

Syntax

```
hm = findobj(h, 'conditions')
```

Description

The `findobj` method of the `handle` class follows the same syntax as the MATLAB `findobj` command, except that the first argument must be an array of handles to objects.

`hm = findobj(h, 'conditions')` searches the handle object array `h` and returns an array of handle objects matching the specified conditions. Only the public members of the objects of `h` are considered when evaluating the conditions.

See Also

`findobj` | `qrandstream`

qrandstream.findprop

Purpose

Find property of MATLAB handle object

Syntax

```
p = findprop(h,'propname')
```

Description

`p = findprop(h,'propname')` finds and returns the `meta.property` object associated with property name `propname` of scalar handle object `h`. `propname` must be a string. It can be the name of a property defined by the class of `h` or a dynamic property added to scalar object `h`.

If no property named `propname` exists for object `h`, an empty `meta.property` array is returned.

See Also

`dynamicprops` | `findobj` | `meta.property` | `qrandstream`

Purpose

F inverse cumulative distribution function

Syntax

```
X = finv(P,V1,V2)
```

Description

`X = finv(P,V1,V2)` computes the inverse of the *F* cdf with numerator degrees of freedom `V1` and denominator degrees of freedom `V2` for the corresponding probabilities in `P`. `P`, `V1`, and `V2` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

`V1` and `V2` parameters must contain real positive values, and the values in `P` must lie on the interval [0 1].

The *F* inverse function is defined in terms of the *F* cdf as

$$x = F^{-1}(p \mid \nu_1,\nu_2) = \{x : F(x \mid \nu_1,\nu_2) = p\}$$

where

$$p = F(x \mid \nu_1,\nu_2) = \int_0^x \frac{\Gamma\left[\frac{(\nu_1+\nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}} \frac{t^{\frac{\nu_1-2}{2}}}{\left[1+\left(\frac{\nu_1}{\nu_2}\right)t\right]^{\frac{\nu_1+\nu_2}{2}}}\,dt$$

Examples

Find a value that should exceed 95% of the samples from an *F* distribution with 5 degrees of freedom in the numerator and 10 degrees of freedom in the denominator.

```
x = finv(0.95,5,10)
x =
  3.3258
```

You would observe values greater than 3.3258 only 5% of the time by chance.

See Also `icdf` | `fcdf` | `fpdf` | `fstat` | `frnd`

How To

- “F Distribution” on page B-25

Purpose

Fit discriminant analysis classifier

Syntax

```
obj = ClassificationDiscriminant.fit(X,Y)
obj = ClassificationDiscriminant.fit(X,Y,Name,Value)
```

Description

`obj = ClassificationDiscriminant.fit(X,Y)` returns a discriminant analysis classifier based on the input variables (also known as predictors, features, or attributes) `X` and output (response) `Y`.

`obj = ClassificationDiscriminant.fit(X,Y,Name,Value)` fits a classifier with additional options specified by one or more `Name,Value` pair arguments. If you use one of the following five options, `obj` is of class `ClassificationPartitionedModel`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Otherwise, `obj` is of class `ClassificationDiscriminant`.

Input Arguments

`X`

Matrix of numeric predictor values. Each column of `X` represents one variable, and each row represents one observation.

`ClassificationDiscriminant.fit` considers `NaN` values in `X` as missing values. `ClassificationDiscriminant.fit` does not use observations with missing values for `X` in the fit.

`Y`

Numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding row of `X`.

`ClassificationDiscriminant.fit` considers `NaN` values in `Y` to be missing values. `ClassificationDiscriminant.fit` does not use observations with missing values for `Y` in the fit.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must

appear inside single quotes (''). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`ClassNames`

Array of class names. Use the data type that exists in `Y`.

Use `ClassNames` to order the classes or to select a subset of classes for training.

Default: Class names that exist in `Y`

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. Alternatively, `Cost` can be a structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same type as `Y`, and `S.ClassificationCosts` containing the cost matrix.

Default: `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`

`crossval`

If `'on'`, creates a cross-validated classifier with 10 folds. You can use `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'` parameters to override this cross-validation setting. You can only use one of these options at a time for creating a cross-validated classifier: `'cvpartition'`, `'holdout'`, `'kfold'`, or `'leaveout'`.

Alternatively, cross validate `obj` later using the `crossval` method.

Default: `'off'`

`cvpartition`

Partition created with `cvpartition` to use in a cross-validated classifier. You can only use one of these options at a time for creating a cross-validated classifier: `'cvpartition'`, `'holdout'`, `'kfold'`, or `'leaveout'`.

`discrimType`

String specifying the discriminant type. Case-insensitive. One of:

- `'linear'`
- `'quadratic'`
- `'diagLinear'`
- `'diagQuadratic'`
- `'pseudoLinear'`
- `'pseudoQuadratic'`

Default: `'linear'`

`fillCoeffs`

String, either `'on'` or `'off'`, specifying whether to populate the `Coeffs` property in the classifier object. Setting to `'on'` can be computationally intensive, especially when cross validating.

Default: `'on'`, except `'off'` when cross validating

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these options at a time for creating a cross-validated classifier: `'cvpartition'`, `'holdout'`, `'kfold'`, or `'leaveout'`.

`kfold`

Number of folds to use in a cross-validated classifier, a positive integer. You can only use one of these options at a time for creating a cross-validated classifier: `'cvpartition'`, `'holdout'`, `'kfold'`, or `'leaveout'`.

Default: `10`

`leaveout`

Use leave-one-out cross validation by setting to `'on'`. You can only use one of these options at a time for creating a cross-validated classifier: `'cvpartition'`, `'holdout'`, `'kfold'`, or `'leaveout'`.

`PredictorNames`

Cell array of names for the predictor variables, in the order in which they appear in `X`.

Default: `{'x1','x2',...}`

`prior`

Prior probabilities for each class. Specify as one of:

- A string:
  - `'empirical'` determines class probabilities from class frequencies in `Y`. If you pass observation weights, they are used to compute the class probabilities.
  - `'uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class)
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as `Y`
  - `S.ClassProbs` containing a vector of corresponding probabilities

Default: `'empirical'`

`ResponseName`

Name of the response variable `Y`, a string.

Default: `'Y'`

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function.

String	Formula
`'symmetric'`	$2x - 1$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'symmetricismax'`	Set score for the class with the largest score to `1`, and scores for all other classes to `-1`.
`'none'`	x
`'logit'`	$1/(1 + e^{-x})$
`'doublelogit'`	$1/(1 + e^{-2x})$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$

You can include your own function handle for transforming scores. Your function should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Default: `'none'`

`weights`

Vector of observation weights. The length of `weights` is the number of rows in `X`. `ClassificationDiscriminant.fit` normalizes the weights to sum to 1.

Default: `ones(size(X,1),1)`

Output Arguments

`obj`

Discriminant analysis classifier. You can use `obj` to predict the response of new data using the `predict` method.

Definitions

Discriminant Classification

The model for discriminant analysis is:

- Each class (`Y`) generates data (`X`) using a multivariate normal distribution. That is, the model assumes `X` has a Gaussian mixture distribution (`gmdistribution`).
  - For linear discriminant analysis, the model has the same covariance matrix for each class, only the means vary.
  - For quadratic discriminant analysis, both means and covariances of each class vary.

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \arg\min_{y=1,\ldots,K} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

For details, see “How the predict Method Classifies” on page 12-6.

Examples

Construct a discriminant analysis classifier for the Fisher iris data:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species)

obj =
ClassificationDiscriminant:
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
         ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
     NObservations: 150
       DiscrimType: 'linear'
                Mu: [3x4 double]
            Coeffs: [3x3 struct]
```

Alternatives

The `classify` function also performs discriminant analysis. `classify` is usually more awkward to use:

- `classify` requires you to fit the classifier every time you make a new prediction.
- `classify` does not perform cross validation.
- `classify` requires you to fit the classifier when changing prior probabilities.

See Also

`ClassificationDiscriminant` | `ClassificationTree.fit`

How To

- “Discriminant Analysis” on page 12-3

ClassificationTree.fit

Purpose

Fit classification tree

Syntax

```
tree = ClassificationTree.fit(X,Y)
tree = ClassificationTree.fit(X,Y,Name,Value)
```

Description

`tree = ClassificationTree.fit(X,Y)` returns a classification tree based on the input variables (also known as predictors, features, or attributes) `X` and output (response) `Y`. `tree` is a binary tree, where each branching node is split based on the values of a column of `X`.

`tree = ClassificationTree.fit(X,Y,Name,Value)` fits a tree with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`. If you use one of the following five options, `tree` is of class `ClassificationPartitionedModel`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Otherwise, `tree` is of class `ClassificationTree`.

Input Arguments

`X`

A matrix of numeric predictor values. Each column of `X` represents one variable, and each row represents one observation.

`ClassificationTree.fit` considers `NaN` values in `X` as missing values. `ClassificationTree.fit` does not use observations with all missing values for `X` in the fit. `ClassificationTree.fit` uses observations with some missing values for `X` to find splits on variables for which these observations have valid values.

`Y`

A numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding row of `X`. For numeric `Y`, consider using `RegressionTree.fit` instead of `ClassificationTree.fit`.

`ClassificationTree.fit` considers `NaN` values in `Y` to be missing values. `ClassificationTree.fit` does not use observations with missing values for `Y` in the fit.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`CategoricalPredictors`

List of categorical predictors. Pass `CategoricalPredictors` as one of:

- A numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of `X` is a categorical variable.
- `'all'`, meaning all predictors are categorical.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in `PredictorNames` values.
- A character matrix, where each row of the matrix is a name of a predictor variable. The names must match entries in `PredictorNames` values. Pad the names with extra blanks so each row of the character matrix has the same length.

Default: `[]`

`ClassNames`

Array of class names. Use the data type that exists in `Y`.

Use `ClassNames` to order the classes or to select a subset of classes for training.

Default: The class names that exist in `Y`

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. Alternatively, `Cost` can be a structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same type as `Y`, and `S.ClassificationCosts` containing the cost matrix.

Default: `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`

`crossval`

If `'on'`, grows a cross-validated decision tree with 10 folds. You can use `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'` parameters to override this cross-validation setting. You can only use one of these four parameters (`'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`) at a time when creating a cross-validated tree.

Alternatively, cross validate `tree` later using the `crossval` method.

Default: `'off'`

`cvpartition`

Partition created with `cvpartition` to use in a cross-validated tree. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`kfold`

Number of folds to use in a cross-validated tree, a positive integer. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: `10`

`leaveout`

Use leave-one-out cross validation by setting to `'on'`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`MergeLeaves`

When `'on'`, `ClassificationTree.fit` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, `ClassificationTree.fit` does not merge leaves.

Default: `'on'`

`MinLeaf`

Each leaf has at least `MinLeaf` observations per tree leaf. If you supply both `MinParent` and `MinLeaf`, `ClassificationTree.fit` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: `1`

`MinParent`

Each branch node in the tree has at least `MinParent` observations. If you supply both `MinParent` and `MinLeaf`, `ClassificationTree.fit` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: `10`

`NVarToSample`

Number of predictors to select at random for each split. Can be a positive integer or `'all'`, which means use all available predictors.

Default: `'all'`

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

Default: `{'x1','x2',...}`

`prior`

Prior probabilities for each class. Specify as one of:

- A string:
  - `'empirical'` determines class probabilities from class frequencies in `Y`. If you pass observation weights, they are used to compute the class probabilities.
  - `'uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class)
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as `Y`
  - `S.ClassProbs` containing a vector of corresponding probabilities

If you set values for both `weights` and `prior`, the weights are renormalized to add up to the value of the prior probability in the respective class.

Default: `'empirical'`

`Prune`

When `'on'`, `ClassificationTree.fit` grows the classification tree, and computes the optimal sequence of pruned subtrees. When `'off'` `ClassificationTree.fit` grows the classification tree without pruning.

Default: `'on'`

`PruneCriterion`

String with the pruning criterion, either `'error'` or `'impurity'`.

Default: `'error'`

`ResponseName`

Name of the response variable `Y`, a string.

Default: `'Response'`

`ScoreTransform`

Function handle for transforming scores, or string representing a built-in transformation function.

String	Formula
`'symmetric'`	$2x - 1$
`'invlogit'`	$\log(x / (1-x))$

String	Formula
`'ismax'`	Set score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'symmetricismax'`	Set score for the class with the largest score to `1`, and scores for all other classes to `-1`.
`'none'`	x
`'logit'`	$1/(1 + e^{-x})$
`'doublelogit'`	$1/(1 + e^{-2x})$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$

You can include your own function handle for transforming scores. Your function should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Default: `'none'`

`SplitCriterion`

Criterion for choosing a split. One of `'gdi'` (Gini's diversity index), `'twoing'` for the twoing rule, or `'deviance'` for maximum deviance reduction (also known as cross entropy).

Default: `'gdi'`

`Surrogate`

When `'on'`, `ClassificationTree.fit` finds surrogate splits at each branch node. This setting improves the accuracy of predictions for data with missing values. The setting also enables

you to compute measures of predictive association between predictors. This setting can use much time and memory.

Default: `'off'`

`weights`

Vector of observation weights. The length of `weights` is the number of rows in `X`. `ClassificationTree.fit` normalizes the weights in each class to add up to the value of the prior probability of the class.

Default: `ones(size(X,1),1)`

Output Arguments

`tree`

A classification tree object. You can use `tree` to predict the response of new data with the `predict` method.

Definitions

Impurity and Node Error

`ClassificationTree` splits nodes based on either *impurity* or *node error*. Impurity means one of several things, depending on your choice of the `SplitCriterion` name-value pair:

- Gini's Diversity Index (`gdi`) — The Gini index of a node is

  $$1 - \sum_i p^2(i),$$

  where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index `0`; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.
- Deviance (`'deviance'`) — With $p(i)$ defined as for the Gini index, the deviance of a node is

$$-\sum_i p(i)\log p(i).$$

A pure node has deviance `0`; otherwise, the deviance is positive.

- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

$$P(L)P(R)\left(\sum_i |L(i)-R(i)|\right)^2,$$

where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.

- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with largest number of training samples at a node, the node error is

$$1-p(j).$$

Examples

Construct a classification tree for the data in `ionosphere.mat`:

```
load ionosphere
tc = ClassificationTree.fit(X,Y)

tc =
ClassificationTree:
           VarNames: {1x34 cell}
    CategoricalVars: []
         ClassNames: {'b'  'g'}
               Cost: [2x2 double]
              Prior: [0.3590 0.6410]
     TransformScore: 'none'
                  X: [351x34 double]
                  Y: {351x1 cell}
                  W: [351x1 double]
        ModelParams: [1x1 classreg.learning.modelparams.TreeParams]
```

See Also

`predict` | `ClassificationTree`

How To

- Chapter 13, “Nonparametric Supervised Learning”

gmdistribution.fit

Purpose

Gaussian mixture parameter estimates

Syntax

```
obj = gmdistribution.fit(X,k)
obj = gmdistribution.fit(...,param1,val1,param2,val2,...)
```

Description

`obj = gmdistribution.fit(X,k)` uses an Expectation Maximization (EM) algorithm to construct an object `obj` of the `gmdistribution` class containing maximum likelihood estimates of the parameters in a Gaussian mixture model with `k` components for data in the n-by-d matrix `X`, where n is the number of observations and d is the dimension of the data.

`gmdistribution` treats `NaN` values as missing data. Rows of `X` with `NaN` values are excluded from the fit.

`obj = gmdistribution.fit(...,param1,val1,param2,val2,...)` provides control over the iterative EM algorithm. Parameters and values are listed below.

Parameter	Value
`'Start'`	Method used to choose initial component parameters. One of the following: • `'randSample'` — To select `k` observations from `X` at random as initial component means. The mixing proportions are uniform. The initial covariance matrices for all components are diagonal, where the element `j` on the diagonal is the variance of `X(:,j)`. This is the default. • `S` — A structure array with fields `mu`, `Sigma`, and `PComponents`. See `gmdistribution` for descriptions of values. • `s` — A vector of length n containing an initial guess of the component index for each point.
`'Replicates'`	A positive integer giving the number of times to repeat the EM algorithm, each time with a new set of

Parameter	Value
	parameters. The solution with the largest likelihood is returned. A value larger than 1 requires the `'randSample'` start method. The default is 1.
`'CovType'`	`'diagonal'` if the covariance matrices are restricted to be diagonal; `'full'` otherwise. The default is `'full'`.
`'SharedCov'`	Logical `true` if all the covariance matrices are restricted to be the same (pooled estimate); logical `false` otherwise.
`'Regularize'`	A nonnegative regularization number added to the diagonal of covariance matrices to make them positive-definite. The default is 0.
`'Options'`	Options structure for the iterative EM algorithm, as created by `statset`. `gmdistribution.fit` uses the parameters `'Display'` with a default value of `'off'`, `'MaxIter'` with a default value of `100`, and `'TolFun'` with a default value of `1e6`.

In some cases, `gmdistribution` may converge to a solution where one or more of the components has an ill-conditioned or singular covariance matrix.

The following issues may result in an ill-conditioned covariance matrix:

- The number of dimension of your data is relatively high and there are not enough observations.
- Some of the features (variables) of your data are highly correlated.
- Some or all the features are discrete.
- You tried to fit the data to too many components.

In general, you can avoid getting ill-conditioned covariance matrices by using one of the following precautions:

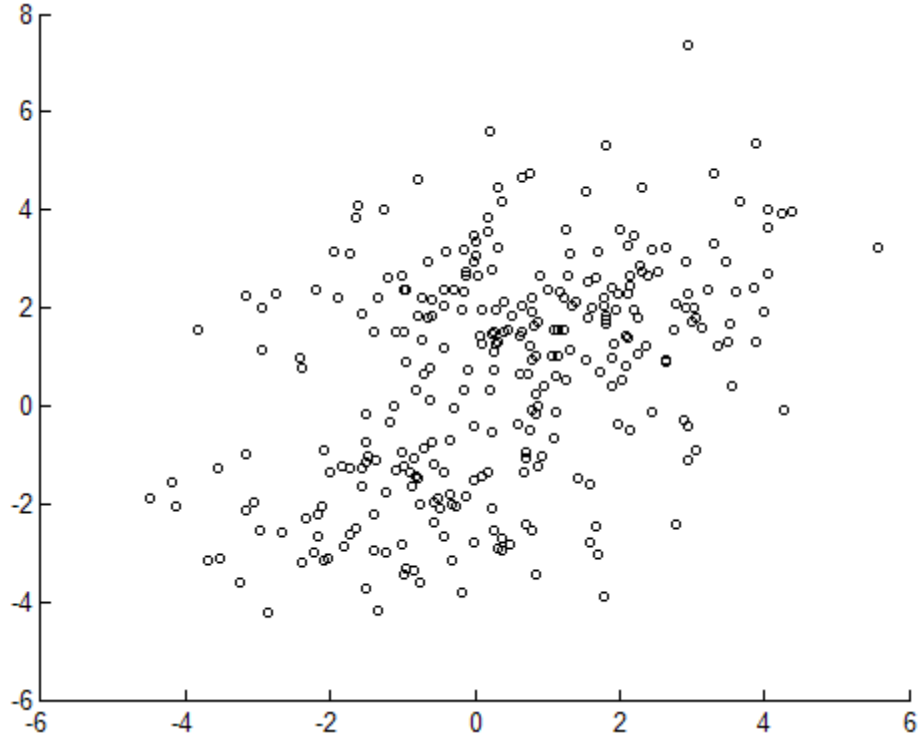
- Pre-process your data to remove correlated features.
- Set `'SharedCov'` to `true` to use an equal covariance matrix for every component.
- Set `'CovType'` to `'diagonal'`.
- Use `'Regularize'` to add a very small positive number to the diagonal of every covariance matrix.
- Try another set of initial values.

In other cases `gmdistribution` may pass through an intermediate step where one or more of the components has an ill-conditioned covariance matrix. Trying another set of initial values may avoid this issue without altering your data or model.

Examples

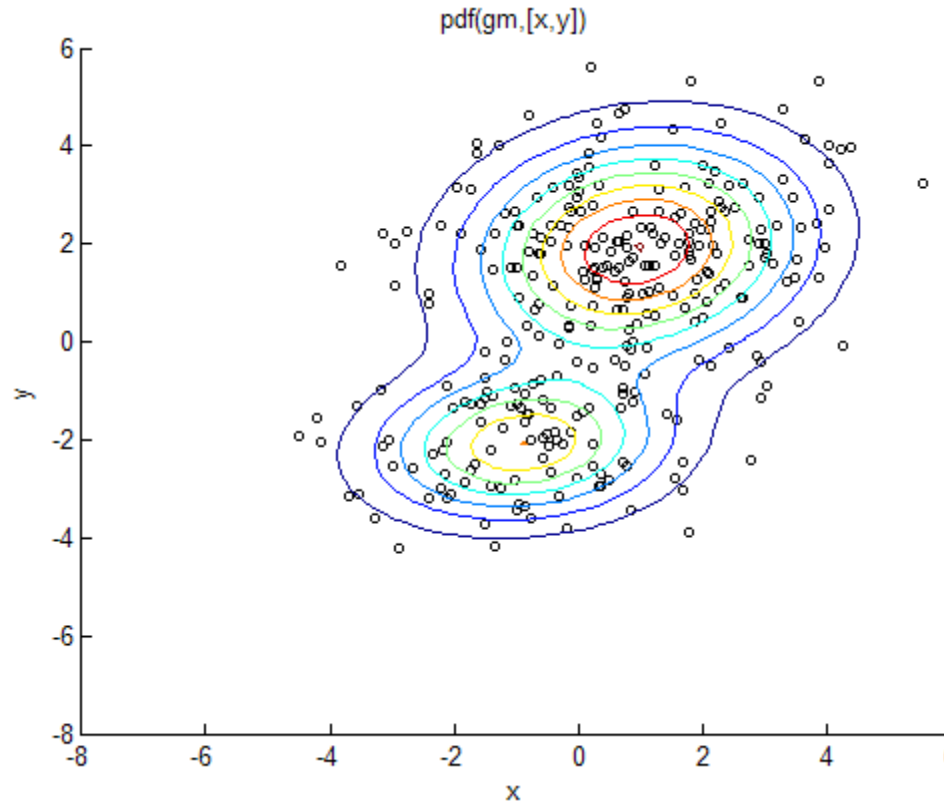
Generate data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function:

```
MU1 = [1 2];
SIGMA1 = [2 0; 0 .5];
MU2 = [-3 -5];
SIGMA2 = [1 0; 0 1];
X = [mvnrnd(MU1,SIGMA1,1000);mvnrnd(MU2,SIGMA2,1000)];

scatter(X(:,1),X(:,2),10,'.')
hold on
```



Next, fit a two-component Gaussian mixture model:

```
options = statset('Display','final');
obj = gmdistribution.fit(X,2,'Options',options);
10 iterations, log-likelihood = -7046.78

h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
```



Among the properties of the fit are the parameter estimates:

```
ComponentMeans = obj.mu
ComponentMeans =
    0.9391    2.0322
   -2.9823   -4.9737

ComponentCovariances = obj.Sigma
ComponentCovariances(:,:,1) =
    1.7786   -0.0528
   -0.0528    0.5312
```

```
ComponentCovariances(:,:,2) =
    1.0491   -0.0150
   -0.0150    0.9816

MixtureProportions = obj.PComponents
MixtureProportions =
    0.5000    0.5000
```

The Akaike information is minimized by the two-component model:

```
AIC = zeros(1,4);
obj = cell(1,4);
for k = 1:4
    obj{k} = gmdistribution.fit(X,k);
    AIC(k)= obj{k}.AIC;
end

[minAIC,numComponents] = min(AIC);
numComponents
numComponents =
     2

model = obj{2}
model =
Gaussian mixture distribution
with 2 components in 2 dimensions
Component 1:
Mixing proportion: 0.500000
Mean:     0.9391    2.0322
Component 2:
Mixing proportion: 0.500000
Mean:    -2.9823   -4.9737
```

Both the Akaike and Bayes information are negative log-likelihoods for the data with penalty terms for the number of estimated parameters. They are often used to determine an appropriate number of components for a model when the number of components is unspecified.

References

[1] McLachlan, G., and D. Peel. *Finite Mixture Models*. Hoboken, NJ: John Wiley & Sons, Inc., 2000.

See Also

`gmdistribution` | `cluster`

Purpose

Create Naive Bayes classifier object by fitting training data

Syntax

```
nb = NaiveBayes.fit(training, class)
nb = NaiveBayes.fit(..., 'param1',val1, 'param2',val2, ...)
```

Description

`nb = NaiveBayes.fit(training, class)` builds a `NaiveBayes` classifier object `nb`. `training` is an `N`-by-`D` numeric matrix of training data. Rows of `training` correspond to observations; columns correspond to features. `class` is a classing variable for `training` (see "Grouped Data" on page 2-34) taking `K` distinct levels. Each element of `class` defines which class the corresponding row of `training` belongs to. `training` and `class` must have the same number of rows.

`nb = NaiveBayes.fit(..., 'param1',val1, 'param2',val2, ...)` specifies one or more of the following name/value pairs:

- `'Distribution'` – a string or a 1-by-`D` cell vector of strings, specifying which distributions `fit` uses to model the data. If the value is a string, `fit` models all the features using one type of distribution. `fit` can also model different features using different types of distributions. If the value is a cell vector, its `j`th element specifies the distribution `fit` uses for the `j`th feature. The available types of distributions are:

`'normal'` (default)	Normal (Gaussian) distribution.
`'kernel'`	Kernel smoothing density estimate.

`'mvmn'`	Multivariate multinomial distribution for discrete data. `fit` assumes each individual feature follows a multinomial model within a class. The parameters for a feature include the probabilities of all possible values that the corresponding feature can take.
`'mn'`	Multinomial distribution for classifying the count-based data such as the bag-of-tokens model. In the bag-of-tokens model, the value of the `j`th feature is the number of occurrences of the `j`th token in this observation, so it must be a non-negative integer. When `'mn'` is used, `fit` considers each observation as multiple trials of a multinomial distribution, and considers each occurrence of a token as one trial. The number of categories (bins) in this multinomial model is the number of distinct tokens, i.e., the number of columns of `training`.

- `'Prior'` – The prior probabilities for the classes, specified as one of the following:

`'empirical'` (default)	`fit` estimates the prior probabilities from the relative frequencies of the classes in `training`.
`'uniform'`	The prior probabilities are equal for all classes.

vector	A numeric vector of length `K` specifying the prior probabilities in the class order of `class`.
structure	A structure `S` containing class levels and their prior probabilities. `S` must have two fields: • `S.prob`: A numeric vector of prior probabilities. • S.class: A vector of the same type as `class`, containing unique class levels indicating the class for the corresponding element of prob. `S.class` must contain all the `K` levels in `class`. It can also contain classes that do not appear in `class`. This can be useful if `training` is a subset of a larger training set. `fit` ignores any classes that appear in `S.class` but not in `class`.

If the prior probabilities don't sum to one, `fit` will normalize them.

- `'KSWidth'` – The bandwidth of the kernel smoothing window. The default is to select a default bandwidth automatically for each combination of feature and class, using a value that is optimal for a Gaussian distribution. You can specify the value as one of the following:

scalar	Width for all features in all classes.
row vector	1-by-`D` vector where the `j`th element is the bandwidth for the `j`th feature in all classes.
column vector	`K`-by-1 vector where the `i`th element specifies the bandwidth for all features in the `i`th class. `K` represents the number of class levels.

matrix	`K`-by-`D` matrix `M` where `M(i,j)` specifies the bandwidth for the `j`th feature in the `i`th class.
structure	A structure `S` containing class levels and their bandwidths. `S` must have two fields: • `S.width` – A numeric array of bandwidths specified as a row vector, or a matrix with `D` columns. • `S.class` – A vector of the same type as `class`, containing unique class levels indicating the class for the corresponding row of width.

- `'KSSupport'` – The regions where the density can be applied. It can be a string, a two-element vector as shown below, or a 1-by-`D` cell array of these values:

`'unbounded'` (default)	The density can extend over the whole real line.
`'positive'`	The density is restricted to positive values.
`[L,U]`	A two-element vector specifying the finite lower bound L and upper bound U for the support of the density.

- `'KSType'` – The type of kernel smoother to use. It can be a string or a 1-by-`D` cell array of strings. Each string can be `'normal'` (default), `'box'`, `'triangle'`, or `'epanechnikov'`.

How To

- “Naive Bayes Classification” on page 12-29
- “Grouped Data” on page 2-34

Purpose

Binary decision tree for regression

Syntax

```
tree = RegressionTree.fit(X,Y)
tree = RegressionTree.fit(X,Y,Name,Value)
```

Description

`tree = RegressionTree.fit(X,Y)` returns a regression tree based on the input variables (also known as predictors, features, or attributes) `X` and output (response) `Y`. `tree` is a binary tree where each branching node is split based on the values of a column of `X`.

`tree = RegressionTree.fit(X,Y,Name,Value)` fits a tree with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`. If you use one of the following five options, `tree` is of class `RegressionPartitionedModel`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Otherwise, `tree` is of class `RegressionTree`.

Input Arguments

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`RegressionTree.fit` considers `NaN` values in `X` as missing values. `RegressionTree.fit` does not use observations with all missing values for `X` the fit. `RegressionTree.fit` uses observations with some missing values for `X` to find splits on variables for which these observations have valid values.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

`RegressionTree.fit` considers `NaN` values in `Y` to be missing values. `RegressionTree.fit` does not use observations with missing values for `Y` in the fit.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`CategoricalPredictors`

List of categorical predictors. Pass `CategoricalPredictors` as one of:

- A numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of `X` is a categorical variable.
- `'all'`, meaning all predictors are categorical.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in the `PredictorNames` property.
- A character matrix, where each row of the matrix is a name of a predictor variable. Pad the names with extra blanks so each row of the character matrix has the same length.

Default: `[]`

`crossval`

If `'on'`, grows a cross-validated decision tree with 10 folds. You can use `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'` parameters to override this cross-validation setting. You can only use one of these four parameters (`'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`) at a time when creating a cross-validated tree.

Alternatively, cross-validate `tree` later using the `crossval` method.

Default: `'off'`

`cvpartition`

A partition created with `cvpartition` to use in cross-validated tree. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'` and `'cvpartition'`.

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'` and `'cvpartition'`.

`kfold`

Number of folds to use in a cross-validated tree, a positive integer. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: `10`

`leaveout`

Use leave-one-out cross validation by setting to `'on'`. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`MergeLeaves`

When `'on'`, `RegressionTree` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, `RegressionTree` does not merge leaves.

Default: `'on'`

`MinLeaf`

Each leaf has at least `MinLeaf` observations per tree leaf. If you supply both `MinParent` and `MinLeaf`, `RegressionTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: `1`

`MinParent`

Each branch node in the tree has at least `MinParent` observations. If you supply both `MinParent` and `MinLeaf`, `RegressionTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: `10`

`NVarToSample`

Number of predictors to select at random for each split. Can be a positive integer or `'all'`, which means use all available predictors.

Default: `'all'`

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

Default: `{'x1','x2',...}`

`Prune`

When `'on'`, `RegressionTree` computes the full tree and the optimal sequence of pruned subtrees. When `'off'` `RegressionTree` computes the full tree without pruning.

Default: `'on'`

`PruneCriterion`

String with the pruning criterion, always `'error'`.

Default: `'error'`

`ResponseName`

Name of the response variable `Y`, a string.

Default: `'Y'`

`ResponseTransform`

Function handle for transforming the raw response values (mean squared error). The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function by dot addressing:

```
tree.ResponseTransform = @function
```

Default: `'none'`

`SplitCriterion`

Criterion for choosing a split, always the string `'MSE'`, meaning mean squared error.

Default: `'MSE'`

`Weights`

Vector of observation weights. The length of `weights` is the number of rows in `X`.

Default: `ones(size(X,1),1)`

Output Arguments

`tree`

A regression tree object. You can use `tree` to predict the response of new data with the `predict` method.

Examples

Load the data in `carsmall.mat`, and make a regression tree to predict the mileage of cars based on their weights and numbers of cylinders:

```
load carsmall
tree = RegressionTree.fit([Weight, Cylinders],MPG,...
                'MinParent',20,...
                'PredictorNames',{'W','C'})

tree =
RegressionTree:
           PredictorNames: {'W'  'C'}
    CategoricalPredictors: []
             ResponseName: 'Y'
        ResponseTransform: 'none'
            NObservations: 94
```

Predict the mileage of a car that weighs 2200 lbs and has four cylinders:

```
predict(tree,[2200,4])

ans =
   29.6111
```

See Also

`predict`

How To

- Chapter 13, "Nonparametric Supervised Learning"

Purpose

Fit probability distribution to data

Syntax

```
PD = fitdist(X, DistName)
[PDCA, GN, GL] = fitdist(X, DistName, 'By', GroupVar)
... = fitdist(..., param1, val1, param2, val2, ...)
```

Description

`PD = fitdist(X, DistName)` fits the probability distribution specified by `DistName` to the data in the column vector `X`, and returns `PD`, an object representing the fitted distribution.

`[PDCA, GN, GL] = fitdist(X, DistName, 'By', GroupVar)` takes a grouping variable, `GroupVar`, fits the specified distribution to the data in `X` from each group, and returns `PDCA`, a cell array of the fitted probability distribution objects. `GroupVar` can also be a cell array of multiple grouping variables. `GN` is a cell array of group labels. `GL` is a cell array of grouping variable levels, with one column for each grouping variable. See "Grouped Data" on page 2-34 for more information.

`... = fitdist(..., param1, val1, param2, val2, ...)` specifies optional parameter name/value pairs, as described in the Parameter/Values table. Parameter and value names are case insensitive.

Input Arguments

`X`

A column vector of data.

> **Note** Any NaN values in `X` are ignored by the fitting calculations. Additionally, any NaN values in the censoring vector or frequency vector will cause the corresponding values in `X` to be ignored by the fitting calculations.

`DistName`

A string specifying a distribution. Choices are:

- `'kernel'` — To fit a nonparametric kernel-smoothing distribution.

- Any of the following to fit a parametric distribution:
  - `'beta'`
  - `'binomial'`
  - `'birnbaumsaunders'`
  - `'exponential'`
  - `'extreme value'` or `'ev'`
  - `'gamma'`
  - `'generalized extreme value'` or `'gev'`
  - `'generalized pareto'` or `'gp'`
  - `'inversegaussian'`
  - `'logistic'`
  - `'loglogistic'`
  - `'lognormal'`
  - `'nakagami'`
  - `'negative binomial'` or `'nbin'`
  - `'normal'`
  - `'poisson'`
  - `'rayleigh'`
  - `'rician'`
  - `'tlocationscale'`
  - `'weibull'` or `'wbl'`

For more information on these parametric distributions, see Appendix B, "Distribution Reference".

GroupVar — A grouping variable or a cell array of multiple grouping variables. For more information on grouping variables, see "Grouped Data" on page 2-34.

Parameter	Values
`'censoring'`	A Boolean vector the same size as *X*, containing `1`s when the corresponding elements in *X* are right-censored observations and `0`s when the corresponding elements are exact observations. Default is a vector of `0`s. **Note** Any NaN values in this censoring vector are ignored by the fitting calculations. Additionally, any NaN values in *X* or the frequency vector will cause the corresponding values in the censoring vector to be ignored by the fitting calculations.
`'frequency'`	A vector the same size as *X*, containing nonnegative integers specifying the frequencies for the corresponding elements in *X*. Default is a vector of `1`s. **Note** Any NaN values in this frequency vector are ignored by the fitting calculations. Additionally, any NaN values in *X* or the censoring vector will cause the corresponding values in the frequency vector to be ignored by the fitting calculations.

Parameter	Values
'options'	A structure created by the statset function to specify control parameters for the iterative fitting algorithm.
'n'	For 'binomial' distributions only, a positive integer specifying the N parameter (number of trials).
'theta'	For 'generalized pareto' distributions only, value specifying the theta (threshold) parameter for the generalized Pareto distribution. Default is 0.
'kernel'	For 'kernel' distributions only, a string specifying the type of kernel smoother to use. Choices are: • 'normal' (default) • 'box' • 'triangle' • 'epanechnikov'
'support'	For 'kernel' distributions only, any of the following to specify the support: • 'unbounded' — Default. If the density can extend over the whole real line. • 'positive' — To restrict it to positive values. • A two-element vector giving finite lower and upper limits for the support of the density.
'width'	For 'kernel' distributions only, a value specifying the bandwidth of the kernel smoothing window. The default is optimal for estimating normal densities, but you may want to choose a smaller value to reveal features such as multiple modes.

Output Arguments

PD	An object in either the `ProbDistUnivKernel` class or the `ProbDistUnivParam` class, which are derived from the `ProbDist` class.
PDCA	A cell array of the fitted probability distribution objects.
GN	A cell array of group labels.
GL	A cell array of grouping variable levels, with one column for each grouping variable.

Examples

Creating a ProbDistUnivKernel Object

1 Load a MAT-file, included with the Statistics Toolbox software, which contains `MPG`, a column vector of data.

```
load carsmall
```

2 Create a `ProbDistUnivKernel` object by fitting a nonparametric kernel-smoothing distribution to the data:

```
ksd = fitdist(MPG,'kernel')

ksd =

kernel distribution

    Kernel = normal
    Bandwidth = 4.11428
    Support = unbounded
```

Creating a ProbDistUnivParam Object

1 Load a MAT-file, included with the Statistics Toolbox software, which contains `MPG`, a column vector of data, and `Origin`, a cell array of seven grouping variables.

```
load carsmall
```

2. Create a cell array of `ProbDistUnivParam` objects by fitting a parametric distribution, namely a Weibull distribution, to the data, and also grouping the data. Since there is only one car from Italy, `fitdist` will return an error, since you cannot fit a distribution to a single observation.

```
wd = fitdist(MPG,'weibull','by',Origin)
```

Algorithms

The `fitdist` function fits most distributions using maximum likelihood. Two exceptions are the normal and lognormal distributions with uncensored data. For the uncensored normal distribution, the estimated value of the sigma parameter is the square root of the unbiased estimate of the variance. For the uncensored lognormal distribution, the estimated value of the sigma parameter is the square root of the unbiased estimate of the variance of the log of the data.

References

[1] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 1, Hoboken, NJ: Wiley-Interscience, 1993.

[2] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 2, Hoboken, NJ: Wiley-Interscience, 1994.

[3] Bowman, A. W., and A. Azzalini. *Applied Smoothing Techniques for Data Analysis*. New York: Oxford University Press, 1997.

Alternatives

`dfittool` — Opens a graphical user interface for displaying fit distributions to data, or for fitting distributions to your data and displaying them over plots of the empirical distributions, by importing data from the workspace.

See Also

`disttool` | `randtool` | `statset` | `ProbDist` | `ProbDistUnivKernel` | `ProbDistUnivParam`

How To

- Appendix B, “Distribution Reference”
- “Grouped Data” on page 2-34

fitensemble

Purpose

Fitted ensemble for classification or regression

Syntax

```
ens = fitensemble(X,Y,method,nlearn,learners)
ens = fitensemble(X,Y,method,nlearn,learners,Name,Value)
```

Description

`ens = fitensemble(X,Y,method,nlearn,learners)` creates an ensemble model that can predict responses to data. The ensemble consists of models listed in `learners`.

`ens = fitensemble(X,Y,method,nlearn,learners,Name,Value)` creates an ensemble model with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Tips

- If `X` has categorical predictors with many levels, use `'GentleBoost'` or `'LogitBoost'` for binary classification. Using other algorithms in this case would likely cause long training times and can exhaust memory.

Input Arguments

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

For classification, `Y` is a categorical variable, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding row of `X`.

For regression, `Y` is a numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

`method`

A case-insensitive string consisting of one of the following.

- For classification with two classes:

  - `'AdaBoostM1'`
  - `'LogitBoost'`
  - `'GentleBoost'`
  - `'RobustBoost'`
  - `'Bag'`
- For classification with three or more classes:
  - `'AdaBoostM2'`
  - `'Bag'`
- For regression:
  - `'LSBoost'`
  - `'Bag'`

Since `'Bag'` applies to all methods, indicate whether you want a classifier or regressor with the `type` name-value pair set to `'classification'` or `'regression'`.

`nlearn`

Number of ensemble learning cycles, a positive integer. At every training cycle, `fitensemble` loops over all learner templates in `learners` and trains one weak learner for every template. The total number of trained learners in `ens` is `nlearn*numel(learners)`.

`nlearn` for ensembles can vary from a few dozen to a few thousand. Usually, an ensemble with a good predictive power needs between a few hundred and a few thousand weak learners. You do not have to train an ensemble for that many cycles at once. You can start by growing a few dozen learners, inspect the ensemble performance and, if necessary, train more weak learners using the `resume` method of the ensemble.

`learners`

One of the following:

- A string with the name of a weak learner, such as `'tree'`
- A single weak learner template you create with `ClassificationTree.template` or `RegressionTree.template`
- A cell array of weak learner templates

Create weak learner templates with `ClassificationTree.template` or `RegressionTree.template`. Usually you should supply only one weak learner template.

Ensemble performance depends on the parameters of the weak learners, and you can get poor performance using weak learners with default parameters. Specify the parameters for the weak learners in the template. Specify parameters for the ensemble in the `fitensemble` name-value pairs.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

All Ensembles:

`CategoricalPredictors`

List of categorical predictors. Pass `CategoricalPredictors` as one of:

- A numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of `X` is a categorical variable.
- `'all'`, meaning all predictors are categorical.

- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in the `PredictorNames` property.
- A character matrix, where each row of the matrix is a name of a predictor variable. The names must match entries in the `PredictorNames` property. Pad the names with extra blanks so each row of the character matrix has the same length.

Default: `[]`

`crossval`

If `'on'`, grows a cross-validated decision tree with 10 folds. You can use `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'` parameters to override this cross-validation setting. You can only use one of these four parameters (`'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`) at a time when creating a cross-validated tree.

Default: `'off'`

`cvpartition`

A partition created with `cvpartition` to use in cross-validated tree. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`fresample`

Fraction of the training set to be selected by resampling for every weak learner. A numeric scalar between `0` and `1`. This parameter has no effect unless you grow an ensemble by bagging or set `'resample'` to `'on'`. The default setting is the one used most often for an ensemble grown by resampling.

Default: `1`

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`kfold`

Number of folds to use in a cross-validated tree, a positive integer. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: `10`

`leaveout`

Use leave-one-out cross validation by setting to `'on'`. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`nprint`

Printout frequency, a positive integer scalar. Set to `'off'` for no printout. Use this parameter to track of how many weak learners have been trained so far. This is useful when you train ensembles with many learners on large datasets. If you use one of the cross-validation options, this parameter defines the printout frequency per number of cross-validation folds.

Default: `'off'`

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

Default: `{'x1','x2',...}`

`replace`

'on' or 'off'. If 'on', sample with replacement; if 'off', sample without replacement. This parameter has no effect unless you grow an ensemble by bagging or set resample to 'on'. If you set resample to 'on' and replace to 'off', fitensemble samples training observations assuming uniform weights, and boosts by reweighting observations.

Default: 'on'

resample

'on' or 'off'. If 'on', grows an ensemble by resampling, with the resampling fraction given by fresample, and sampling with or without replacement given by replace.

- Boosting — When 'off', the boosting algorithm reweights observations at every learning iteration. When 'on', the algorithm samples training observations using updated weights as the multinomial sampling probabilities.
- Bagging — You can use only the default value of this parameter ('on').

Default: 'off' for boosting, 'on' for bagging

ResponseName

Name of the response variable Y, a string.

Default: 'Y'

type

A string, either 'classification' or 'regression'. Specify type when the method is 'bag'.

weights

Vector of observation weights. The length of weights is the number of rows in X.

Default: `ones(size(X,1),1)`

Classification Ensembles:

`classnames`

Array of class names. Specify a data type the same as exists in `Y`.

Default: The class names that exist in `Y`

`cost`

Square matrix `C`, where `C(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. Alternatively, `cost` can be a structure `S` having two fields: `S.ClassNames` containing the group names as a categorical variable, character array, or cell array of strings; and `S.ClassificationCosts` containing the cost matrix `C`.

Default: `C(i,j)=1` if `i~=j`, and `C(i,j)=0` if `i=j`

`prior`

Prior probabilities for each class. Specify as one of:

- A string:
  - `'empirical'` determines class probabilities from class frequencies in `Y`. If you pass observation weights, they are used to compute the class probabilities.
  - `'uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class)
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a categorical variable, character array, or cell array of strings

- `S.ClassProbs` containing a vector of corresponding probabilities

If you set values for both `weights` and `prior`, the weights are renormalized to add up to the value of the prior probability in the respective class.

Default: `'empirical'`

AdaBoostM1, AdaBoostM2, LogitBoost, GentleBoost, and LSBoost:

`LearnRate`

Learning rate for shrinkage, a numeric scalar between 0 and 1. If you set the learning rate to a smaller value than `1`, the ensemble requires more learning iterations but often achieves a better accuracy. `0.1` is a popular choice for ensemble grown with shrinkage.

Default: `1`

RobustBoost:

`RobustErrorGoal`

Target classification error for `RobustBoost`, a numeric scalar from `0` to `1`. Usually there is an optimal range for this parameter for your training data. If you set the error goal too low or too high, `RobustBoost` can produce a model with poor classification accuracy.

Default: `0.1`

`RobustMaxMargin`

Maximal classification margin for `RobustBoost` in the training set, a nonnegative numeric scalar. `RobustBoost` minimizes the

number of observations in the training set with classification margins below `RobustMaxMargin`.

Default: `0`

`RobustMarginSigma`

Spread of the distribution of classification margins over the training set for `RobustBoost`, a numeric positive scalar. You should consult literature on `RobustBoost` before setting this parameter

Default: `0.1`

Output Arguments

`ens`

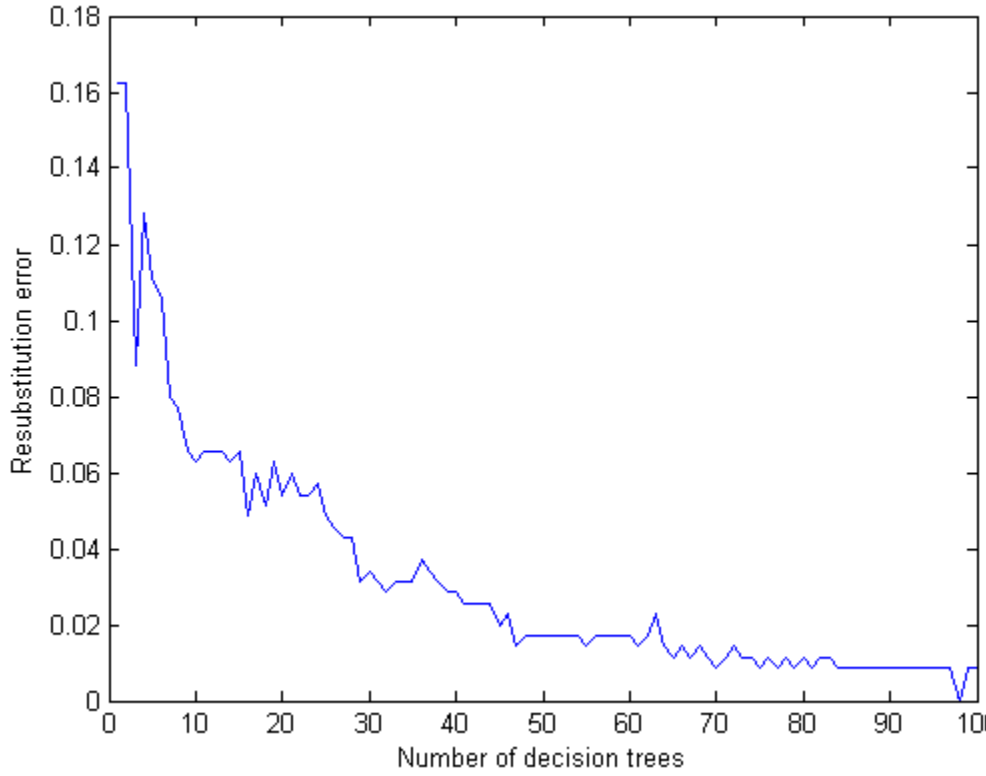
Ensemble object for predicting characteristics. The class of `ens` depends on settings. In the following table, cross-validation names are `crossval`, `kfold`, `holdout`, `leaveout`, and `cvpartition`.

Settings	Class
`resample` name-value pair is `'off'`, and you don't set a cross-validation name-value pair.	`ClassificationEnsemble`
`resample` name-value pair is `'off'`, and you don't set a cross-validation name-value pair.	`RegressionEnsemble`
`resample` name-value pair is `'on'`, `type` is `'classification'`, and you don't set a cross-validation name-value pair.	`ClassificationBaggedEnsemble`
`resample` name-value pair is `'on'`, `type` is `'regression'`, and you don't set a cross-validation name-value pair.	`RegressionBaggedEnsemble`
`method` is a classification method, and you set a cross-validation name-value pair.	`ClassificationPartitionedEnsemble`
`method` is a regression method, and you set a cross-validation name-value pair.	`RegressionPartitionedEnsemble`

Examples

Train a boosting ensemble, and inspect the resubstitution loss:

```
load ionosphere;
ada = fitensemble(X,Y,'AdaBoostM1',100,'tree');
plot(resubLoss(ada,'mode','cumulative'));
xlabel('Number of decision trees');
ylabel('Resubstitution error');
```



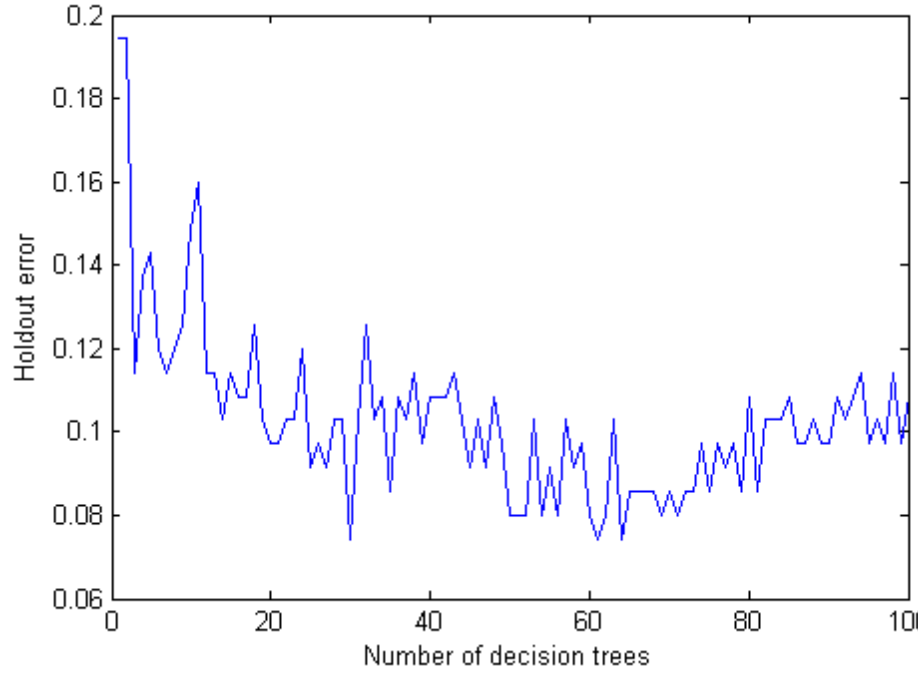
Train a regression ensemble to predict car mileage based on the number of cylinders, engine displacement, horsepower, and weight. Predict the mileage for a four-cylinder car with a 200 cubic inch displacement, 150 horsepower, weighing 3000 lbs.

```
load carsmall
X = [Cylinders Displacement Horsepower Weight];
xnames = {'Cylinders' 'Displacement' 'Horsepower' 'Weight'};
t = RegressionTree.template('Surrogate','on');
rens = fitensemble(X,MPG,'LSBoost',100,t,'PredictorNames',xnames)

rens =
classreg.learning.regr.RegressionEnsemble:
         PredictorNames: {'Cylinders' 'Displacement' 'Horsepower' 'Weight'}
  CategoricalPredictors: []
           ResponseName: 'Y'
      ResponseTransform: 'none'
          NObservations: 94
               NTrained: 100
                 Method: 'LSBoost'
           LearnerNames: {'Tree'}
   ReasonForTermination: [1x77 char]
                FitInfo: [100x1 double]
     FitInfoDescription: [2x83 char]
         Regularization: []

predict(rens,[4 200 150 3000])

ans =
   20.4982
```

Train and estimate generalization error on a holdout sample:

```
load ionosphere;
ada = fitensemble(X,Y,'AdaBoostM1',100,'Tree',...
```

```
    'holdout',0.5);
plot(kfoldLoss(ada,'mode','cumulative'));
xlabel('Number of decision trees');
ylabel('Holdout error');
```



See Also

`ClassificationEnsemble` | `RegressionEnsemble` | `ClassificationBaggedEnsemble` | `RegressionBaggedEnsemble` | `ClassificationPartitionedEnsemble` | `RegressionPartitionedEnsemble` | `ClassificationTree.template` | `RegressionTree.template`

How To

- Chapter 13, “Nonparametric Supervised Learning”

categorical.flipdim

Purpose

Flip categorical array along specified dimension

Syntax

```
B = flipdim(A,dim)
```

Description

`B = flipdim(A,dim)` returns the categorical array `A` with dimension `dim` flipped.

See Also

`fliplr` | `flipud` | `permute` | `rot90`

Purpose

Flip categorical matrix in left/right direction

Syntax

```
B = fliplr(A)
```

Description

`B = fliplr(A)` returns the 2-D categorical matrix `A` with rows preserved and columns flipped in the left/right direction.

See Also

`flipdim` | `flipud` | `permute` | `rot90`

categorical.flipud

Purpose

Flip categorical matrix in up/down direction

Syntax

```
B = flipud(A)
```

Description

`B = flipud(A)` returns the 2-D categorical matrix `A` with rows preserved and columns flipped in the up/down direction.

See Also

`flipdim` | `fliplr` | `permute` | `rot90`

Purpose

F probability density function

Syntax

```
Y = fpdf(X,V1,V2)
```

Description

`Y = fpdf(X,V1,V2)` computes the *F* pdf at each of the values in `X` using the corresponding numerator degrees of freedom `V1` and denominator degrees of freedom `V2`. `X`, `V1`, and `V2` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. `V1` and `V2` parameters must contain real positive values, and the values in `X` must lie on the interval [0 ∞).

The probability density function for the *F* distribution is

$$y = f(x \mid \nu_1,\nu_2) = \frac{\Gamma\left[\frac{(\nu_1+\nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}} \frac{x^{\frac{\nu_1-2}{2}}}{\left[1+\left(\frac{\nu_1}{\nu_2}\right)x\right]^{\frac{\nu_1+\nu_2}{2}}}$$

Examples

```
y = fpdf(1:6,2,2)
y =
  0.2500   0.1111   0.0625   0.0400   0.0278   0.0204

z = fpdf(3,5:10,5:10)
z =
  0.0689   0.0659   0.0620   0.0577   0.0532   0.0487
```

See Also

`pdf` | `fcdf` | `finv` | `fstat` | `frnd`

How To

- "F Distribution" on page B-25

Purpose

Fractional factorial design

Syntax

```
X = fracfact(gen)
[X,conf] = fracfact(gen)
[X,conf] = fracfact(gen,Name,Value)
```

Description

`X = fracfact(gen)` creates the two-level fractional factorial design defined by the generator string `gen`.

`[X,conf] = fracfact(gen)` returns a cell array of strings containing the confounding pattern for the design.

`[X,conf] = fracfact(gen,Name,Value)` creates a fractional factorial designs with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`gen`

Either a cell array of strings where each cell contains one "word," or a string consisting of "words" separated by spaces. "Words" consist of case-sensitive letters or groups of letters, where `'a'` represents string `1`, `'b'` represents string `2`, ..., `'A'` represents string `27`, ..., `'Z'` represents string `52`.

Each word defines how the corresponding factor's levels are defined as products of generators from a `2^K` full-factorial design. `K` is the number of letters of the alphabet in `gen`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`FactorNames`

Cell array specifying the name for each factor.

Default: `{'X1','X2',...}`

`MaxInt`

Positive integer setting the maximum level of interaction to include in the confounding output.

Default: `2`

Output Arguments

`X`

The two-level fractional factorial design. `X` is a matrix of size `N`-by-`P`, where

- `N = 2^K`, where `K` is the number of letters of the alphabet in `gen`.
- `P` is the number of words in `gen`.

Because `X` is a two-level design, the components of `X` are `–1`. For the meaning of `X`, see "Fractional Factorial Designs" on page 15-5.

`conf`

Cell array of strings containing the confounding pattern for the design.

Examples

Generate a fractional factorial design for four variables, where the fourth variable is the product of the first three:

```
x = fracfact('a b c abc')

x =
     -1    -1    -1    -1
     -1    -1     1     1
     -1     1    -1     1
     -1     1     1    -1
      1    -1    -1     1
      1    -1     1    -1
      1     1    -1    -1
      1     1     1     1
```

Find generators for a six-factor design that uses four factors and achieves resolution IV using `fracfactgen`. Use the result to specify the design:

```
generators = fracfactgen('a b c d e f',4, ... % 4 factors
    4) % resolution 4

generators =
    'a'
    'b'
    'c'
    'd'
    'bcd'
    'acd'

x = fracfact(generators)

x =
    -1    -1    -1    -1    -1    -1
    -1    -1    -1     1     1     1
    -1    -1     1    -1     1     1
    -1    -1     1     1    -1    -1
    -1     1    -1    -1     1    -1
    -1     1    -1     1    -1     1
    -1     1     1    -1    -1     1
    -1     1     1     1     1    -1
     1    -1    -1    -1    -1     1
     1    -1    -1     1     1    -1
     1    -1     1    -1     1    -1
     1    -1     1     1    -1     1
     1     1    -1    -1     1     1
     1     1    -1     1    -1    -1
     1     1     1    -1    -1    -1
     1     1     1     1     1     1
```

References

[1] Box, G. E. P., W. G. Hunter, and J. S. Hunter. *Statistics for Experimenters*. Hoboken, NJ: Wiley-Interscience, 1978.

See Also

`ff2n` | `fracfactgen` | `fullfact` | `hadamard`

How To

- "Fractional Factorial Designs" on page 15-5

fracfactgen

Purpose

Fractional factorial design generators

Syntax

```
generators = fracfactgen(terms)
generators = fracfactgen(terms,k)
generators = fracfactgen(terms,k,R)
generators = fracfactgen(terms,k,R,basic)
```

Description

`generators = fracfactgen(terms)` uses the Franklin-Bailey algorithm to find generators for the smallest two-level fractional-factorial design for estimating linear model terms specified by `terms`. `terms` is a string consisting of words formed from the `52` case-sensitive letters `a-Z`, separated by spaces. Use `'a'-'z'` for the first 26 factors, and, if necessary, `'A'-'Z'` for the remaining factors. For example, `terms = 'a b c ab ac'`. Single-character words indicate main effects to be estimated; multiple-character words indicate interactions. Alternatively, `terms` is an m-by-n matrix of `0`s and `1`s where m is the number of model terms to be estimated and n is the number of factors. For example, if `terms` contains rows `[0 1 0 0]` and `[1 0 0 1]`, then the factor `b` and the interaction between factors `a` and `d` are included in the model. `generators` is a cell array of strings with one generator per cell. Pass `generators` to `fracfact` to produce the fractional-factorial design and corresponding confounding pattern.

`generators = fracfactgen(terms,k)` returns generators for a two-level fractional-factorial design with 2^k-runs, if possible. If `k` is `[]`, `fracfactgen` finds the smallest design.

`generators = fracfactgen(terms,k,R)` finds a design with resolution `R`, if possible. The default resolution is `3`.

A design of *resolution* R is one in which no n-factor interaction is confounded with any other effect containing less than $R - n$ factors. Thus a resolution III design does not confound main effects with one another but may confound them with two-way interactions, while a resolution IV design does not confound either main effects or two-way interactions but may confound two-way interactions with each other.

If `fracfactgen` is unable to find a design at the requested resolution, it tries to find a lower-resolution design sufficient to calibrate the model.

If it is successful, it returns the generators for the lower-resolution design along with a warning. If it fails, it returns an error.

`generators = fracfactgen(terms,k,R,basic)` also accepts a vector `basic` specifying the indices of factors that are to be treated as basic. These factors receive full-factorial treatments in the design. The default includes factors that are part of the highest-order interaction in `terms`.

Examples

Suppose you wish to determine the effects of four two-level factors, for which there may be two-way interactions. A full-factorial design would require $2^4 = 16$ runs. The `fracfactgen` function finds generators for a resolution IV (separating main effects) fractional-factorial design that requires only $2^3 = 8$ runs:

```
generators = fracfactgen('a b c d',3,4)
generators =
    'a'
    'b'
    'c'
    'abc'
```

The more economical design and the corresponding confounding pattern are returned by `fracfact`:

```
[dfF,confounding] = fracfact(generators)
dfF =
    -1    -1    -1    -1
    -1    -1     1     1
    -1     1    -1     1
    -1     1     1    -1
     1    -1    -1     1
     1    -1     1    -1
     1     1    -1    -1
     1     1     1     1
confounding =
    'Term'     'Generator'    'Confounding'
    'X1'       'a'            'X1'
    'X2'       'b'            'X2'
```

```
'X3'       'c'            'X3'
'X4'       'abc'          'X4'
'X1*X2'    'ab'           'X1*X2 + X3*X4'
'X1*X3'    'ac'           'X1*X3 + X2*X4'
'X1*X4'    'bc'           'X1*X4 + X2*X3'
'X2*X3'    'bc'           'X1*X4 + X2*X3'
'X2*X4'    'ac'           'X1*X3 + X2*X4'
'X3*X4'    'ab'           'X1*X2 + X3*X4'
```

The confounding pattern shows, for example, that the two-way interaction between `X1` and `X2` is confounded by the two-way interaction between `X3` and `X4`.

References

[1] Box, G. E. P., W. G. Hunter, and J. S. Hunter. *Statistics for Experimenters*. Hoboken, NJ: Wiley-Interscience, 1978.

See Also

`fracfact | hadamard`

How To

- "Fractional Factorial Designs" on page 15-5

Purpose

Friedman's test

Syntax

```
p = friedman(X,reps)
p = friedman(X,reps,displayopt)
[p,table] = friedman(...)
[p,table,stats] = friedman(...)
```

Description

`p = friedman(X,reps)` performs the nonparametric Friedman's test to compare column effects in a two-way layout. Friedman's test is similar to classical balanced two-way ANOVA, but it tests only for column effects after adjusting for possible row effects. It does not test for row effects or interaction effects. Friedman's test is appropriate when columns represent treatments that are under study, and rows represent nuisance effects (blocks) that need to be taken into account but are not of any interest.

The different columns of `X` represent changes in a factor A. The different rows represent changes in a blocking factor B. If there is more than one observation for each combination of factors, input `reps` indicates the number of replicates in each "cell," which must be constant.

The matrix below illustrates the format for a set-up where column factor A has three levels, row factor B has two levels, and there are two replicates (`reps=2`). The subscripts indicate row, column, and replicate, respectively.

$$\begin{bmatrix} x_{111} & x_{121} & x_{131} \\ x_{112} & x_{122} & x_{132} \\ x_{211} & x_{221} & x_{231} \\ x_{212} & x_{222} & x_{232} \end{bmatrix}$$

Friedman's test assumes a model of the form

$$x_{ijk} = \mu + \alpha_i + \beta_j + \varepsilon_{ijk}$$

where μ is an overall location parameter, α_i represents the column effect, β_j represents the row effect, and ε_{ijk} represents the error. This test ranks the data within each level of B, and tests for a difference across levels of A. The `p` that `friedman` returns is the p value for the null hypothesis that $\alpha_i = 0$. If the p value is near zero, this casts doubt on the null hypothesis. A sufficiently small p value suggests that at least one column-sample median is significantly different than the others; i.e., there is a main effect due to factor A. The choice of a critical p value to determine whether a result is "statistically significant" is left to the researcher. It is common to declare a result significant if the p value is less than 0.05 or 0.01.

`friedman` also displays a figure showing an ANOVA table, which divides the variability of the ranks into two or three parts:

- The variability due to the differences among the column effects
- The variability due to the interaction between rows and columns (if reps is greater than its default value of 1)
- The remaining variability not explained by any systematic source

The ANOVA table has six columns:

- The first shows the source of the variability.
- The second shows the Sum of Squares (SS) due to each source.
- The third shows the degrees of freedom (df) associated with each source.
- The fourth shows the Mean Squares (MS), which is the ratio SS/df.
- The fifth shows Friedman's chi-square statistic.
- The sixth shows the p value for the chi-square statistic.

`p = friedman(X,reps,displayopt)` enables the ANOVA table display when *`displayopt`* is `'on'` (default) and suppresses the display when *`displayopt`* is `'off'`.

`[p,table] = friedman(...)` returns the ANOVA table (including column and row labels) in cell array `table`. (You can copy a text version of the ANOVA table to the clipboard by selecting `Copy Text` from the **Edit** menu.

`[p,table,stats] = friedman(...)` returns a `stats` structure that you can use to perform a follow-up multiple comparison test. The `friedman` test evaluates the hypothesis that the column effects are all the same against the alternative that they are not all the same. Sometimes it is preferable to perform a test to determine which pairs of column effects are significantly different, and which are not. You can use the `multcompare` function to perform such tests by supplying the `stats` structure as input.

Assumptions

Friedman's test makes the following assumptions about the data in `X`:

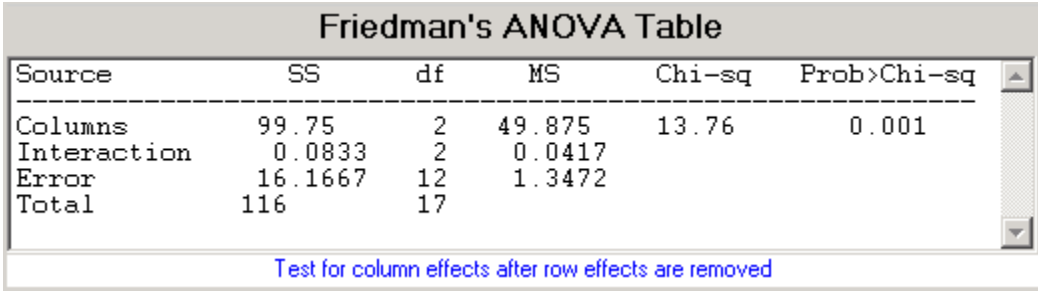
- All data come from populations having the same continuous distribution, apart from possibly different locations due to column and row effects.
- All observations are mutually independent.

The classical two-way ANOVA replaces the first assumption with the stronger assumption that data come from normal distributions.

Examples

Let's repeat the example from the `anova2` function, this time applying Friedman's test. Recall that the data below come from a study of popcorn brands and popper type (Hogg 1987). The columns of the matrix `popcorn` are brands (Gourmet, National, and Generic). The rows are popper type (Oil and Air). The study popped a batch of each brand three times with each popper. The values are the yield in cups of popped popcorn.

```
load popcorn
popcorn
popcorn =
  5.5000  4.5000  3.5000
  5.5000  4.5000  4.0000
  6.0000  4.0000  3.0000
  6.5000  5.0000  4.0000
  7.0000  5.5000  5.0000
  7.0000  5.0000  4.5000

p = friedman(popcorn,3)
p =
  0.0010
```



The small p value of `0.001` indicates the popcorn brand affects the yield of popcorn. This is consistent with the results from `anova2`.

References

[1] Hogg, R. V., and J. Ledolter. *Engineering Statistics*. New York: MacMillan, 1987.

[2] Hollander, M., and D. A. Wolfe. *Nonparametric Statistical Methods*. Hoboken, NJ: John Wiley & Sons, Inc., 1999.

See Also

`anova2`

How To

- `multcompare`

- kruskalwallis

frnd

Purpose

F random numbers

Syntax

```
R = frnd(V1,V2)
R = frnd(V1,V2,m,n,...)
R = frnd(V1,V2,[m,n,...])
```

Description

`R = frnd(V1,V2)` generates random numbers from the *F* distribution with numerator degrees of freedom `V1` and denominator degrees of freedom `V2`. `V1` and `V2` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `V1` or `V2` is expanded to a constant array with the same dimensions as the other input.

`R = frnd(V1,V2,m,n,...)` or `R = frnd(V1,V2,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the *F* distribution with parameters `V1` and `V2`. `V1` and `V2` can each be scalars or arrays of the same size as `R`.

Examples

```
n1 = frnd(1:6,1:6)
n1 =
  0.0022  0.3121  3.0528  0.3189  0.2715  0.9539

n2 = frnd(2,2,[2 3])
n2 =
  0.3186  0.9727  3.0268
  0.2052 148.5816  0.2191

n3 = frnd([1 2 3;4 5 6],1,2,3)
n3 =
  0.6233  0.2322  31.5458
  2.5848  0.2121  4.4955
```

See Also

`random` | `fpdf` | `fcdf` | `finv` | `fstat`

How To

- "F Distribution" on page B-25

Purpose

F mean and variance

Syntax

```
[M,V] = fstat(V1,V2)
```

Description

`[M,V] = fstat(V1,V2)` returns the mean of and variance for the F distribution with numerator degrees of freedom `V1` and denominator degrees of freedom `V2`. `V1` and `V2` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `V1` or `V2` is expanded to a constant arrays with the same dimensions as the other input.

The mean of the F distribution for values of ν_2 greater than 2 is

$$\frac{\nu_2}{\nu_2 - 2}$$

The variance of the F distribution for values of ν_2 greater than 4 is

$$\frac{2\nu_2^2(\nu_1 + \nu_2 - 2)}{\nu_1(\nu_2 - 2)^2(\nu_2 - 4)}$$

The mean of the F distribution is undefined if ν_2 is less than 3. The variance is undefined for ν_2 less than 5.

Examples

`fstat` returns `NaN` when the mean and variance are undefined.

```
[m,v] = fstat(1:5,1:5)
m =
    NaN  NaN  3.0000  2.0000  1.6667
v =
    NaN  NaN  NaN  NaN  8.8889
```

See Also

`fpdf` | `fcdf` | `finv` | `frnd`

How To

- "F Distribution" on page B-25

fsurfht

Purpose

Interactive contour plot

Syntax

```
fsurfht(fun,xlims,ylims)
fsurfht(fun,xlims,ylims,p1,p2,p3,p4,p5)
```

Description

`fsurfht(fun,xlims,ylims)` is an interactive contour plot of the function specified by the text variable `fun`. The *x*-axis limits are specified by `xlims` in the form `[xmin xmax]`, and the *y*-axis limits are specified by `ylims` in the form `[ymin ymax]`.

`fsurfht(fun,xlims,ylims,p1,p2,p3,p4,p5)` allows for five optional parameters that you can supply to the function `fun`.

The intersection of the vertical and horizontal reference lines on the plot defines the current *x* value and *y* value. You can drag these reference lines and watch the calculated *z*-values (at the top of the plot) update simultaneously. Alternatively, you can type the *x* value and *y* value into editable text fields on the *x*-axis and *y*-axis.

Examples

Plot the Gaussian likelihood function for the `gas.mat` data.

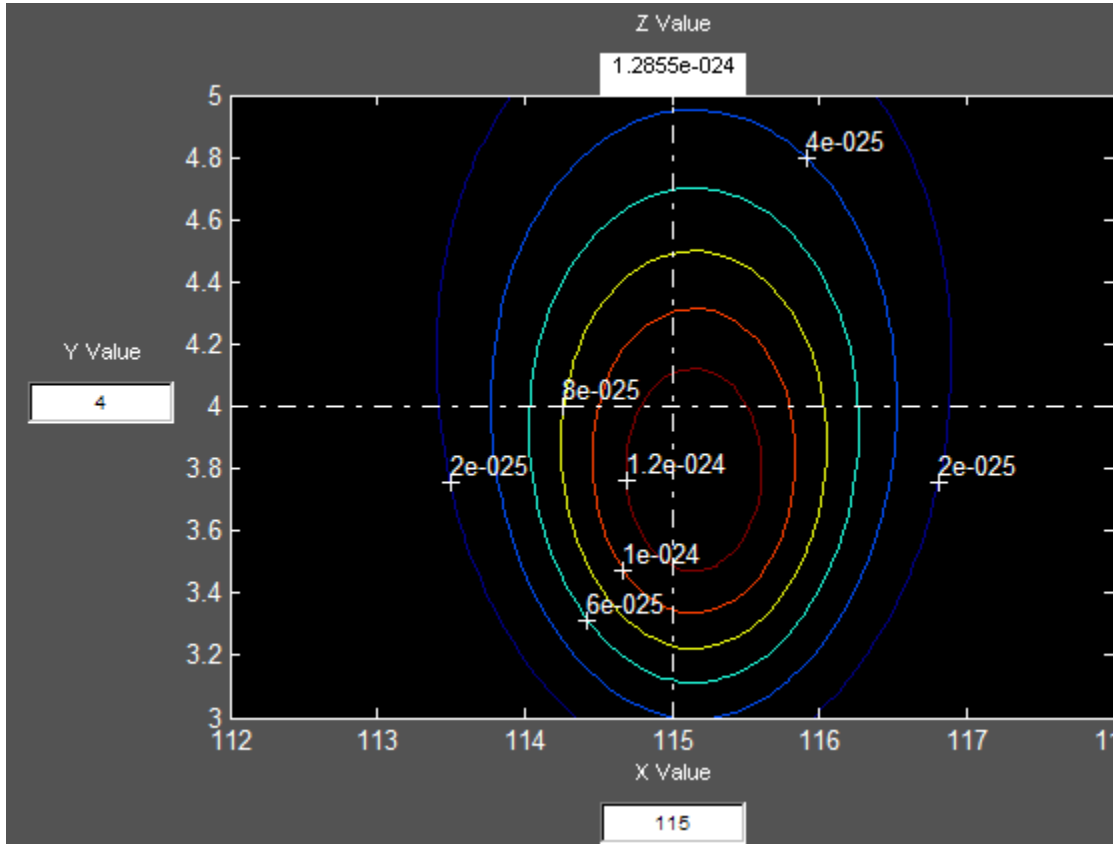
```
load gas
```

Create a function containing the following commands, and name it `gauslike.m`.

```
function z = gauslike(mu,sigma,p1)
n = length(p1);
z = ones(size(mu));
for i = 1:n
z = z .* (normpdf(p1(i),mu,sigma));
end
```

The `gauslike` function calls `normpdf`, treating the data sample as fixed and the parameters μ and σ as variables. Assume that the gas prices are normally distributed, and plot the likelihood surface of the sample.

```
fsurfht('gauslike',[112 118],[3 5],price1)
```



The sample mean is the *x* value at the maximum, but the sample standard deviation is *not* the *y* value at the maximum.

```
mumax = mean(price1)
mumax =
 115.1500
sigmamax = std(price1)*sqrt(19/20)
sigmamax =
  3.7719
```

Purpose

Full factorial design

Syntax

```
dFF = fullfact(levels)
```

Description

`dFF = fullfact(levels)` gives factor settings `dFF` for a full factorial design with n factors, where the number of levels for each factor is given by the vector `levels` of length n. `dFF` is m-by-n, where m is the number of treatments in the full-factorial design. Each row of `dFF` corresponds to a single treatment. Each column contains the settings for a single factor, with integer values from one to the number of levels.

Examples

The following generates an eight-run full-factorial design with two levels in the first factor and four levels in the second factor:

```
dFF = fullfact([2 4])
dFF =
   1   1
   2   1
   1   2
   2   2
   1   3
   2   3
   1   4
   2   4
```

See Also

`ff2n`

Purpose

Gage repeatability and reproducibility study

Syntax

```
gagerr(y,{part,operator})
gagerr(y,GROUP)
gagerr(y,part)
gagerr(...,param1,val1,param2,val2,...)
[TABLE, stats] = gagerr(...)
```

Description

`gagerr(y,{part,operator})` performs a gage repeatability and reproducibility study on measurements in `y` collected by `operator` on `part`. `y` is a column vector containing the measurements on different parts. `part` and `operator` are categorical variables, numeric vectors, character matrices, or cell arrays of strings. The number of elements in `part` and `operator` should be the same as in `y`.

`gagerr` prints a table in the command window in which the decomposition of variance, standard deviation, study var (5.15 x standard deviation) are listed with respective percentages for different sources. Summary statistics are printed below the table giving the number of distinct categories (NDC) and the percentage of Gage R&R of total variations (PRR).

`gagerr` also plots a bar graph showing the percentage of different components of variations. Gage R&R, repeatability, reproducibility, and part-to-part variations are plotted as four vertical bars. Variance and study var are plotted as two groups.

To determine the capability of a measurement system using NDC, use the following guidelines:

- If NDC > 5, the measurement system is capable.
- If NDC < 2, the measurement system is not capable.
- Otherwise, the measurement system may be acceptable.

To determine the capability of a measurement system using PRR, use the following guidelines:

- If PRR < 10%, the measurement system is capable.
- If PRR > 30%, the measurement system is not capable.
- Otherwise, the measurement system may be acceptable.

`gagerr(y,GROUP)` performs a gage R&R study on measurements in `y` with `part` and `operator` represented in `GROUP`. `GROUP` is a numeric matrix whose first and second columns specify different parts and operators, respectively. The number of rows in `GROUP` should be the same as the number of elements in `y`. (See "Grouped Data" on page 2-34.)

`gagerr(y,part)` performs a gage R&R study on measurements in `y` without operator information. The assumption is that all variability is contributed by `part`.

`gagerr(...,param1,val1,param2,val2,...)` performs a gage R&R study using one or more of the following parameter name/value pairs:

- `'spec'` — A two-element vector that defines the lower and upper limit of the process, respectively. In this case, summary statistics printed in the command window include Precision-to-Tolerance Ratio (PTR). Also, the bar graph includes an additional group, the percentage of tolerance.

  To determine the capability of a measurement system using PTR, use the following guidelines:

  - If PTR < 0.1, the measurement system is capable.
  - If PTR > 0.3, the measurement system is not capable.
  - Otherwise, the measurement system may be acceptable.
- `'printtable'` — A string with a value `'on'` or `'off'` that indicates whether the tabular output should be printed in the command window or not. The default value is `'on'`.
- `'printgraph'` — A string with a value `'on'` or `'off'` that indicates whether the bar graph should be plotted or not. The default value is `'on'`.

- `'randomoperator'` — A logical value, `true` or `false`, that indicates whether the effect of `operator` is random or not. The default value is `true`.
- `'model'` — The model to use, specified by one of:
  - `'linear'` — Main effects only (default)
  - `'interaction'` — Main effects plus two-factor interactions
  - `'nested'` — Nest `operator` in `part`

  The default value is `'linear'`.

`[TABLE, stats] = gagerr(...)` returns a 6-by-5 matrix `TABLE` and a structure `stats`. The columns of `TABLE`, from left to right, represent variance, percentage of variance, standard deviations, study var, and percentage of study var. The rows of `TABLE`, from top to bottom, represent different sources of variations: gage R&R, repeatability, reproducibility, operator, operator and part interactions, and part. `stats` is a structure containing summary statistics for the performance of the measurement system. The fields of `stats` are:

- `ndc` — Number of distinct categories
- `prr` — Percentage of gage R&R of total variations
- `ptr` — Precision-to-tolerance ratio. The value is `NaN` if the parameter `'spec'` is not given.

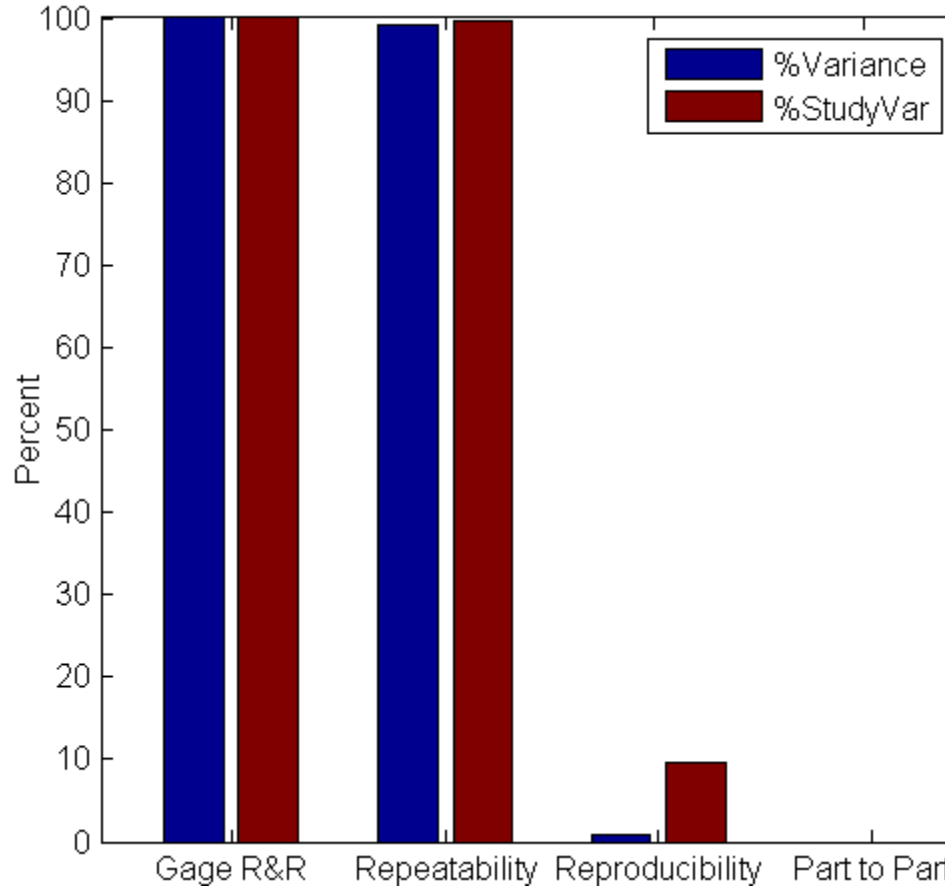
Examples

Conduct a gage R&R study for a simulated measurement system using a mixed ANOVA model without interactions:

```
y = randn(100,1);                                % measurements
part = ceil(3*rand(100,1));                      % parts
operator = ceil(4*rand(100,1));                  % operators
gagerr(y,{part, operator},'randomoperator',true) % analysis

Source            Variance     % Variance      sigma      5.15*sigma    % 5.15*sigma
================================================================================
```

Gage R&R	0.77	100.00	0.88	4.51	100.00
Repeatability	0.76	99.08	0.87	4.49	99.54
Reproducibility	0.01	0.92	0.08	0.43	9.61
Operator	0.01	0.92	0.08	0.43	9.61
Part	0.00	0.00	0.00	0.00	0.00
Total	0.77	100.00	0.88	4.51	

```
              Number of distinct categories (NDC):  0
              % of Gage R&R of total variations (PRR): 100.00

Note: The last column of the above table does not have to sum to 100%
```



How To

- “Grouped Data” on page 2-34

Purpose

Gamma cumulative distribution function

Syntax

```
gamcdf(X,A,B)
[P,PLO,PUP] = gamcdf(X,A,B,pcov,alpha)
```

Description

`gamcdf(X,A,B)` computes the gamma cdf at each of the values in `X` using the corresponding shape parameters in `A` and scale parameters in `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `A` and `B` must be positive.

The gamma cdf is

$$p = F(x \mid a,b) = \frac{1}{b^a \Gamma(a)} \int_0^x t^{a-1} e^{\frac{-t}{b}} dt$$

The result, p, is the probability that a single observation from a gamma distribution with parameters a and b will fall in the interval $[0\ x]$.

`[P,PLO,PUP] = gamcdf(X,A,B,pcov,alpha)` produces confidence bounds for `P` when the input parameters `A` and `B` are estimates. `pcov` is a 2-by-2 matrix containing the covariance matrix of the estimated parameters. `alpha` has a default value of 0.05, and specifies `100(1-alpha)`% confidence bounds. `PLO` and `PUP` are arrays of the same size as `P` containing the lower and upper confidence bounds.

`gammainc` is the gamma distribution with b fixed at 1.

Examples

```
a = 1:6;
b = 5:10;
prob = gamcdf(a.*b,a,b)
prob =
  0.6321  0.5940  0.5768  0.5665  0.5595  0.5543
```

The mean of the gamma distribution is the product of the parameters, ab. In this example, the mean approaches the median as it increases (i.e., the distribution becomes more symmetric).

See Also

`cdf` | `gampdf` | `gaminv` | `gamstat` | `gamfit` | `gamlike` | `gamrnd` | `gamma`

How To

- "Gamma Distribution" on page B-27

Purpose

Gamma parameter estimates

Syntax

```
phat = gamfit(data)
[phat,pci] = gamfit(data)
[phat,pci] = gamfit(data,alpha)
[...] = gamfit(data,alpha,censoring,freq,options)
```

Description

`phat = gamfit(data)` returns the maximum likelihood estimates (MLEs) for the parameters of the gamma distribution given the data in vector `data`.

`[phat,pci] = gamfit(data)` returns MLEs and 95% percent confidence intervals. The first row of `pci` is the lower bound of the confidence intervals; the last row is the upper bound.

`[phat,pci] = gamfit(data,alpha)` returns `100(1 - alpha)`% confidence intervals. For example, `alpha = 0.01` yields 99% confidence intervals.

`[...] = gamfit(data,alpha,censoring)` accepts a Boolean vector of the same size as `data` that is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = gamfit(data,alpha,censoring,freq)` accepts a frequency vector of the same size as `data`. `freq` typically contains integer frequencies for the corresponding elements in `data`, but may contain any nonnegative values.

`[...] = gamfit(data,alpha,censoring,freq,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates. The gamma fit function accepts an `options` structure which can be created using the function `statset`. Enter `statset('gamfit')` to see the names and default values of the parameters that `gamfit` accepts in the `options` structure.

Examples

Fit a gamma distribution to random data generated from a specified gamma distribution:

```
a = 2; b = 4;
data = gamrnd(a,b,100,1);

[p,ci] = gamfit(data)
p =
  2.1990  3.7426
ci =
  1.6840  2.8298
  2.7141  4.6554
```

References

[1] Hahn, Gerald J., and S. S. Shapiro. *Statistical Models in Engineering*. Hoboken, NJ: John Wiley & Sons, Inc., 1994, p. 88.

See Also

`mle` | `gamlike` | `gampdf` | `gamcdf` | `gaminv` | `gamstat` | `gamrnd`

How To

- "Gamma Distribution" on page B-27

Purpose

Gamma inverse cumulative distribution function

Syntax

```
X = gaminv(P,A,B)
[X,XLO,XUP] = gamcdf(P,A,B,pcov,alpha)
```

Description

`X = gaminv(P,A,B)` computes the inverse of the gamma cdf with shape parameters in `A` and scale parameters in `B` for the corresponding probabilities in `P`. `P`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `A` and `B` must all be positive, and the values in `P` must lie on the interval [0 1].

The gamma inverse function in terms of the gamma cdf is

$$x = F^{-1}(p \mid a,b) = \{x : F(x \mid a,b) = p\}$$

where

$$p = F(x \mid a,b) = \frac{1}{b^a \Gamma(a)} \int_0^x t^{a-1} e^{\frac{-t}{b}} dt$$

`[X,XLO,XUP] = gamcdf(P,A,B,pcov,alpha)` produces confidence bounds for `P` when the input parameters `A` and `B` are estimates. `pcov` is a 2-by-2 matrix containing the covariance matrix of the estimated parameters. `alpha` has a default value of 0.05, and specifies `100(1-alpha)`% confidence bounds. `PLO` and `PUP` are arrays of the same size as `P` containing the lower and upper confidence bounds.

Algorithms

There is no known analytical solution to the integral equation above. `gaminv` uses an iterative approach (Newton's method) to converge on the solution.

Examples

This example shows the relationship between the gamma cdf and its inverse function.

```
a = 1:5;
b = 6:10;
x = gaminv(gamcdf(1:5,a,b),a,b)
x =
  1.0000  2.0000  3.0000  4.0000  5.0000
```

See Also

icdf | gamcdf | gampdf | gamstat | gamfit | gamlike | gamrnd

How To

- "Gamma Distribution" on page B-27

Purpose

Gamma negative log-likelihood

Syntax

```
nlogL = gamlike(params,data)
[nlogL,AVAR] = gamlike(params,data)
```

Description

`nlogL = gamlike(params,data)` returns the negative of the gamma log-likelihood of the parameters, `params`, given `data`. `params(1)=A`, shape parameters, and `params(2)=B`, scale parameters.

`[nlogL,AVAR] = gamlike(params,data)` also returns `AVAR`, which is the asymptotic variance-covariance matrix of the parameter estimates when the values in `params` are the maximum likelihood estimates. `AVAR` is the inverse of Fisher's information matrix. The diagonal elements of `AVAR` are the asymptotic variances of their respective parameters.

`[...] = gamlike(params,data,censoring)` accepts a Boolean vector of the same size as `data` that is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = gamfit(params,data,censoring,freq)` accepts a frequency vector of the same size as `data`. `freq` typically contains integer frequencies for the corresponding elements in `data`, but may contain any non-negative values.

`gamlike` is a utility function for maximum likelihood estimation of the gamma distribution. Since `gamlike` returns the negative gamma log-likelihood function, minimizing `gamlike` using `fminsearch` is the same as maximizing the likelihood.

Examples

Compute the negative log-likelihood of parameter estimates computed by the `gamfit` function:

```
a = 2; b = 3;
r = gamrnd(a,b,100,1);

[nlogL,AVAR] = gamlike(gamfit(r),r)
nlogL =
  267.5648
AVAR =
```

```
    0.0788   -0.1104
   -0.1104    0.1955
```

See Also

gamfit | gampdf | gamcdf | gaminv | gamstat | gamrnd

How To

- “Gamma Distribution” on page B-27

Purpose

Gamma probability density function

Syntax

```
Y = gampdf(X,A,B)
```

Description

`Y = gampdf(X,A,B)` computes the gamma pdf at each of the values in `X` using the corresponding shape parameters in `A` and scale parameters in `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `A` and `B` must all be positive, and the values in `X` must lie on the interval $[0\ \infty)$.

The gamma pdf is

$$y = f(x \mid a,b) = \frac{1}{b^a \Gamma(a)} x^{a-1} e^{\frac{-x}{b}}$$

The gamma probability density function is useful in reliability models of lifetimes. The gamma distribution is more flexible than the exponential distribution in that the probability of a product surviving an additional period may depend on its current age. The exponential and χ^2 functions are special cases of the gamma function.

Examples

The exponential distribution is a special case of the gamma distribution.

```
mu = 1:5;

y = gampdf(1,1,mu)
y =
  0.3679  0.3033  0.2388  0.1947  0.1637

y1 = exppdf(1,mu)
y1 =
  0.3679  0.3033  0.2388  0.1947  0.1637
```

See Also

`pdf` | `gamcdf` | `gaminv` | `gamstat` | `gamfit` | `gamlike` | `gamrnd`

How To

- "Gamma Distribution" on page B-27

Purpose

Gamma random numbers

Syntax

```
R = gamrnd(A,B)
R = gamrnd(A,B,m,n,...)
R = gamrnd(A,B,[m,n,...])
```

Description

`R = gamrnd(A,B)` generates random numbers from the gamma distribution with shape parameters in `A` and scale parameters in `B`. `A` and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `A` or `B` is expanded to a constant array with the same dimensions as the other input.

`R = gamrnd(A,B,m,n,...)` or `R = gamrnd(A,B,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the gamma distribution with parameters `A` and `B`. `A` and `B` can each be scalars or arrays of the same size as `R`.

Examples

```
n1 = gamrnd(1:5,6:10)
n1 =
  9.1132  12.8431  24.8025  38.5960 106.4164

n2 = gamrnd(5,10,[1 5])
n2 =
  30.9486  33.5667  33.6837  55.2014  46.8265

n3 = gamrnd(2:6,3,1,5)
n3 =
  12.8715  11.3068  3.0982  15.6012  21.6739
```

See Also

`randg` | `random` | `gampdf` | `gamcdf` | `gaminv` | `gamstat` | `gamfit` | `gamlike`

How To

- "Gamma Distribution" on page B-27

gamstat

Purpose

Gamma mean and variance

Syntax

```
[M,V] = gamstat(A,B)
```

Description

`[M,V] = gamstat(A,B)` returns the mean of and variance for the gamma distribution with shape parameters in `A` and scale parameters in `B`. `A` and `B` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `M` and `V`. A scalar input for `A` or `B` is expanded to a constant array with the same dimensions as the other input.

The mean of the gamma distribution with parameters a and b is ab. The variance is ab^2.

Examples

```
[m,v] = gamstat(1:5,1:5)
m =
   1   4   9  16  25
v =
   1   8  27  64  125

[m,v] = gamstat(1:5,1./(1:5))
m =
   1   1   1   1   1
v =
  1.0000  0.5000  0.3333  0.2500  0.2000
```

See Also

`gampdf` | `gamcdf` | `gaminv` | `gamfit` | `gamlike` | `gamrnd`

How To

- "Gamma Distribution" on page B-27

Purpose

Greater than or equal relation for handles

Syntax

```
h1 >= h2
```

Description

`h1 >= h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise `>=` result.

If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = ge(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `eq` | `gt` | `le` | `lt` | `ne`

geocdf

Purpose

Geometric cumulative distribution function

Syntax

```
Y = geocdf(X,P)
```

Description

`Y = geocdf(X,P)` computes the geometric cdf at each of the values in `X` using the corresponding probabilities in `P`. `X` and `P` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `P` must lie on the interval [0 1].

The geometric cdf is

$$y = F(x \mid p) = \sum_{i=0}^{floor(x)} pq^i$$

where $q = 1 - p$.

The result, y, is the probability of observing up to x trials before a success, when the probability of success in any given trial is p.

Examples

Suppose you toss a fair coin repeatedly. If the coin lands face up (heads), that is a success. What is the probability of observing three or fewer tails before getting a heads?

```
p = geocdf(3,0.5)
p =
  0.9375
```

See Also

`cdf` | `geopdf` | `geoinv` | `geostat` | `geornd` | `mle`

How To

- "Geometric Distribution" on page B-41

Purpose

Geometric inverse cumulative distribution function

Syntax

```
X = geoinv(Y,P)
```

Description

`X = geoinv(Y,P)` returns the smallest positive integer `X` such that the geometric cdf evaluated at `X` is equal to or exceeds `Y`. You can think of `Y` as the probability of observing `X` successes in a row in independent trials where `P` is the probability of success in each trial.

`Y` and `P` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `P` or `Y` is expanded to a constant array with the same dimensions as the other input. The values in `P` and `Y` must lie on the interval [0 1].

Examples

The probability of correctly guessing the result of 10 coin tosses in a row is less than 0.001 (unless the coin is not fair).

```
psychic = geoinv(0.999,0.5)
psychic =
   9
```

The example below shows the inverse method for generating random numbers from the geometric distribution.

```
rndgeo = geoinv(rand(2,5),0.5)
rndgeo =
   0   1   3   1   0
   0   1   0   2   0
```

See Also

`icdf` | `geocdf` | `geopdf` | `geostat` | `geornd`

How To

- "Geometric Distribution" on page B-41

geomean

Purpose

Geometric mean

Syntax

```
m = geomean(x)
geomean(X,dim)
```

Description

`m = geomean(x)` calculates the geometric mean of a sample. For vectors, `geomean(x)` is the geometric mean of the elements in `x`. For matrices, `geomean(X)` is a row vector containing the geometric means of each column. For N-dimensional arrays, `geomean` operates along the first nonsingleton dimension of `X`.

`geomean(X,dim)` takes the geometric mean along the dimension `dim` of `X`.

The geometric mean is

$$m = \left[\prod_{i=1}^{n} x_i\right]^{\frac{1}{n}}$$

Examples

The arithmetic mean is greater than or equal to the geometric mean.

```
x = exprnd(1,10,6);

geometric = geomean(x)
geometric =
  0.7466  0.6061  0.6038  0.2569  0.7539  0.3478

average = mean(x)
average =
  1.3509  1.1583  0.9741  0.5319  1.0088  0.8122
```

See Also

`mean` | `median` | `harmmean` | `trimmean`

How To

- "Geometric Distribution" on page B-41

Purpose

Geometric probability density function

Syntax

```
Y = geopdf(X,P)
```

Description

`Y = geopdf(X,P)` computes the geometric pdf at each of the values in `X` using the corresponding probabilities in `P`. `X` and `P` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `P` must lie on the interval [0 1].

The geometric pdf is

$$y = f(x \mid p) = pq^x I_{(0,1,\ldots)}(x)$$

where $q = 1 - p$.

Examples

Suppose you toss a fair coin repeatedly. If the coin lands face up (heads), that is a success. What is the probability of observing exactly three tails before getting a heads?

```
p = geopdf(3,0.5)
p =
  0.0625
```

See Also

`pdf` | `geocdf` | `geoinv` | `geostat` | `geornd`

How To

- "Geometric Distribution" on page B-41

geornd

Purpose

Geometric random numbers

Syntax

```
R = geornd(P)
R = geornd(P,m,n,...)
R = geornd(P,[m,n,...])
```

Description

`R = geornd(P)` generates geometric random numbers with probability parameter `P`. `P` can be a vector, a matrix, or a multidimensional array. The size of `R` is the size of `P`. The geometric distribution is useful when you want to model the number of successive failures preceding a success, where the probability of success in any given trial is the constant `P`. The parameters in `P` must lie in the interval [0 1].

`R = geornd(P,m,n,...)` or `R = geornd(P,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the geometric distribution with probability parameter `P`. `P` can be a scalar or an array of the same size as `R`.

Examples

```
r1 = geornd(1 ./ 2.^(1:6))
r1 =
   2  10   2   5   2  60

r2 = geornd(0.01,[1 5])
r2 =
  65  18  334  291  63

r3 = geornd(0.5,1,6)
r3 =
   0   7   1   3   1   0
```

See Also

`random` | `geopdf` | `geocdf` | `geoinv` | `geostat`

How To

- "Geometric Distribution" on page B-41

Purpose

Geometric mean and variance

Syntax

```
[M,V] = geostat(P)
```

Description

`[M,V] = geostat(P)` returns the mean of and variance for the geometric distribution with corresponding probabilities in `P`.

The mean of the geometric distribution with parameter p is q/p, where $q = 1\text{-}p$. The variance is q/p^2.

Examples

```
[m,v] = geostat(1./(1:6))
m =
    0  1.0000  2.0000  3.0000  4.0000  5.0000
v =
    0  2.0000  6.0000  12.0000  20.0000  30.0000
```

See Also

`geopdf` | `geocdf` | `geoinv` | `geornd`

How To

- "Geometric Distribution" on page B-41

dataset.get

Purpose

Access dataset array properties

Syntax

```
get(A)
s = get(A)
p = get(A,PropertyName)
p = get(A,{PropertyName1,PropertyName2,...})
```

Description

`get(A)` displays a list of property/value pairs for the dataset array `A`.

`s = get(A)` returns the values in a scalar structure `s` with field names given by the properties.

`p = get(A,PropertyName)` returns the value of the property specified by the string *`PropertyName`*.

`p = get(A,{PropertyName1,PropertyName2,...})` allows multiple property names to be specified and returns their values in a cell array.

Examples

Create a dataset array from Fisher's iris data and access the information:

```
load fisheriris
NumObs = size(meas,1);
NameObs = strcat({'Obs'},num2str((1:NumObs)','%-d'));
iris = dataset({nominal(species),'species'},...
               {meas,'SL','SW','PL','PW'},...
               'ObsNames',NameObs);

get(iris)
   Description: ''
   Units: {}
   DimNames: {'Observations' 'Variables'}
   UserData: []
   ObsNames: {150x1 cell}
   VarNames: {'species' 'SL' 'SW' 'PL' 'PW'}

ON = get(iris,'ObsNames');
ON(1:3)
```

```
ans =
    'Obs1'
    'Obs2'
    'Obs3'
```

See Also

set | summary

categorical.getlabels

Purpose

Access categorical array labels

Syntax

```
labels = getlabels(A)
```

Description

`labels = getlabels(A)` returns the labels of the levels in the categorical array `A` as a cell array of strings `labels`. For ordinal `A`, the labels are returned in the order of the levels.

Examples

Example 1

Display levels in a nominal and an ordinal array:

```
standings = nominal({'Leafs','Canadiens','Bruins'});
getlabels(standings)
ans =
    'Bruins'  'Canadiens'  'Leafs'

standings = ordinal(1:3,{'Leafs','Canadiens','Bruins'});
getlabels(standings)
ans =
    'Leafs'  'Canadiens'  'Bruins'
```

Example 2

Display age groups containing data in `hospital.mat`:

```
load hospital
edges = 0:10:100;
labels = strcat(num2str((0:10:90)','%d'),{'s'});
AgeGroup = ordinal(hospital.Age,labels,[],edges);
AgeGroup = droplevels(AgeGroup);
getlabels(AgeGroup)
ans =
    '20s'    '30s'    '40s'    '50s'
```

See Also

`getlevels` | `setlabels`

Purpose

Get categorical array levels

Syntax

```
S = getlevels(A)
```

Description

`S = getlevels(A)` returns the levels for the categorical array `A`. `S` is a vector with the same type as `A`.

See Also

`getlabels`

gevcdf

Purpose

Generalized extreme value cumulative distribution function

Syntax

```
P = gevcdf(X,k,sigma,mu)
```

Description

`P = gevcdf(X,k,sigma,mu)` returns the cdf of the generalized extreme value (GEV) distribution with shape parameter `k`, scale parameter `sigma`, and location parameter, `mu`, evaluated at the values in `X`. The size of `P` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `k`, `sigma`, and `mu` are 0, 1, and 0, respectively.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblcdf` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evcdf` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`cdf` | `gevpdf` | `gevinv` | `gevstat` | `gevfit` | `gevlike` | `gevrnd`

How To

- "Generalized Extreme Value Distribution" on page B-32

Purpose

Generalized extreme value parameter estimates

Syntax

```
parmhat = gevfit(X)
[parmhat,parmci] = gevfit(X)
[parmhat,parmci] = gevfit(X,alpha)
[...] = gevfit(X,alpha,options)
```

Description

`parmhat = gevfit(X)` returns maximum likelihood estimates of the parameters for the generalized extreme value (GEV) distribution given the data in X. `parmhat(1)` is the shape parameter, `k`, `parmhat(2)` is the scale parameter, `sigma`, and `parmhat(3)` is the location parameter, `mu`.

`[parmhat,parmci] = gevfit(X)` returns 95% confidence intervals for the parameter estimates.

`[parmhat,parmci] = gevfit(X,alpha)` returns `100(1-alpha)`% confidence intervals for the parameter estimates.

`[...] = gevfit(X,alpha,options)` specifies control parameters for the iterative algorithm used to compute ML estimates. This argument can be created by a call to `statset`. See `statset('gevfit')` for parameter names and default values. Pass in `[]` for `alpha` to use the default values.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblfit` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evfit` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution is defined for `k*(X-mu)/sigma > -1`.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`mle` | `gevlike` | `gevpdf` | `gevcdf` | `gevinv` | `gevstat` | `gevrnd`

How To

- "Generalized Extreme Value Distribution" on page B-32

Purpose

Generalized extreme value inverse cumulative distribution function

Syntax

```
X = gevinv(P,k,sigma,mu)
```

Description

`X = gevinv(P,k,sigma,mu)` returns the inverse cdf of the generalized extreme value (GEV) distribution with shape parameter `k`, scale parameter `sigma`, and location parameter `mu`, evaluated at the values in `P`. The size of `X` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `k`, `sigma`, and `mu` are 0, 1, and 0, respectively.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblinv` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evinv` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`icdf` | `gevcdf` | `gevpdf` | `gevstat` | `gevfit` | `gevlike` | `gevrnd`

How To

- "Generalized Extreme Value Distribution" on page B-32

gevlike

Purpose

Generalized extreme value negative log-likelihood

Syntax

```
nlogL = gevlike(params,data)
[nlogL,ACOV] = gevlike(params,data)
```

Description

`nlogL = gevlike(params,data)` returns the negative of the log-likelihood `nlogL` for the generalized extreme value (GEV) distribution, evaluated at parameters `params`. `params(1)` is the shape parameter, `k`, `params(2)` is the scale parameter, `sigma`, and `params(3)` is the location parameter, `mu`.

`[nlogL,ACOV] = gevlike(params,data)` returns the inverse of Fisher's information matrix, `ACOV`. If the input parameter values in `params` are the maximum likelihood estimates, the diagonal elements of `ACOV` are their asymptotic variances. `ACOV` is based on the observed Fisher's information, not the expected information.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wbllike` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evlike` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah.*Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`gevfit` | `gevpdf` | `gevcdf` | `gevinv` | `gevstat` | `gevrnd`

How To

- "Generalized Extreme Value Distribution" on page B-32

Purpose

Generalized extreme value probability density function

Syntax

```
Y = gevpdf(X,k,sigma,mu)
```

Description

`Y = gevpdf(X,k,sigma,mu)` returns the pdf of the generalized extreme value (GEV) distribution with shape parameter `k`, scale parameter `sigma`, and location parameter, `mu`, evaluated at the values in `X`. The size of `Y` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `k`, `sigma`, and `mu` are 0, 1, and 0, respectively.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblpdf` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evcdf` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`pdf` | `gevcdf` | `gevinv` | `gevstat` | `gevfit` | `gevlike` | `gevrnd`

How To

- "Generalized Extreme Value Distribution" on page B-32

gevrnd

Purpose

Generalized extreme value random numbers

Syntax

```
R = gevrnd(k,sigma,mu)
R = gevrnd(k,sigma,mu,m,n,...)
R = gevrnd(k,sigma,mu,[m,n,...])
```

Description

`R = gevrnd(k,sigma,mu)` returns an array of random numbers chosen from the generalized extreme value (GEV) distribution with shape parameter `k`, scale parameter `sigma`, and location parameter, `mu`. The size of `R` is the common size of the input arguments if all are arrays. If any parameter is a scalar, the size of `R` is the size of the other parameters.

`R = gevrnd(k,sigma,mu,m,n,...)` or `R = gevrnd(k,sigma,mu,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the GEV distribution with parameters `k`, `sigma`, and `mu`. The `k`, `sigma`, `mu` parameters can each be scalars or arrays of the same size as `R`.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblrnd` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evrnd` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`random` | `gevpdf` | `gevcdf` | `gevinv` | `gevstat` | `gevfit` | `gevlike`

How To

- "Generalized Extreme Value Distribution" on page B-32

gevstat

Purpose

Generalized extreme value mean and variance

Syntax

```
[M,V] = gevstat(k,sigma,mu)
```

Description

`[M,V] = gevstat(k,sigma,mu)` returns the mean of and variance for the generalized extreme value (GEV) distribution with shape parameter `k`, scale parameter `sigma`, and location parameter, `mu`. The sizes of `M` and `V` are the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `k`, `sigma`, and `mu` are 0, 1, and 0, respectively.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblstat` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evstat` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`gevpdf` | `gevcdf` | `gevinv` | `gevfit` | `gevlike` | `gevrnd`

How To

- "Generalized Extreme Value Distribution" on page B-32

Purpose

Interactively add line to plot

Syntax

```
gline(h)
gline
hline = gline(...)
```

Description

`gline(h)` allows you to draw a line segment in the figure with handle `h` by clicking the pointer at the two endpoints. A rubber-band line tracks the pointer movement.

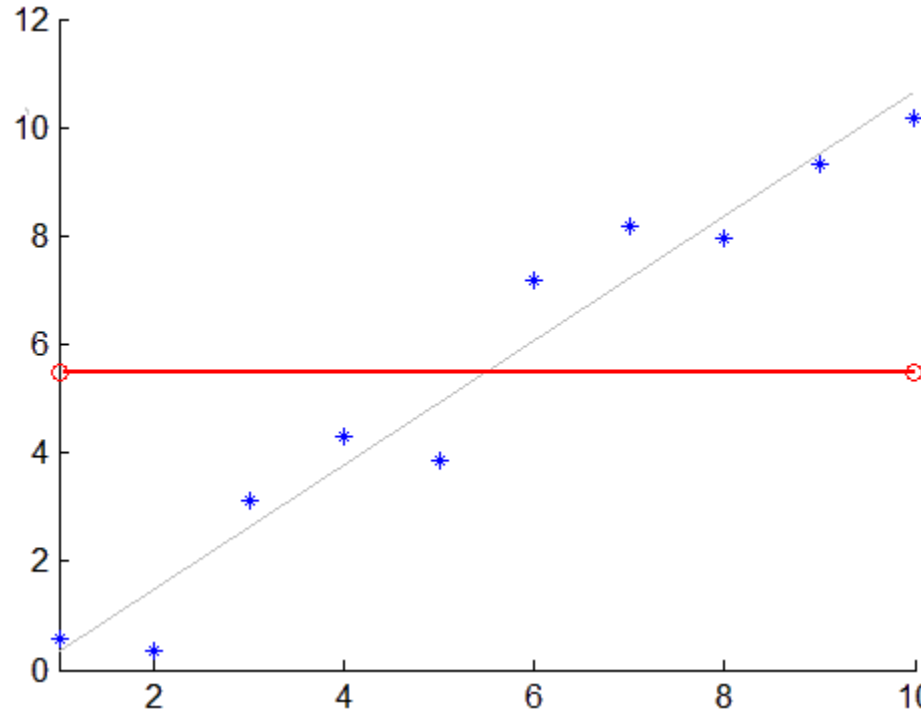
`gline` with no input arguments defaults to `h = gcf` and draws in the current figure.

`hline = gline(...)` returns the handle `hline` to the line.

Examples

Use `gline` to connect two points in a plot:

```
x = 1:10;

y = x + randn(1,10);
scatter(x,y,25,'b','*')

lsline

mu = mean(y);
hold on
plot([1 10],[mu mu],'ro')

hline = gline; % Connect circles
set(hline,'Color','r')
```



See Also

`refline` | `refcurve` | `lsline`

Purpose

Generalized linear model regression

Syntax

```
b = glmfit(X,y,distr)
b = glmfit(X,y,distr,param1,val1,param2,val2,...)
[b,dev] = glmfit(...)
[b,dev,stats] = glmfit(...)
```

Description

`b = glmfit(X,y,distr)` returns a p-by-1 vector `b` of coefficient estimates for a generalized linear regression of the responses in `y` on the predictors in `X`, using the distribution *`distr`*. `X` is an n-by-p matrix of p predictors at each of n observations. *`distr`* can be any of the following strings: `'binomial'`, `'gamma'`, `'inverse gaussian'`, `'normal'` (the default), and `'poisson'`.

In most cases, `y` is an n-by-1 vector of observed responses. For the binomial distribution, `y` can be a binary vector indicating success or failure at each observation, or a two column matrix with the first column indicating the number of successes for each observation and the second column indicating the number of trials for each observation.

This syntax uses the canonical link (see below) to relate the distribution to the predictors.

Note By default, `glmfit` adds a first column of 1s to `X`, corresponding to a constant term in the model. Do not enter a column of 1s directly into `X`. You can change the default behavior of `glmfit` using the `'constant'` parameter, below.

`glmfit` treats `NaN`s in either `X` or `y` as missing values, and ignores them.

`b = glmfit(X,y,distr,param1,val1,param2,val2,...)` additionally allows you to specify optional parameter name/value pairs to control the model fit. Acceptable parameters are as follows:

Parameter	Value	Description
`'link'`	`'identity'`, default for the distribution `'normal'`	$\mu = Xb$
	`'log'`, default for the distribution `'poisson'`	$\log(\mu) = Xb$
	`'logit'`, default for the distribution `'binomial'`	$\log(\mu/(1-\mu)) = Xb$
	`'probit'`	$\text{norminv}(\mu) = Xb$
	`'comploglog'`	$\log(-\log(1-\mu)) = Xb$
	`'reciprocal'`	$1/\mu = Xb$
	`'loglog'`, default for the distribution `'gamma'`	$\log(-\log(\mu)) = Xb$
	`p` (a number), default for the distribution `'inverse gaussian'` (with $p = -2$)	$\mu^p = Xb$
	cell array of the form `{FL FD FI}`, containing three function handles, created using `@`, that define the link (`FL`), the derivative of the link (`FD`), and the inverse link (`FI`).	User-specified link function

Parameter	Value	Description
'estdisp'	'on'	Estimates a dispersion parameter for the binomial or Poisson distribution
	'off' (Default for binomial or Poisson distribution)	Uses the theoretical value of 1.0 for those distributions
'offset'	Vector	Used as an additional predictor variable, but with a coefficient value fixed at 1.0
'weights'	Vector of prior weights, such as the inverses of the relative variance of each observation	
'constant'	'on' (default)	Includes a constant term in the model. The coefficient of the constant term is the first element of b.
	'off'	Omit the constant term

[b,dev] = glmfit(...)returns dev, the deviance of the fit at the solution vector. The deviance is a generalization of the residual sum of squares. It is possible to perform an analysis of deviance to compare several models, each a subset of the other, and to test whether the model with more terms is significantly better than the model with fewer terms.

[b,dev,stats] = glmfit(...) returns dev and stats.

stats is a structure with the following fields:

- beta — Coefficient estimates b
- dfe — Degrees of freedom for error
- s — Theoretical or estimated dispersion parameter

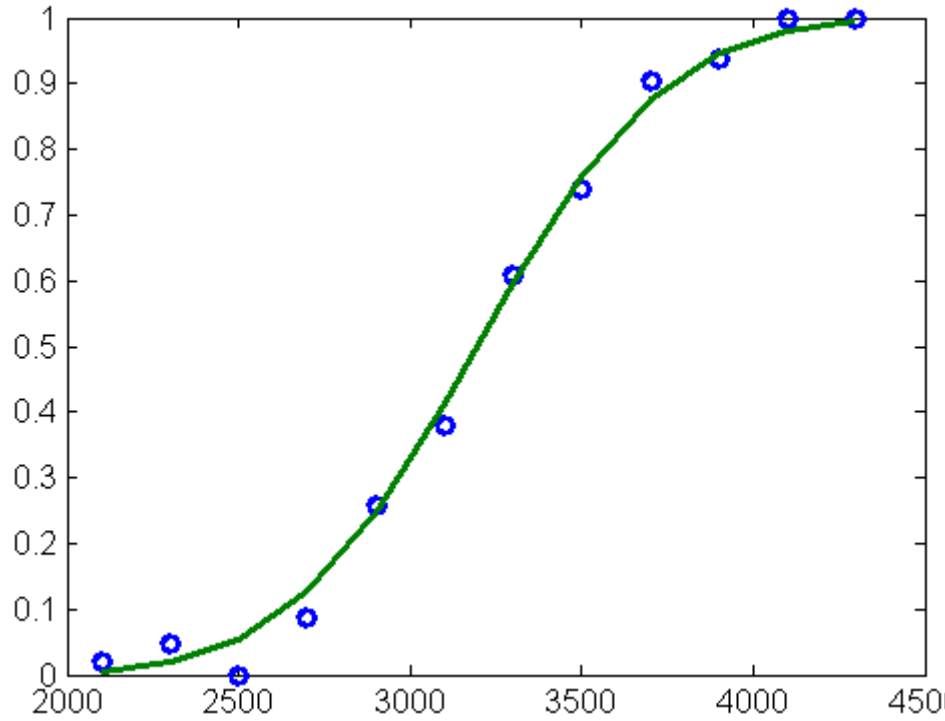
- `sfit` — Estimated dispersion parameter
- `se` — Vector of standard errors of the coefficient estimates `b`
- `coeffcorr` — Correlation matrix for `b`
- `covb` — Estimated covariance matrix for B
- `t` — *t* statistics for `b`
- `p` — *p*-values for `b`
- `resid` — Vector of residuals
- `residp` — Vector of Pearson residuals
- `residd` — Vector of deviance residuals
- `resida` — Vector of Anscombe residuals

If you estimate a dispersion parameter for the binomial or Poisson distribution, then `stats.s` is set equal to `stats.sfit`. Also, the elements of `stats.se` differ by the factor `stats.s` from their theoretical values.

Examples

Fit a probit regression model for `y` on `x`. Each `y(i)` is the number of successes in `n(i)` trials.

```
x = [2100 2300 2500 2700 2900 3100 ...
     3300 3500 3700 3900 4100 4300]';
n = [48 42 31 34 31 21 23 23 21 16 17 21]';
y = [1 2 0 3 8 8 14 17 19 15 17 21]';
b = glmfit(x,[y n],'binomial','link','probit');
yfit = glmval(b, x,'probit','size', n);
plot(x, y./n,'o',x,yfit./n,'-','LineWidth',2)
```



References

[1] Dobson, A. J. *An Introduction to Generalized Linear Models*. New York: Chapman & Hall, 1990.

[2] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

[3] Collett, D. *Modeling Binary Data*. New York: Chapman & Hall, 2002.

See Also

`glmval` | `regress` | `regstats`

Purpose

Generalized linear model values

Syntax

```
yhat = glmval(b,X,link)
[yhat,dylo,dyhi] = glmval(b,X,link,stats)
[...] = glmval(...,param1,val1,param2,val2,...)
```

Description

`yhat = glmval(b,X,link)` computes predicted values for the generalized linear model with link function `link` and predictors `X`. Distinct predictor variables should appear in different columns of `X`. `b` is a vector of coefficient estimates as returned by the `glmfit` function. `link` can be any of the strings used as values for the `link` parameter in the `glmfit` function.

Note By default, `glmval` adds a first column of 1s to `X`, corresponding to a constant term in the model. Do not enter a column of 1s directly into `X`. You can change the default behavior of `glmval` using the `'constant'` parameter, below.

`[yhat,dylo,dyhi] = glmval(b,X,link,stats)` also computes 95% confidence bounds for the predicted values. When the `stats` structure output of the `glmfit` function is specified, `dylo` and `dyhi` are also returned. `dylo` and `dyhi` define a lower confidence bound of `yhat-dylo`, and an upper confidence bound of `yhat+dyhi`. Confidence bounds are nonsimultaneous, and apply to the fitted curve, not to a new observation.

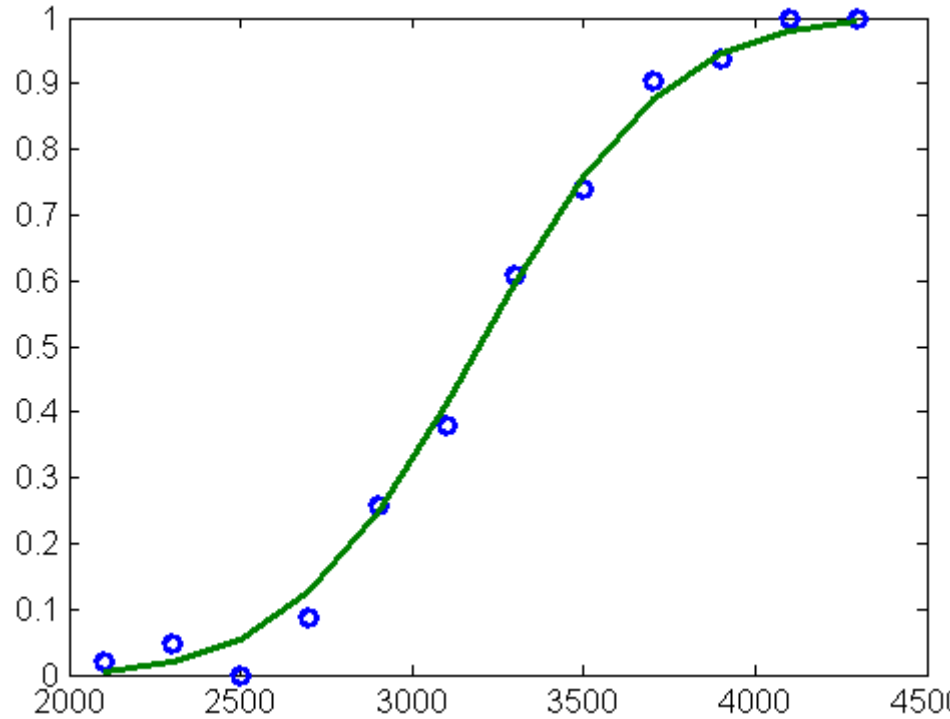
`[...] = glmval(...,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs to control the predicted values. Acceptable parameters are:

Parameter	Value
`'confidence'` — the confidence level for the confidence bounds	A scalar between 0 and 1
`'size'` — the size parameter (N) for a binomial model	A scalar, or a vector with one value for each row of X
`'offset'` — used as an additional predictor variable, but with a coefficient value fixed at 1.0	A vector
`'constant'`	• `'on'` — Includes a constant term in the model. The coefficient of the constant term is the first element of `b`. • `'off'` — Omit the constant term

Examples

Fit a probit regression model for `y` on `x`. Each `y(i)` is the number of successes in `n(i)` trials.

```
x = [2100 2300 2500 2700 2900 3100 ...
     3300 3500 3700 3900 4100 4300]';
n = [48 42 31 34 31 21 23 23 21 16 17 21]';
y = [1 2 0 3 8 8 14 17 19 15 17 21]';
b = glmfit(x,[y n],'binomial','link','probit');
yfit = glmval(b,x,'probit','size',n);
plot(x, y./n,'o',x,yfit./n,'-','LineWidth',2)
```



References

[1] Dobson, A. J. *An Introduction to Generalized Linear Models.* New York: Chapman & Hall, 1990.

[2] McCullagh, P., and J. A. Nelder. *Generalized Linear Models.* New York: Chapman & Hall, 1990.

[3] Collett, D. *Modeling Binary Data.* New York: Chapman & Hall, 2002.

See Also

`glmfit`

Purpose

Glyph plot

Syntax

```
glyphplot(X)
glyphplot(X,'glyph','face')
glyphplot(X,'glyph','face','features',f)
glyphplot(X,...,'grid',[rows,cols])
glyphplot(X,...,'grid',[rows,cols],'page',p)
glyphplot(X,...,'centers',C)
glyphplot,...,'centers',C,'radius',r)
glyphplot(X,...,'obslabels',labels)
glyphplot(X,...,'standardize',method)
glyphplot(X,...,prop1,val1,...)
h = glyphplot(X,...)
```

Description

`glyphplot(X)` creates a star plot from the multivariate data in the *n*-by-*p* matrix `X`. Rows of `X` correspond to observations, columns to variables. A star plot represents each observation as a "star" whose *i*th spoke is proportional in length to the *i*th coordinate of that observation. `glyphplot` standardizes `X` by shifting and scaling each column separately onto the interval `[0,1]` before making the plot, and centers the glyphs on a rectangular grid that is as close to square as possible. `glyphplot` treats `NaN`s in `X` as missing values, and does not plot the corresponding rows of `X`. `glyphplot(X,'glyph','star')` is a synonym for `glyphplot(X)`.

`glyphplot(X,'glyph','face')` creates a face plot from `X`. A face plot represents each observation as a "face," whose *i*th facial feature is drawn with a characteristic proportional to the *i*th coordinate of that observation. The features are described in "Face Features" on page 20-677Face Features.

`glyphplot(X,'glyph','face','features',f)` creates a face plot where the *i*th element of the index vector `f` defines which facial feature will represent the *i*th column of `X`. `f` must contain integers from `0` to `17`, where `0` indicate that the corresponding column of `X` should not be plotted. See "Face Features" on page 20-677 for more information.

`glyphplot(X,...,'grid',[rows,cols])` organizes the glyphs into a `rows`-by-`cols` grid.

`glyphplot(X,...,'grid',[rows,cols],'page',p)` organizes the glyph into one or more pages of a `rows`-by-`cols` grid, and displays the page `p`. If `p` is a vector, `glyphplot` displays multiple pages in succession. If `p` is `'all'`, `glyphplot` displays all pages. If `p` is `'scroll'`, `glyphplot` displays a single plot with a scrollbar.

`glyphplot(X,...,'centers',C)` creates a plot with each glyph centered at the locations in the n-by-2 matrix `C`.

`glyphplot,...,'centers',C,'radius',r)` creates a plot with glyphs positioned using `C`, and scale the glyphs so the largest has radius `r`.

`glyphplot(X,...,'obslabels',labels)` labels each glyph with the text in the character array or cell array of strings `labels`. By default, the glyphs are labelled `1:N`. Use `''` for blank labels.

`glyphplot(X,...,'standardize',`*`method`*`)` standardizes `X` before making the plot. Choices for *`method`* are

- `'column'` — Maps each column of `X` separately onto the interval [0,1]. This is the default.
- `'matrix'` — Maps the entire matrix `X` onto the interval `[0,1]`.
- `'PCA'` — Transforms `X` to its principal component scores, in order of decreasing eigenvalue, and maps each one onto the interval `[0,1]`.
- `'off'` — No standardization. Negative values in `X` may make a star plot uninterpretable.

`glyphplot(X,...,`*`prop1`*`,`*`val1`*`,...)` sets properties to the specified property values for all line graphics objects created by `glyphplot`.

`h = glyphplot(X,...)` returns a matrix of handles to the graphics objects created by `glyphplot`. For a star plot, `h(:,1)` and `h(:,2)` contain handles to the line objects for each star's perimeter and spokes, respectively. For a face plot, `h(:,1)` and `h(:,2)` contain object handles

to the lines making up each face and to the pupils, respectively. `h(:,3)` contains handles to the text objects for the labels, if present.

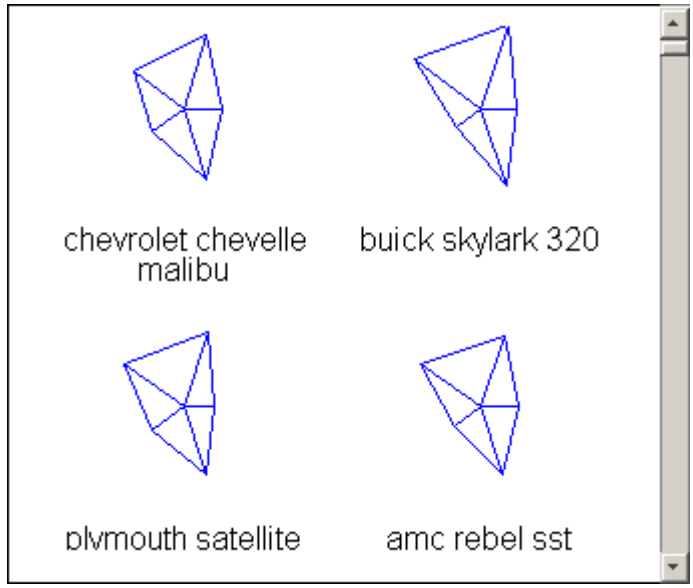
Face Features

The following table describes the correspondence between the columns of the vector `f`, the value of the `'Features'` input parameter, and the facial features of the glyph plot. If `X` has fewer than 17 columns, unused features are displayed at their default value.

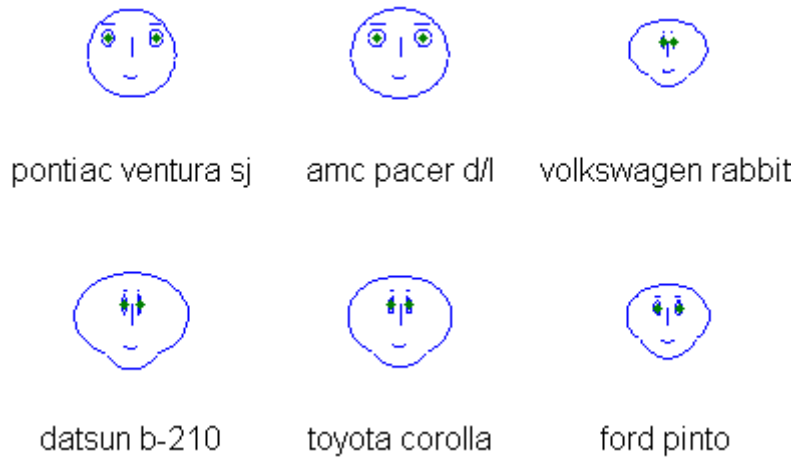
Column	Facial Feature
1	Size of face
2	Forehead/jaw relative arc length
3	Shape of forehead
4	Shape of jaw
5	Width between eyes
6	Vertical position of eyes
7	Height of eyes
8	Width of eyes (this also affects eyebrow width)
9	Angle of eyes (this also affects eyebrow angle)
10	Vertical position of eyebrows
11	Width of eyebrows (relative to eyes)
12	Angle of eyebrows (relative to eyes)
13	Direction of pupils
14	Length of nose
15	Vertical position of mouth
16	Shape of mouth
17	Mouth arc length

Examples

```
load carsmall
X = [Acceleration Displacement Horsepower MPG Weight];

glyphplot(X,'standardize','column',...
            'obslabels',Model,...
            'grid',[2 2],...
            'page','scroll');
```




```
glyphplot(X,'glyph','face',...
            'obslabels',Model,...
            'grid',[2 3],...
            'page',9);
```



See Also

`andrewsplot` | `parallelcoords`

gmdistribution

Purpose

Gaussian mixture models

Description

An object of the `gmdistribution` class defines a Gaussian mixture distribution, which is a multivariate distribution that consists of a mixture of one or more multivariate Gaussian distribution components. The number of components for a given `gmdistribution` object is fixed. Each multivariate Gaussian component is defined by its mean and covariance, and the mixture is defined by a vector of mixing proportions.

Construction

To create a Gaussian mixture distribution by specifying the distribution parameters, use the `gmdistribution` constructor. To fit a Gaussian mixture distribution model to data, use `gmdistribution.fit`.

fit	Gaussian mixture parameter estimates
gmdistribution	Construct Gaussian mixture distribution

Methods

cdf	Cumulative distribution function for Gaussian mixture distribution
cluster	Construct clusters from Gaussian mixture distribution
disp	Display Gaussian mixture distribution object
display	Display Gaussian mixture distribution object
fit	Gaussian mixture parameter estimates
mahal	Mahalanobis distance to component means

pdf	Probability density function for Gaussian mixture distribution
posterior	Posterior probabilities of components
random	Random numbers from Gaussian mixture distribution
subsasgn	Subscripted reference for Gaussian mixture distribution object
subsref	Subscripted reference for Gaussian mixture distribution object

Properties

All objects of the class have the properties listed in the following table.

CovType	Type of covariance matrices
DistName	Type of distribution
Mu	Input matrix of means `MU`
NComponents	Number k of mixture components
NDimensions	Dimension d of multivariate Gaussian distributions
PComponents	Input vector of mixing proportions
SharedCov	`true` if all covariance matrices are restricted to be the same
Sigma	Input array of covariances

Objects constructed with `fit` have the additional properties listed in the following table.

AIC	Akaike Information Criterion
BIC	Bayes Information Criterion
Converged	Determine if algorithm converged
Iters	Number of iterations
NlogL	Negative of log-likelihood
RegV	Value of `'Regularize'` parameter

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

References

McLachlan, G., and D. Peel, Finite Mixture Models, John Wiley & Sons, New York, 2000.

How To

- “Normal Distribution” on page B-83

Purpose

Construct Gaussian mixture distribution

Syntax

```
obj = gmdistribution(mu,sigma,p)
```

Description

`obj = gmdistribution(mu,sigma,p)` constructs an object `obj` of the `gmdistribution` class defining a Gaussian mixture distribution.

`mu` is a k-by-d matrix specifying the d-dimensional mean of each of the k components.

`sigma` specifies the covariance of each component. The size of `sigma` is:

- d-by-d-by-k if there are no restrictions on the form of the covariance. In this case, `sigma(:,:,I)` is the covariance of component `I`.
- 1-by-d-by-k if the covariance matrices are restricted to be diagonal, but not restricted to be same across components. In this case, `sigma(:,:,I)` contains the diagonal elements of the covariance of component I.
- d-by-d matrix if the covariance matrices are restricted to be the same across components, but not restricted to be diagonal. In this case, `sigma` is the pooled estimate of covariance.
- 1-by-d if the covariance matrices are restricted to be diagonal and the same across components. In this case, `sigma` contains the diagonal elements of the pooled estimate of covariance.

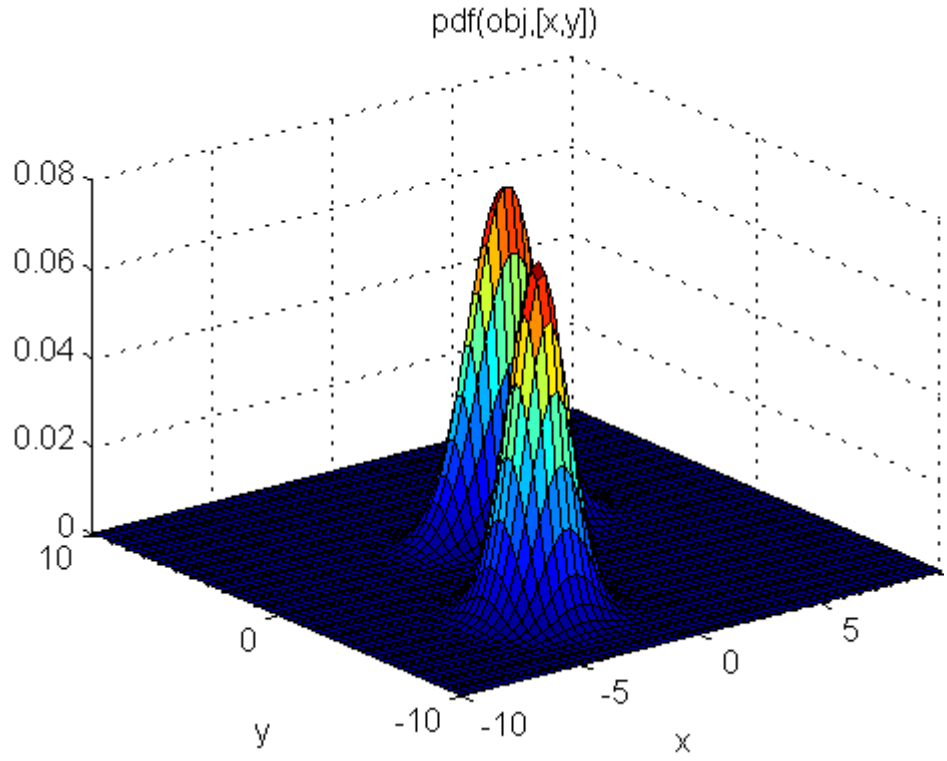
`p` is an optional 1-by-k vector specifying the mixing proportions of each component. If `p` does not sum to `1`, `gmdistribution` normalizes it. The default is equal proportions.

Examples

Create a `gmdistribution` object defining a two-component mixture of bivariate Gaussian distributions:

```
mu = [1 2;-3 -5];
sigma = cat(3,[2 0;0 .5],[1 0;0 1]);
p = ones(1,2)/2;
obj = gmdistribution(mu,sigma,p);
```

```
ezsurf(@(x,y)pdf(obj,[x y]),[-10 10],[-10 10])
```



References

[1] McLachlan, G., and D. Peel. *Finite Mixture Models*. Hoboken, NJ: John Wiley & Sons, Inc., 2000.

See Also

`fit` | `pdf` | `cdf` | `random` | `cluster` | `posterior` | `mahal`

Purpose

Add case names to plot

Syntax

```
gname(cases)
gname
h = gname(cases,line_handle)
```

Description

`gname(cases)` displays a figure window and waits for you to press a mouse button or a keyboard key. The input argument `cases` is a character array or a cell array of strings, in which each row of the character array or each element of the cell array contains the case name of a point. Moving the mouse over the graph displays a pair of cross-hairs. If you position the cross-hairs near a point with the mouse and click once, the graph displays the label corresponding to that point. Alternatively, you can click and drag the mouse to create a rectangle around several points. When you release the mouse button, the graph displays the labels for all points in the rectangle. Right-click a point to remove its label. When you are done labelling points, press the **Enter** or **Escape** key to stop labeling.

`gname` with no arguments labels each case with its case number.

`cases` typically contains unique case names for each point, and is a cell array of strings or a character matrix with each row representing a name. `cases` can also be any grouping variable, which `gname` converts to labels.

`h = gname(cases,line_handle)` returns a vector of handles to the text objects on the plot. Use the scalar `line_handle` to identify the correct line if there is more than one line object on the plot.

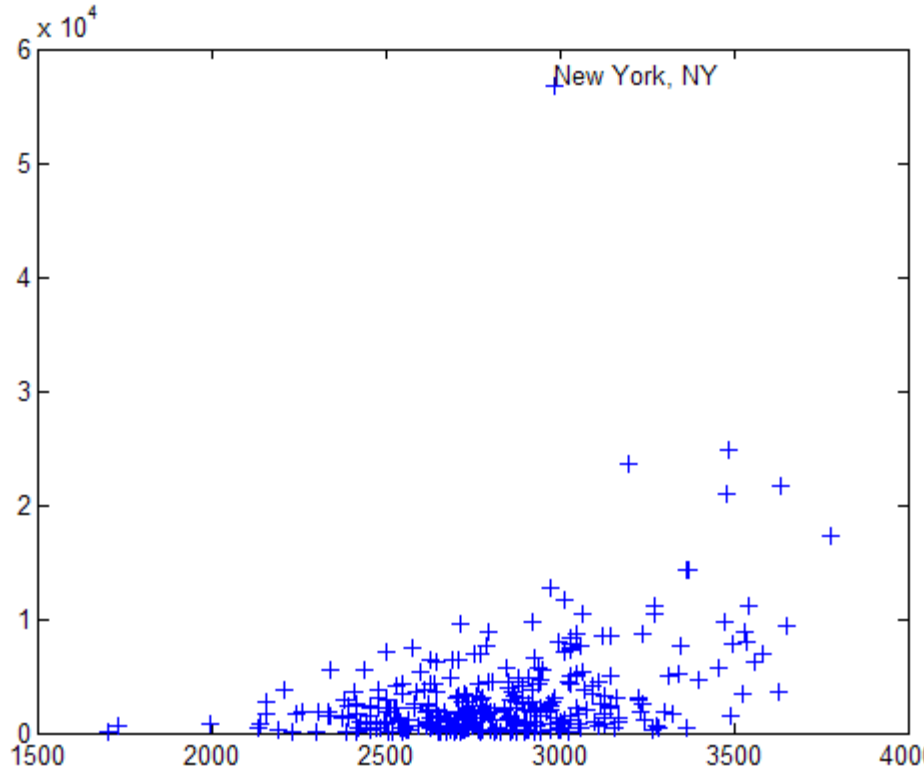
You can use `gname` to label plots created by the `plot`, `scatter`, `gscatter`, `plotmatrix`, and `gplotmatrix` functions.

Examples

This example uses the city ratings data sets to find out which cities are the best and worst for education and the arts.

```
load cities
education = ratings(:,6);
arts = ratings(:,7);
```

```
plot(education,arts,'+')
gname(names)
```



Click the point at the top of the graph to display its label, “New York.”

See Also

`gtext` | `gscatter` | `gplotmatrix`

Purpose

Generalized Pareto cumulative distribution function

Syntax

```
P = gpcdf(X,K,sigma,theta)
```

Description

`P = gpcdf(X,K,sigma,theta)` returns the cdf of the generalized Pareto (GP) distribution with the tail index (shape) parameter `K`, scale parameter `sigma`, and threshold (location) parameter, `theta`, evaluated at the values in `X`. The size of `P` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `K`, `sigma`, and `theta` are 0, 1, and 0, respectively.

When `K = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `K > 0` and `theta = sigma/K`, the GP is equivalent to the Pareto distribution. The mean of the GP is not finite when $K \geq 1$, and the variance is not finite when $K \geq 1/2$. When $K \geq 0$, the GP has positive density for

`X > theta`, or, when

$K < 0,\ 0 \leq \frac{X-\theta}{\sigma} \leq -\frac{1}{K}$.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`cdf` | `gppdf` | `gpinv` | `gpstat` | `gpfit` | `gplike` | `gprnd`

How To

• "Generalized Pareto Distribution" on page B-37

Purpose

Generalized Pareto parameter estimates

Syntax

```
parmhat = gpfit(X)
[parmhat,parmci] = gpfit(X)
[parmhat,parmci] = gpfit(X,alpha)
[...] = gpfit(X,alpha,options)
```

Description

`parmhat = gpfit(X)` returns maximum likelihood estimates of the parameters for the two-parameter generalized Pareto (GP) distribution given the data in `X`. `parmhat(1)` is the tail index (shape) parameter, `K` and `parmhat(2)` is the scale parameter, `sigma`. `gpfit` does not fit a threshold (location) parameter.

`[parmhat,parmci] = gpfit(X)` returns 95% confidence intervals for the parameter estimates.

`[parmhat,parmci] = gpfit(X,alpha)` returns `100(1-alpha)`% confidence intervals for the parameter estimates.

`[...] = gpfit(X,alpha,options)` specifies control parameters for the iterative algorithm used to compute ML estimates. This argument can be created by a call to `statset`. See `statset('gpfit')` for parameter names and default values.

Other functions for the generalized Pareto, such as `gpcdf` allow a threshold parameter, `theta`. However, `gpfit` does not estimate theta. It is assumed to be known, and subtracted from `X` before calling `gpfit`.

When `K = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `K > 0` and `theta = sigma/K`, the GP is equivalent to the Pareto distribution. The mean of the GP is not finite when $K \geq 1$, and the variance is not finite when $K \geq 1/2$. When $K \geq 0$, the GP has positive density for

`X > theta`, or, when

$$0 \leq \frac{X-\theta}{\sigma} \leq -\frac{1}{K}$$

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`mle` | `gplike` | `gppdf` | `gpcdf` | `gpinv` | `gpstat` | `gprnd`

How To

- "Generalized Pareto Distribution" on page B-37

gpinv

Purpose

Generalized Pareto inverse cumulative distribution function

Syntax

```
X = gpinv(P,K,sigma,theta)
```

Description

`X = gpinv(P,K,sigma,theta)` returns the inverse cdf for a generalized Pareto (GP) distribution with tail index (shape) parameter `K`, scale parameter `sigma`, and threshold (location) parameter `theta`, evaluated at the values in `P`. The size of `X` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `K`, `sigma`, and `theta` are 0, 1, and 0, respectively.

When `K = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `K > 0` and `theta = sigma/K`, the GP is equivalent to the Pareto distribution. The mean of the GP is not finite when $K \geq 1$, and the variance is not finite when $K \geq 1/2$. When $K \geq 0$, the GP has positive density for

`X > theta`, or, when

$K < 0,\ 0 \leq \frac{X-\theta}{\sigma} \leq -\frac{1}{K}$.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`icdf` | `gpcdf` | `gppdf` | `gpstat` | `gpfit` | `gplike` | `gprnd`

How To

- "Generalized Pareto Distribution" on page B-37

Purpose

Generalized Pareto negative log-likelihood

Syntax

```
nlogL = gplike(params,data)
[nlogL,ACOV] = gplike(params,data)
```

Description

`nlogL = gplike(params,data)` returns the negative of the log-likelihood `nlogL` for the two-parameter generalized Pareto (GP) distribution, evaluated at parameters `params`. `params(1)` is the tail index (shape) parameter, `K`, `params(2)` is the scale parameter, `sigma`, and `params(3)` is the threshold (location) parameter, `mu`.

`[nlogL,ACOV] = gplike(params,data)` returns the inverse of Fisher's information matrix, `ACOV`. If the input parameter values in `params` are the maximum likelihood estimates, the diagonal elements of `ACOV` are their asymptotic variances. `ACOV` is based on the observed Fisher's information, not the expected information.

When `K = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `K > 0` and `theta = sigma/K`, the GP is equivalent to the Pareto distribution. The mean of the GP is not finite when $K \geq 1$, and the variance is not finite when $K \geq 1/2$. When $K \geq 0$, the GP has positive density for

`X > theta`, or, when

$K < 0,\ 0 \leq \frac{X-\theta}{\sigma} \leq -\frac{1}{K}$.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`gpfit` | `gppdf` | `gpcdf` | `gpinv` | `gpstat` | `gprnd`

How To

- "Generalized Pareto Distribution" on page B-37

gppdf

Purpose

Generalized Pareto probability density function

Syntax

```
P = gppdf(X,K,sigma,theta)
```

Description

`P = gppdf(X,K,sigma,theta)` returns the pdf of the generalized Pareto (GP) distribution with the tail index (shape) parameter `K`, scale parameter `sigma`, and threshold (location) parameter, `theta`, evaluated at the values in `X`. The size of `P` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `K`, `sigma`, and `theta` are 0, 1, and 0, respectively.

When `K = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `K > 0` and `theta = sigma/K`, the GP is equivalent to the Pareto distribution. The mean of the GP is not finite when $K \geq 1$, and the variance is not finite when $K \geq 1/2$. When $K \geq 0$, the GP has positive density for

`X > theta`, or, when

$K < 0,\ 0 \leq \frac{X-\theta}{\sigma} \leq -\frac{1}{K}$.

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`pdf` | `gpcdf` | `gpinv` | `gpstat` | `gpfit` | `gplike` | `gprnd`

How To

- "Generalized Pareto Distribution" on page B-37

Purpose

Matrix of scatter plots by group

Syntax

```
gplotmatrix(x,y,group)
gplotmatrix(x,y,group,clr,sym,siz)
gplotmatrix(x,y,group,clr,sym,siz,doleg)
gplotmatrix(x,y,group,clr,sym,siz,doleg,dispopt)
gplotmatrix(x,y,group,clr,sym,siz,doleg,dispopt,xnam,ynam)
[h,ax,bigax] = gplotmatrix(...)
```

Description

`gplotmatrix(x,y,group)` creates a matrix of scatter plots. Each individual set of axes in the resulting figure contains a scatter plot of a column of `x` against a column of `y`. All plots are grouped by the grouping variable `group`. (See "Grouped Data" on page 2-34.)

`x` and `y` are matrices with the same number of rows. If `x` has p columns and `y` has q columns, the figure contains a p-by-q matrix of scatter plots. If you omit `y` or specify it as the empty matrix, `[]`, `gplotmatrix` creates a square matrix of scatter plots of columns of `x` against each other.

`group` is a grouping variable that can be a categorical variable, vector, string array, or cell array of strings. `group` must have the same number of rows as `x` and `y`. Points with the same value of `group` are placed in the same group, and appear on the graph with the same marker and color. Alternatively, `group` can be a cell array containing several grouping variables (such as `{g1 g2 g3}`); in that case, observations are in the same group if they have common values of all grouping variables.

`gplotmatrix(x,y,group,clr,sym,siz)` specifies the color, marker type, and size for each group. *`clr`* is a string array of colors recognized by the `plot` function. The default for *`clr`* is `'bgrcmyk'`. *`sym`* is a string array of symbols recognized by the `plot` command, with the default value `'.'`. `siz` is a vector of sizes, with the default determined by the `DefaultLineMarkerSize` property. If you do not specify enough values for all groups, `gplotmatrix` cycles through the specified values as needed.

`gplotmatrix(x,y,group,clr,sym,siz,doleg)` controls whether a legend is displayed on the graph (*`doleg`* is `'on'`, the default) or not (*`doleg`* is `'off'`).

`gplotmatrix(x,y,group,clr,sym,siz,doleg,dispopt)` controls what appears along the diagonal of a plot matrix of `y` versus `x`. Allowable values are `'none'`, to leave the diagonals blank, `'hist'`, to plot histograms, or `'variable'`, to write the variable names. `gplotmatrix` displays histograms along the diagonal only when there is only one variable (i.e., `gplotmatrix(x,[],[],[],[],[],'hist')`.

`gplotmatrix(x,y,group,clr,sym,siz,doleg,dispopt,xnam,ynam)` specifies the names of the columns in the `x` and `y` arrays. These names are used to label the *x*- and *y*-axes. `xnam` and `ynam` must be character arrays or cell arrays of strings, with one name for each column of `x` and `y`, respectively.

`[h,ax,bigax] = gplotmatrix(...)` returns three arrays of handles. `h` is an array of handles to the lines on the graphs. The array's third dimension corresponds to groups in G. `ax` is a matrix of handles to the axes of the individual plots. If *`dispopt`* is `'hist'`, `ax` contains one extra row of handles to invisible axes in which the histograms are plotted. `bigax` is a handle to big (invisible) axes framing the entire plot matrix. `bigax` is fixed to point to the current axes, so a subsequent `title`, `xlabel`, or `ylabel` command will produce labels that are centered with respect to the entire plot matrix.

Examples

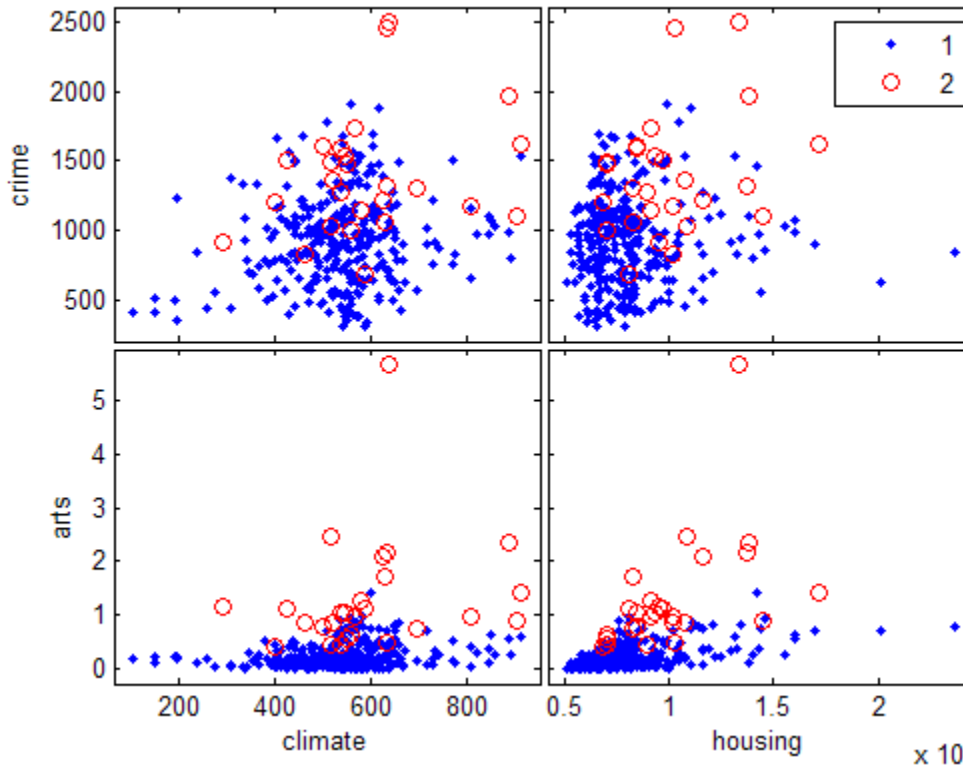
Load the `cities` data. The `ratings` array has ratings of the cities in nine categories (category names are in the array `categories`). `group` is a code whose value is 2 for the largest cities. You can make scatter plots of the first three categories against the other four, grouped by the city size code:

```
load discrim
gplotmatrix(ratings(:,1:2),ratings(:,[4 7]),group)
```

The output figure (not shown) has an array of graphs with each city group represented by a different color. The graphs are a little easier to read if you specify colors and plotting symbols, label the axes with the rating categories, and move the legend off the graphs:

```
gplotmatrix(ratings(:,1:2),ratings(:,[4 7]),group,...
```

```
'br','.o',[],'on','',categories(1:2,:),...
 categories([4 7],:))
```



See Also `grpstats` | `gscatter` | `plotmatrix`

How To

- “Grouped Data” on page 2-34

gprnd

Purpose

Generalized Pareto random numbers

Syntax

```
R = gprnd(K,sigma,theta)
R = gprnd(K,sigma,theta,m,n,...)
R = gprnd(K,sigma,theta,[m,n,...])
```

Description

`R = gprnd(K,sigma,theta)` returns an array of random numbers chosen from the generalized Pareto (GP) distribution with tail index (shape) parameter `K`, scale parameter `sigma`, and threshold (location) parameter, `theta`. The size of `R` is the common size of the input arguments if all are arrays. If any parameter is a scalar, the size of `R` is the size of the other parameters.

`R = gprnd(K,sigma,theta,m,n,...)` or `R = gprnd(K,sigma,theta,[m,n,...])` generates an `m`-by-`n`-by-... array. The `K`, `sigma`, `theta` parameters can each be scalars or arrays of the same size as `R`.

When `K = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `K > 0` and `theta = sigma/K`, the GP is equivalent to the Pareto distribution. The mean of the GP is not finite when $K \geq 1$, and the variance is not finite when $K \geq 1/2$. When $K \geq 0$, the GP has positive density for

`X > theta`, or, when

$$0 \leq \frac{X-\theta}{\sigma} \leq -\frac{1}{K}$$

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`random` | `gppdf` | `gpcdf` | `gpinv` | `gpstat` | `gpfit` | `gplike`

Purpose

Generalized Pareto mean and variance

Syntax

```
[M,V] = gpstat(K,sigma,theta)
```

Description

`[M,V] = gpstat(K,sigma,theta)` returns the mean of and variance for the generalized Pareto (GP) distribution with the tail index (shape) parameter `K`, scale parameter `sigma`, and threshold (location) parameter, `theta`.

The default value for `theta` is 0.

When `K = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `K > 0` and `theta = sigma/K`, the GP is equivalent to the Pareto distribution. The mean of the GP is not finite when $K \geq 1$, and the variance is not finite when $K \geq 1/2$. When $K \geq 0$, the GP has positive density for `X > theta`, or when

$$K < 0,\ 0 \leq \frac{X-\theta}{\sigma} \leq -\frac{1}{K}.$$

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance.* New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications.* London: Imperial College Press, 2000.

See Also

`gppdf` | `gpcdf` | `gpinv` | `gpfit` | `gplike` | `gprnd`

TreeBagger.growTrees

Purpose

Train additional trees and add to ensemble

Syntax

```
B = growTrees(B,ntrees)
B = growTrees(B,ntrees,'param1',val1,'param2',val2,...)
```

Description

`B = growTrees(B,ntrees)` grows `ntrees` new trees and appends them to those trees already stored in the ensemble `B`.

`B = growTrees(B,ntrees,'param1',val1,'param2',val2,...)` pecifies optional parameter name/value pairs:

`'nprint'`	Specifies that a diagnostic message showing training progress should display after every `value` training cycles (grown trees). Default is no diagnostic messages.
`'options'`	A struct that specifies options that govern computation when growing the ensemble of decision trees. One option requests that the computation of decision trees on multiple bootstrap replicates uses multiple processors, if the Parallel Computing Toolbox is available. Two options specify the random number streams to use in selecting bootstrap replicates. You can create this argument with a call to `statset`. You can retrieve values of the individual fields with a call to `statget`. Applicable `statset` parameters are: • `'UseParallel'` — If `'always'` and if a `matlabpool` of the Parallel Computing Toolbox is open, compute decision trees drawn on separate boostrap replicates in parallel. If the Parallel Computing Toolbox is not installed, or a `matlabpool` is not open, computation occurs in serial mode. Default is `'never'`, or serial computation.

- `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. Default is `'never'`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
- `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `growTrees` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case
  - You have an open MATLAB pool
  - `UseParallel` is `'always'`
  - `UseSubstreams` is `'never'`

  In that case, use a cell array the same size as the MATLAB pool.

For more information on using parallel computing, see Chapter 17, "Parallel Statistics".

See Also

`classregtree`

grp2idx

Purpose

Create index vector from grouping variable

Syntax

```
[G,GN]=grp2idx(S)
[G,GN,GL] = grp2idx(S)
```

Description

`[G,GN]=grp2idx(S)` creates an index vector `G` from the grouping variable `S`. `S` can be a categorical, numeric, or logical vector; a cell vector of strings; or a character matrix with each row representing a group label. The result `G` is a vector taking integer values from 1 up to the number `K` of distinct groups. `GN` is a cell array of strings representing group labels. `GN(G)` reproduces `S` (aside from any differences in type).

The order of `GN` depends on the grouping variable:

- For numeric and logical grouping variables, the order is the sorted order of `S`.
- For categorical grouping variables, the order is the order of `getlabels(S)`.
- For string grouping variables, the order is the order of first appearance in `S`.

`[G,GN,GL] = grp2idx(S)` returns a column vector `GL` representing the group levels. The set of groups and their order in `GL` and `GN` are the same, except that `GL` has the same type as `S`. If `S` is a character matrix, `GL(G,:)` reproduces `S`, otherwise `GL(G)` reproduces `S`.

`grp2idx` treats `NaN`s (numeric or logical), empty strings (char or cell array of strings), or `<undefined>` values (categorical) in `S` as missing values and returns `NaN`s in the corresponding rows of `G`. `GN` and `GL` don't include entries for missing values.

Examples

Load the data in `hospital.mat` and create a categorical grouping variable:

```
load hospital
edges = 0:10:100;
labels = strcat(num2str((0:10:90)','%d'),{'s'});
```

```
AgeGroup = ordinal(hospital.Age,labels,[],edges);

ages = hospital.Age(1:5)
ages =
    38
    43
    38
    40
    49

group = AgeGroup(1:5)
group =
     30s
     40s
     30s
     40s
     40s

indices = grp2idx(group)
indices =
     4
     5
     4
     5
     5
```

See Also

gscatter | grpstats | crosstab | getlabels

How To

- “Grouped Data” on page 2-34

Purpose

Summary statistics by group

Syntax

```
means = grpstats(X)
means = grpstats(X,group)
grpstats(X,group,alpha)
dsstats = grpstats(ds,groupvars)
[A,B,...] = grpstats(X,group,whichstats)
[...] = grpstats(...,whichstats,'Param1',VAL1,'Param2',VAL2,
   ...)
```

Description

`means = grpstats(X)` computes the mean of the entire sample without grouping, where `X` is a matrix of observations.

`means = grpstats(X,group)` returns the means of each column of `X` by `group`. The array, `group` defines the grouping such that two elements of `X` are in the same group if their corresponding `group` values are the same. (See "Grouped Data" on page 2-34.) The grouping variable `group` can be a categorical variable, vector, string array, or cell array of strings. It can also be a cell array containing several grouping variables (such as `{g1 g2 g3}`) to group the values in `X` by each unique combination of grouping variable values.

`grpstats(X,group,alpha)` displays a plot of the means versus index with `100(1-alpha)`% confidence intervals around each mean.

`dsstats = grpstats(ds,groupvars)`, when `ds` is a dataset array, returns a dataset `dsstats` that contains the mean, computed by group, for variables in `ds`. `groupvars` specifies the grouping variables in `ds` that define the groups, and is a positive integer, a vector of positive integers, the name of a dataset variable, a cell array containing one or more dataset variable names, or a logical vector. A grouping variable may be a vector of categorical, logical, or numeric values, a character array of strings, or a cell vector of strings. `dsstats` contains those grouping variables, plus one variable giving the number of observations in `ds` for each group, as well as one variable for each of the remaining dataset variables in `ds`. These variables must be numeric or logical. `dsstats` contains one observation for each group of observations in `ds`.

`groupvars` can be `[]` or omitted to compute the mean of each variable across the entire dataset without grouping.

`grpstats` treats `NaNs` as missing values, and removes them.

`grpstats` ignores empty group names.

`[A,B,...] = grpstats(X,group,whichstats)` returns the statistics specified in *`whichstats`*. The input *`whichstats`* can be a single function handle or name, or a cell array containing multiple function handles or names. The number of outputs (`A`,`B`, ...) must match the number function handles and names in *`whichstats`*. Acceptable names are as follows:

- `'mean'` — mean
- `'sem'` — standard error of the mean
- `'numel'` — count, or number of non-`NaN` elements
- `'gname'` — group name
- `'std'` — standard deviation
- `'var'` — variance
- `'min'` — minimum
- `'max'` — maximum
- `'range'` — maximum - minimum
- `'meanci'` — 95% confidence interval for the mean
- `'predci'` — 95% prediction interval for a new observation

Each function included in *`whichstats`* must accept a column vector of data and compute a descriptive statistic for it. For example, `@median` and `@skewness` are suitable functions to apply to a numeric input. A function must return the same size output each time `grpstats` calls it, even if the input for some groups is empty. The function typically returns a scalar value, but may return an *nvals*-by-1 column vector if the descriptive statistic is not a scalar (a confidence interval, for example). The size of each output `A`, `B`, ... is *ngroups*-by-*ncols*-by-*nvals*,

where *ngroups* is the number of groups, *ncols* is the number of columns in the data `X`, and *nvals* is the number of values returned by the function for data from a single group in one column of `X`. If `X` is a vector of data, then the size of each output `A`, `B`, ... is *ngroups*-by-*nvals*.

A function included in *`whichstats`* may also be written to accept a matrix of data and compute a descriptive statistic for each column. The function should return either a row vector, or an *nvals*-by-*ncols* matrix if the descriptive statistic is not a scalar.

For the case when data are contained in a numeric matrix X, a function specified in `whichstats` may also be written to accept a matrix of data and ompute a descriptive statistic for each column. The function should return either a row vector, or an `nvals`-by-`ncols` matrix if the descriptive statistic is not a scalar.

`[...] = grpstats(...,whichstats,'Param1',VAL1,'Param2',VAL2,...)` specifies additional parameter name/value pairs chosen from the following:

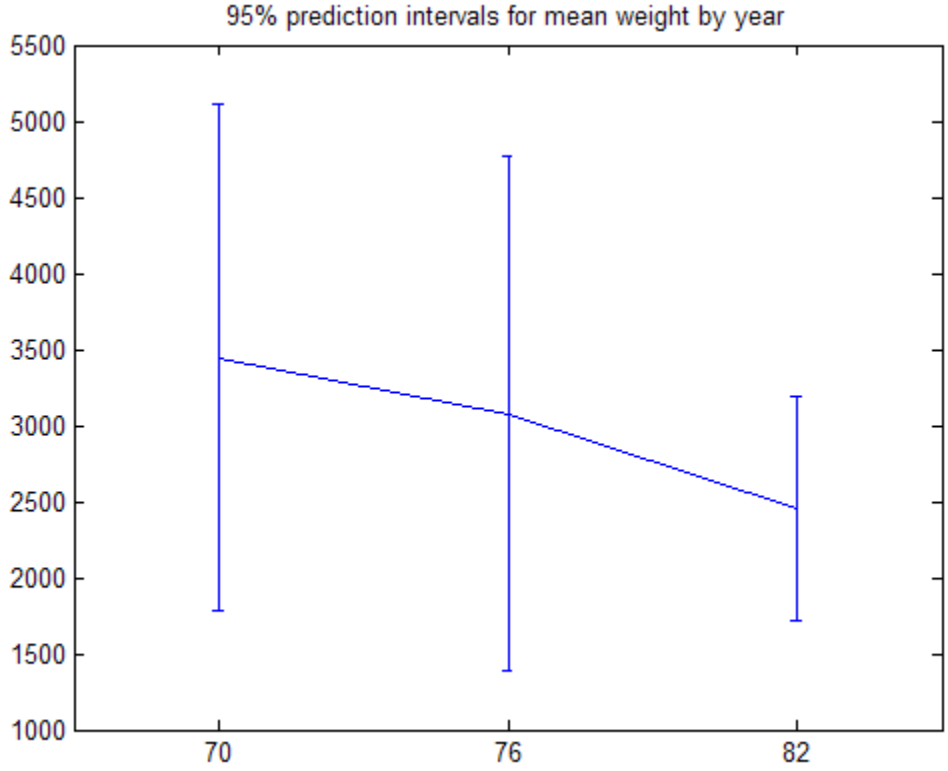
`'Alpha'`	A value from 0 to 1 that specifies the confidence level as `100(1-alpha)%` for the `'meanci'` and `'predci'` options. Default is 0.05.
`'DataVars'`	The names of the variables in `ds` to which the functions in `whichstats` should be applied. `dsstats` contains one summary statistic variable for each of these data variables. `datavars` is a positive integer, a vector of positive integers, a variable name, a cell array containing

	one or more variable names, or a logical vector.
`'VarNames'`	The names of the variables in `dsstats`. By default, `grpstats` uses the names from `ds` for the grouping variable names, and constructs names for the summary statistic variables based on the function name and the data variable names from `ds`.

`dsstats` contains `ngroupvars + 1 + ndatavars*nfuns` variables, where `ngroupvars` is the number of variables specified in `groupvars`, `ndatavars` is the number of variables specified in `datavars`, and `nfuns` is the number of summary statistics specified in `whichstats`.

Examples

```
load carsmall
[m,p,g] = grpstats(Weight,Model_Year,...
                   {'mean','predci','gname'})
n = length(m)
errorbar((1:n)',m,p(:,2)-m)
set(gca,'xtick',1:n,'xticklabel',g)
title('95% prediction intervals for mean weight by year')
```



See Also `gscatter | grp2idx | dataset.grpstats`

How To

- “Grouped Data” on page 2-34

Purpose

Summary statistics by group for dataset arrays

Syntax

```
B = grpstats(A,groupvars)
B = grpstats(A,groupvars,whichstats)
B = grpstats(A,groupvars,whichstats,...,'DataVars',vars)
B = grpstats(A,groupvars,whichstats,...,'VarNames',names)
```

Description

`B = grpstats(A,groupvars)` returns a dataset array `B` that contains the means, computed by group, for variables in the dataset array `A`. The optional input `groupvars` specifies the variables in `A` that define the groups. `groupvars` can be a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. `groupvars` can also be `[]` or omitted to compute the means of the variables in `A` without grouping. Grouping variables can be vectors of categorical, logical, or numeric values, a character array of strings, or a cell vector of strings. (See "Grouped Data" on page 2-34.)

`B` contains the grouping variables, plus a variable giving the number of observations in `A` for each group, plus a variable for each of the remaining variables in `A`. `B` contains one observation for each group of observations in `A`.

`grpstats` treats `NaN`s as missing values, and removes them.

`B = grpstats(A,groupvars,whichstats)` returns a dataset array `B` with variables for each of the statistics specified in *`whichstats`*, applied to each of the nongrouping variables in `A`. *`whichstats`* can be a single function handle or name, or a cell array containing multiple function handles or names. The names can be chosen from among the following:

- `'mean'` — mean
- `'sem'` — standard error of the mean
- `'numel'` — count, or number of non-`NaN` elements
- `'gname'` — group name
- `'std'` — standard deviation

- `'var'` — variance
- `'meanci'` — 95% confidence interval for the mean
- `'predci'` — 95% prediction interval for a new observation

Each function included in *`whichstats`* must accept a subset of the rows of a dataset variable, and compute column-wise descriptive statistics for it. A function should typically return a value that has one row but is otherwise the same size as its input data. For example, `@median` and `@skewness` are suitable functions to apply to a numeric dataset variable.

A summary statistic function may also return values with more than one row, provided the return values have the same number of rows each time `grpstats` applies the function to different subsets of data from a given dataset variable. For a dataset variable that is `nobs`-by-`m`-by-... if a summary statistic function returns values that are `nvals`-by-`m`-by-... then the corresponding summary statistic variable in `B` is `ngroups`-by-`m`-by-...-by-`nvals`, where `ngroups` is the number of groups in `A`.

`B = grpstats(A,groupvars,`*`whichstats`*`,...,'DataVars',vars)` specifies the variables in `A` to which the functions in *`whichstats`* should be applied. The output dataset arrays contain one summary statistic variable for each of the specified variables. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

`B = grpstats(A,groupvars,`*`whichstats`*`,...,'VarNames',names)` specifies the names of the variables in `B`. By default, `grpstats` uses the names from `A` for the grouping variables, and constructs names for the summary statistic variables based on the function name and the data variable names. The number of variables in `B` is `ngroupvars + 1 + ndatavars*nfuns`, where `ngroupvars` is the number of variables specified in `groupvars`, `ndatavars` is the number of variables specified in `vars`, and `nfuns` is the number of summary statistics specified in *`whichstats`*.

Examples

Compute blood pressure statistics for the data in `hospital.mat`, by sex and smoker status:

```
load hospital
grpstats(hospital,...
         {'Sex','Smoker'},...
         {@median,@iqr},...
         'DataVars','BloodPressure')
ans =
              Sex       Smoker    GroupCount
 Female_0     Female    false     40
 Female_1     Female    true      13
 Male_0       Male      false     26
 Male_1       Male      true      21

              median_BloodPressure
 Female_0     119.5            79
 Female_1       129            91
 Male_0         119            79
 Male_1         129            92

              iqr_BloodPressure
 Female_0      6.5          5.5
 Female_1        8          5.5
 Male_0          7            6
 Male_1       10.5          4.5
```

See Also

`grpstats` | `summary`

Purpose

Scatter plot by group

Syntax

```
gscatter(x,y,group)
gscatter(x,y,group,clr,sym,siz)
gscatter(x,y,group,clr,sym,siz,doleg)
gscatter(x,y,group,clr,sym,siz,doleg,xnam,ynam)
h = gscatter(...)
```

Description

`gscatter(x,y,group)` creates a scatter plot of `x` and `y`, grouped by `group`. `x` and `y` are vectors of the same size. `group` is a grouping variable in the form of a categorical variable, vector, string array, or cell array of strings. (See "Grouped Data" on page 2-34.) Alternatively, `group` can be a cell array containing several grouping variables (such as `{g1 g2 g3}`), in which case observations are in the same group if they have common values of all grouping variables. Points in the same group and appear on the graph with the same marker and color.

`gscatter(x,y,group,clr,sym,siz)` specifies the color, marker type, and size for each group. *`clr`* is a string array of colors recognized by the `plot` function. The default for *`clr`* is `'bgrcmyk'`. *`sym`* is a string array of symbols recognized by the `plot` command, with the default value `'.'`. `siz` is a vector of sizes, with the default determined by the `'DefaultLineMarkerSize'` property. If you do not specify enough values for all groups, `gscatter` cycles through the specified values as needed.

`gscatter(x,y,group,clr,sym,siz,doleg)` controls whether a legend is displayed on the graph (*`doleg`* is `'on'`, the default) or not (*`doleg`* is `'off'`).

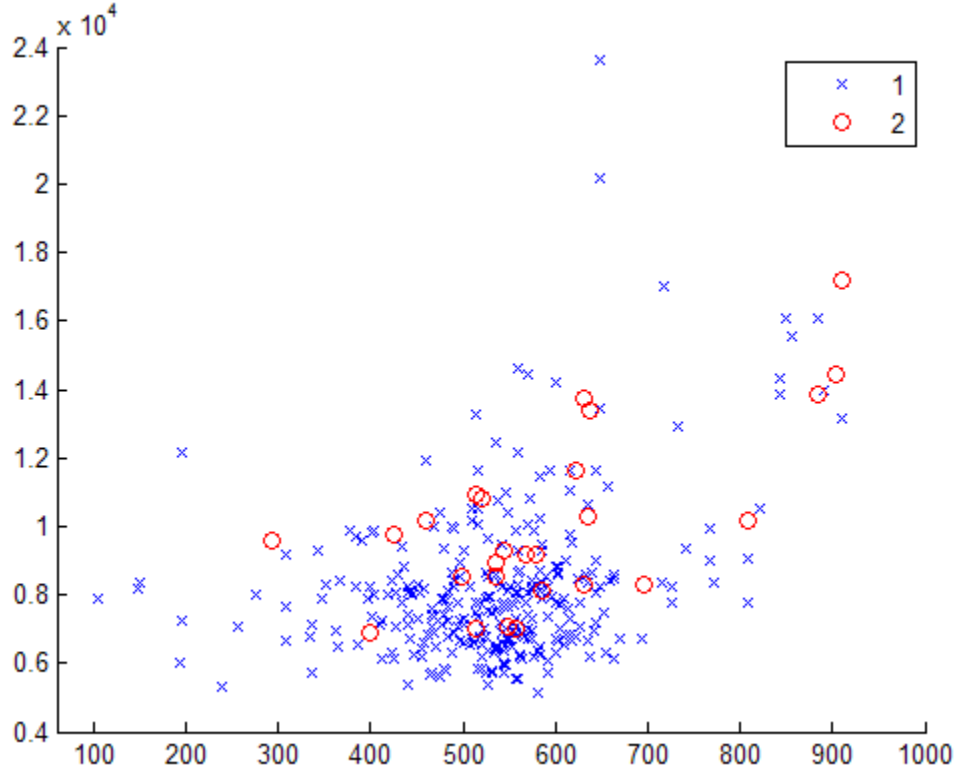
`gscatter(x,y,group,clr,sym,siz,doleg,xnam,ynam)` specifies the name to use for the *x*-axis and *y*-axis labels. If the `x` and `y` inputs are simple variable names and `xnam` and `ynam` are omitted, `gscatter` labels the axes with the variable names.

`h = gscatter(...)` returns an array of handles to the lines on the graph.

Examples

Load the `cities` data and look at the relationship between the ratings for climate (first column) and housing (second column) grouped by city size. We'll also specify the colors and plotting symbols.

```
load discrim
gscatter(ratings(:,1),ratings(:,2),group,'br','xo')
```



See Also

`gplotmatrix` | `grpstats` | `scatter`

How To

- "Grouped Data" on page 2-34

Purpose

Greater than relation for handles

Syntax

```
h1 > h2
```

Description

`h1 > h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise > result.

If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = gt(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `eq` | `ge` | `le` | `lt` | `ne`

haltonset

Superclasses

qrandset

Purpose

Halton quasi-random point sets

Description

`haltonset` is a quasi-random point set class that produces points from the Halton sequence.

Construction

haltonset	Construct Halton quasi-random point set

Methods

Inherited Methods

Methods in the following table are inherited from `qrandset`.

disp	Display qrandset object
end	Last index in indexing expression for point set
length	Length of point set
ndims	Number of dimensions in matrix
net	Generate quasi-random point set
scramble	Scramble quasi-random point set
size	Number of dimensions in matrix
subsref	Subscripted reference for qrandset

Properties

Inherited Properties

Properties in the following table are inherited from `qrandset`.

Dimensions	Number of dimensions
Leap	Interval between points

ScrambleMethod	Settings that control scrambling
Skip	Number of initial points to omit from sequence
Type	Name of sequence on which point set `P` is based

Copy Semantics

Handle. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

References

[1] Kocis, L., and W. J. Whiten, "Computational Investigations of Low-Discrepancy Sequences," ACM Transactions on Mathematical Software, Vol. 23, No. 2, pp. 266-294, 1997.

See Also

`sobolset`

How To

- “Quasi-Random Point Sets” on page 6-16

haltonset

Purpose

Construct Halton quasi-random point set

Syntax

```
p = haltonset(d)
p = haltonset(d,prop1,val1,prop2,val2,...)
```

Description

`p = haltonset(d)` constructs a `d`-dimensional point set `p` of the `haltonset` class, with default property settings.

`p = haltonset(d,prop1,val1,prop2,val2,...)` specifies property name/value pairs used to construct `p`.

The object `p` returned by `haltonset` encapsulates properties of a specified quasi-random sequence. The point set is finite, with a length determined by the `Skip` and `Leap` properties and by limits on the size of point set indices (maximum value of 2^{53}). Values of the point set are not generated and stored in memory until you access `p` using `net` or parenthesis indexing.

Examples

Generate a 3-D Halton point set, skip the first 1000 values, and then retain every 101st point:

```
p = haltonset(3,'Skip',1e3,'Leap',1e2)
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none
```

Use `scramble` to apply reverse-radix scrambling:

```
p = scramble(p,'RR2')
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : RR2
```

Use `net` to generate the first four points:

```
X0 = net(p,4)
X0 =
    0.0928    0.6950    0.0029
    0.6958    0.2958    0.8269
    0.3013    0.6497    0.4141
    0.9087    0.7883    0.2166
```

Use parenthesis indexing to generate every third point, up to the 11th point:

```
X = p(1:3:11,:)
X =
    0.0928    0.6950    0.0029
    0.9087    0.7883    0.2166
    0.3843    0.9840    0.9878
    0.6831    0.7357    0.7923
```

References

[1] Kocis, L., and W. J. Whiten. "Computational Investigations of Low-Discrepancy Sequences." *ACM Transactions on Mathematical Software*. Vol. 23, No. 2, 1997, pp. 266–294.

See Also

`net` | `scramble` | `sobolset`

harmmean

Purpose

Harmonic mean

Syntax

```
m = harmmean(X)
harmmean(X,dim)
```

Description

`m = harmmean(X)` calculates the harmonic mean of a sample. For vectors, `harmmean(x)` is the harmonic mean of the elements in `x`. For matrices, `harmmean(X)` is a row vector containing the harmonic means of each column. For *N*-dimensional arrays, `harmmean` operates along the first nonsingleton dimension of `X`.

`harmmean(X,dim)` takes the harmonic mean along dimension `dim` of `X`.

The harmonic mean is

$$m = \frac{n}{\sum_{i=1}^{n} \frac{1}{x_i}}$$

Examples

The arithmetic mean is greater than or equal to the harmonic mean.

```
x = exprnd(1,10,6);

harmonic = harmmean(x)
harmonic =
  0.3382  0.3200  0.3710  0.0540  0.4936  0.0907

average = mean(x)
average =
  1.3509  1.1583  0.9741  0.5319  1.0088  0.8122
```

See Also

`mean` | `median` | `geomean` | `trimmean`

Purpose

Bivariate histogram

Syntax

```
hist3(X)
hist3(X,nbins)
hist3(X,ctrs)
hist3(X,'Edges',edges)
N = hist3(X,...)
[N,C] = hist3(X,...)
hist3(...,param1,val1,param2,val2,...)
```

Description

`hist3(X)` bins the elements of the *m*-by-2 matrix `X` into a 10-by-10 grid of equally spaced containers, and plots a histogram. Each column of **`X`** corresponds to one dimension in the bin grid.

`hist3(X,nbins)` plots a histogram using an `nbins(1)`-by-`nbins(2)` grid of bins. `hist3(X,'Nbins',nbins)` is equivalent to `hist3(X,nbins)`.

`hist3(X,ctrs)`, where `ctrs` is a two-element cell array of numeric vectors with monotonically non-decreasing values, uses a 2-D grid of bins centered on `ctrs{1}` in the first dimension and on `ctrs{2}` in the second. `hist3` assigns rows of `X` falling outside the range of that grid to the bins along the outer edges of the grid, and ignores rows of `X` containing `NaN`s. `hist3(X,'Ctrs',ctrs)` is equivalent to `hist3(X,ctrs)`.

`hist3(X,'Edges',edges)`, where `edges` is a two-element cell array of numeric vectors with monotonically non-decreasing values, uses a 2-D grid of bins with edges at `edges{1}` in the first dimension and at `edges{2}` in the second. The (*i*, *j*)th bin includes the value `X(k,:)` if

```
edges{1}(i) <= X(k,1) < edges{1}(i+1)
edges{2}(j) <= X(k,2) < edges{2}(j+1)
```

Rows of `X` that fall on the upper edges of the grid, `edges{1}(end)` or `edges{2}(end)`, are counted in the `(I,j)`th or `(i,J)`th bins, where `I` and `J` are the lengths of `edges{1}` and `edges{2}`. `hist3` does not count rows of `X` falling outside the range of the grid. Use `-Inf` and `Inf` in `edges` to include all non-`NaN` values.

`N = hist3(X,...)` returns a matrix containing the number of elements of `X` that fall in each bin of the grid, and does not plot the histogram.

`[N,C] = hist3(X,...)` returns the positions of the bin centers in a 1-by-2 cell array of numeric vectors, and does not plot the histogram. `hist3(ax,X,...)` plots onto an `axes` with handle `ax` instead of the current `axes`. See the `axes` reference page for more information about handles to plots.

`hist3(...,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` allows you to specify graphics parameter name/value pairs to fine-tune the plot.

Examples

Example 1

Make a 3-D figure using a histogram with a density plot underneath:

```
load seamount
dat = [-y,x]; % Grid corrected for negative y-values
hold on
hist3(dat) % Draw histogram in 2D

n = hist3(dat); % Extract histogram data;
                % default to 10x10 bins
n1 = n';
n1( size(n,1) + 1 ,size(n,2) + 1 ) = 0;
```

Generate grid for 2-D projected view of intensities:

```
xb = linspace(min(dat(:,1)),max(dat(:,1)),size(n,1)+1);
yb = linspace(min(dat(:,2)),max(dat(:,2)),size(n,1)+1);
```

Make a pseudocolor plot:

```
h = pcolor(xb,yb,n1);
```

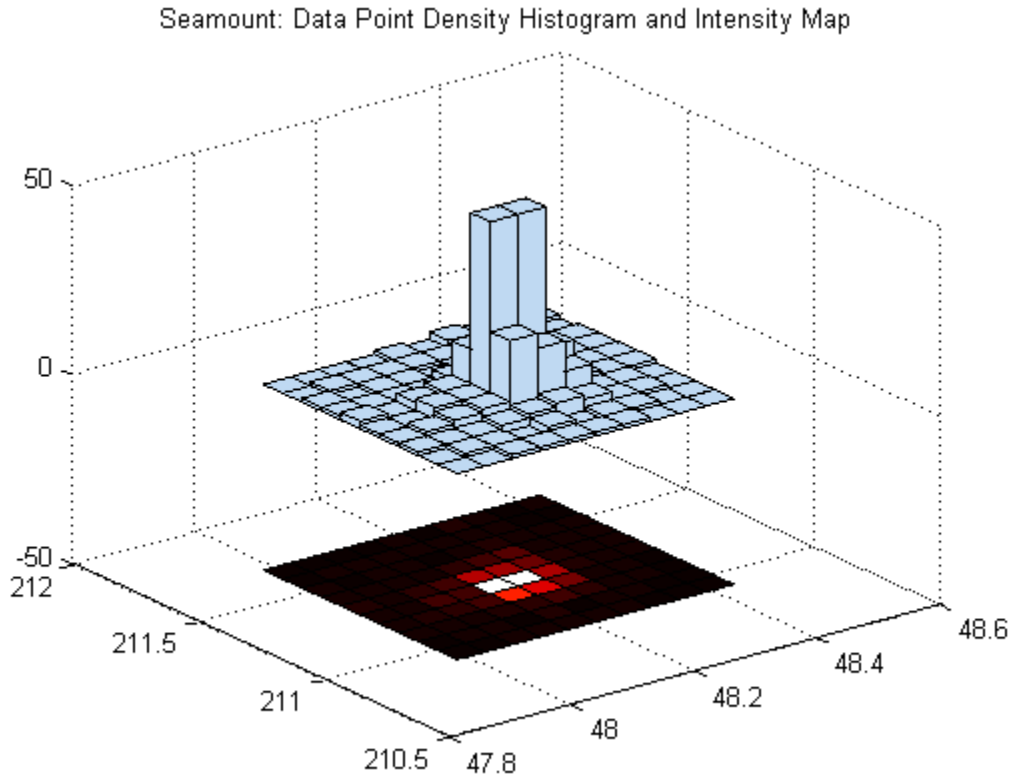
Set the z-level and colormap of the displayed grid:

```
set(h, 'zdata', ones(size(n1)) * -max(max(n)))
colormap(hot) % heat map
title('Seamount: ...
```

```
      Data Point Density Histogram and Intensity Map');
grid on
```

Display the default 3-D perspective view:

```
view(3);
```



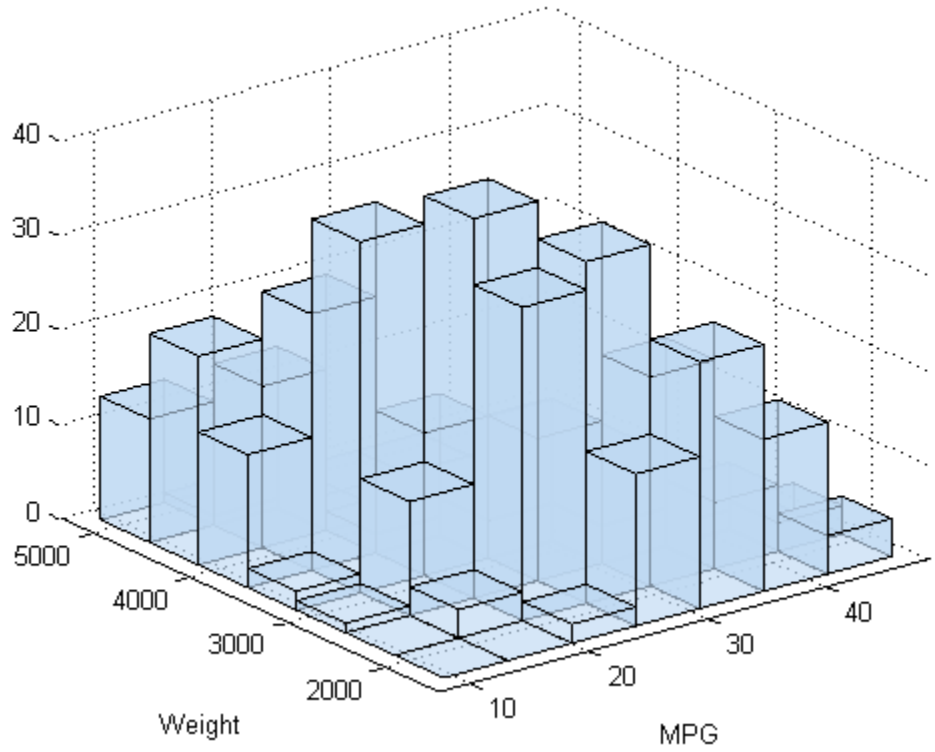
Example 2

Use the car data to make a histogram on a 7-by-7 grid of bins.

```
load carbig
X = [MPG,Weight];
hist3(X,[7 7]);
xlabel('MPG'); ylabel('Weight');
```

Make a histogram with semi-transparent bars:

```
hist3(X,[7 7],'FaceAlpha',.65);
xlabel('MPG'); ylabel('Weight');
set(gcf,'renderer','opengl');
```



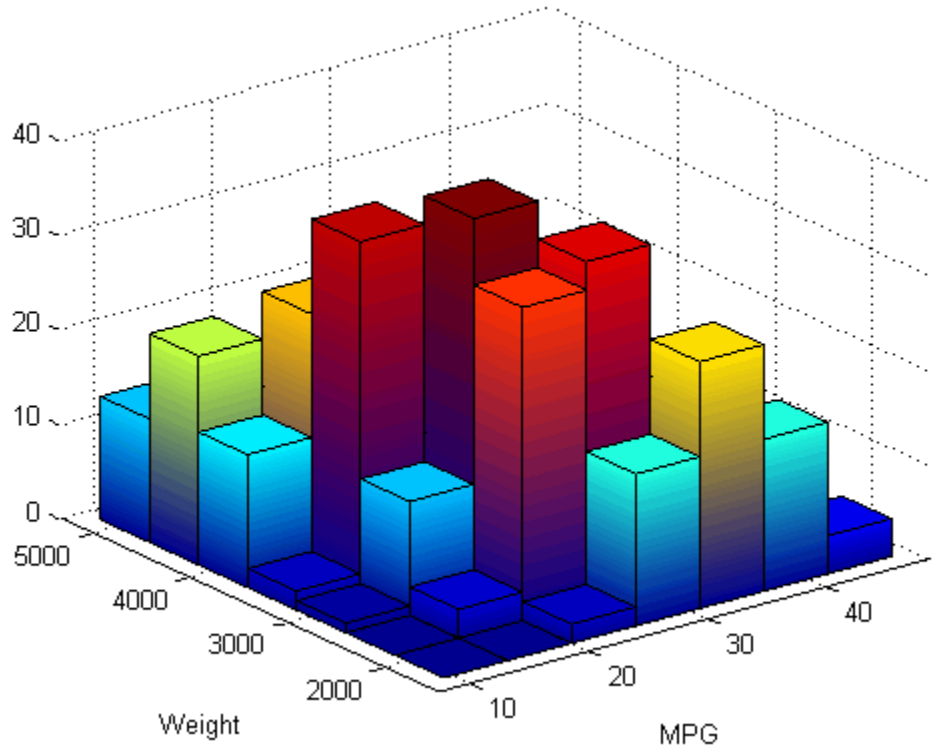
Specify bin centers, different in each direction; get back counts, but don't make the plot.

```
cnt = hist3(X, {0:10:50 2000:500:5000});
```

Example 3

Make a histogram with bars colored according to height.

```
load carbig
X = [MPG,Weight];
hist3(X,[7 7]);
xlabel('MPG'); ylabel('Weight');
set(gcf,'renderer','opengl');
set(get(gca,'child'),'FaceColor','interp','CDataMode',...
'auto');
```



See Also `accumarray` | `bar` | `bar3` | `hist` | `histc`

Purpose

Plot histogram of categorical data

Syntax

```
hist(Y)
hist(Y,X)
hist(ax,...)
N = hist(...)
[N,X] = hist(...)
```

Description

`hist(Y)` plots a histogram bar plot of the counts for each level of the categorical vector `Y`. If `Y` is an *m*-by-*n* categorical matrix, `hist` computes counts for each column of `Y`, and plots a group of *n* bars for each categorical level.

`hist(Y,X)` plots bars only for the levels specified in `X`. `X` is a categorical vector or a cell array of level names as strings.

`hist(ax,...)` plots into the axes with handle `ax` instead of `gca`.

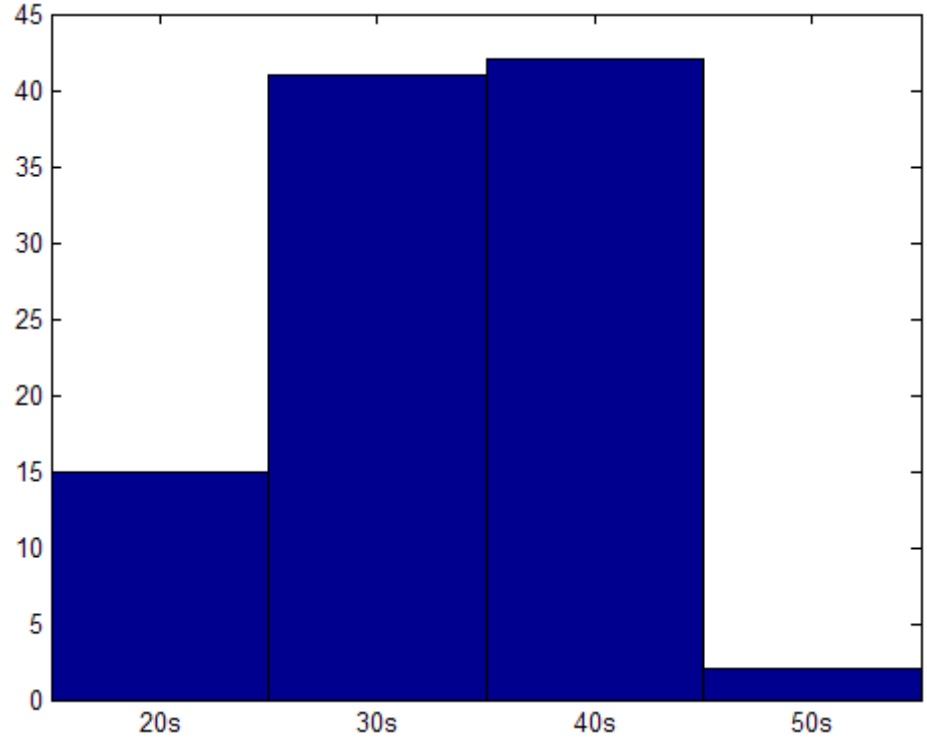
`N = hist(...)` returns the counts for each categorical level. If `Y` is a matrix, `hist` works down the columns of `Y` and returns a matrix of counts with one column for each coluimn of `Y` and one row for each cetegorical level.

`[N,X] = hist(...)` returns the categorical levels corresponding to each count in `N`, or corresponding to each column of `N` if `Y` is a matrix.

Examples

Create a histogram of age groups from the hospital.mat dataset:

```
load hospital
edges = 0:10:100;
labels = strcat(num2str((0:10:90)','%d'),{'s'});
AgeGroup = ordinal(hospital.Age,labels,[],edges);
AgeGroup = droplevels(AgeGroup);
hist(AgeGroup)
```



See Also

`hist` | `categorical.levelcounts` | `categorical.getlevels`

Purpose

Histogram with normal fit

Syntax

```
histfit(data)
histfit(data,nbins)
histfit(data,nbins,dist)
h = histfit(...)
```

Description

`histfit(data)` plots a histogram of the values in the vector `data` using the number of bins equal to the square root of the number of elements in `data`, then superimposes a fitted normal distribution.

`histfit(data,nbins)` uses `nbins` bins for the histogram.

`histfit(data,nbins,dist)` plots a histogram with a density from the distribution specified by `dist`, one of the following strings:

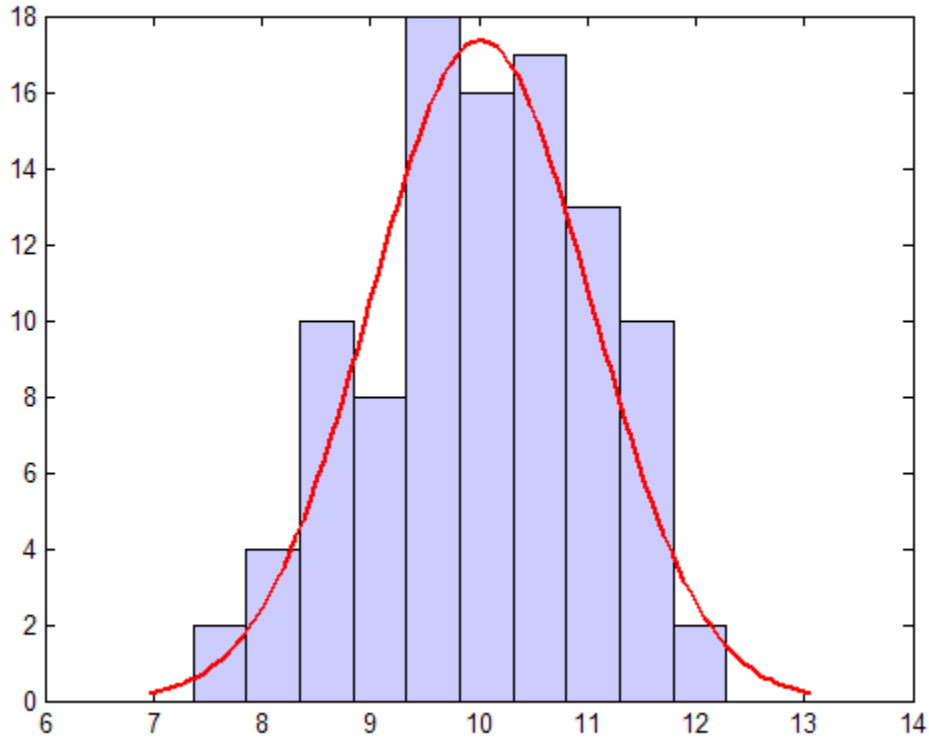
- `'beta'`
- `'birnbaumsaunders'`
- `'exponential'`
- `'extreme value'` or `ev'`
- `'gamma'`
- `'generalized extreme value'` or `'gev'`
- `'generalized pareto'` or `'gp'`
- `'inversegaussian'`
- `'logistic'`
- `'loglogistic'`
- `'lognormal'`
- `'nakagami'`
- `'negative binomial'` or `'nbin'`
- `'normal'` (default)
- `'poisson'`

- 'rayleigh'
- 'rician'
- 'tlocationscale'
- 'weibull' or 'wbl'

h = histfit(...) returns a vector of handles h, where h(1) is the handle to the histogram and h(2) is the handle to the normal curve.

Examples

```
r = normrnd(10,1,100,1);
histfit(r)
h = get(gca,'Children');
set(h(2),'FaceColor',[.8 .8 1])
```



See Also `hist` | `normfit`

hmmdecode

Purpose

Hidden Markov model posterior state probabilities

Syntax

```
PSTATES = hmmdecode(seq,TRANS,EMIS)
[PSTATES,logpseq] = hmmdecode(...)
[PSTATES,logpseq,FORWARD,BACKWARD,S] = hmmdecode(...)
hmmdecode(...,'Symbols',SYMBOLS)
```

Description

`PSTATES = hmmdecode(seq,TRANS,EMIS)` calculates the posterior state probabilities, `PSTATES`, of the sequence `seq`, from a hidden Markov model. The posterior state probabilities are the conditional probabilities of being at state k at step i, given the observed sequence of symbols, `sym`. You specify the model by a transition probability matrix, `TRANS`, and an emissions probability matrix, `EMIS`. `TRANS(i,j)` is the probability of transition from state `i` to state `j`. `EMIS(k,seq)` is the probability that symbol `seq` is emitted from state `k`.

`PSTATES` is an array with the same length as `seq` and one row for each state in the model. The (i, j)th element of `PSTATES` gives the probability that the model is in state i at the jth step, given the sequence `seq`.

Note The function `hmmdecode` begins with the model in state 1 at step 0, prior to the first emission. `hmmdecode` computes the probabilities in `PSTATES` based on the fact that the model begins in state 1.

`[PSTATES,logpseq] = hmmdecode(...)` returns `logpseq`, the logarithm of the probability of sequence `seq`, given transition matrix `TRANS` and emission matrix `EMIS`.

`[PSTATES,logpseq,FORWARD,BACKWARD,S] = hmmdecode(...)` returns the forward and backward probabilities of the sequence scaled by `S`.

`hmmdecode(...,'Symbols',SYMBOLS)` specifies the symbols that are emitted. `SYMBOLS` can be a numeric array or a cell array of the names of the symbols. The default symbols are integers `1` through `N`, where `N` is the number of possible emissions.

References

[1] Durbin, R., S. Eddy, A. Krogh, and G. Mitchison. *Biological Sequence Analysis*. Cambridge, UK: Cambridge University Press, 1998.

Examples

```
trans = [0.95,0.05;
         0.10,0.90];
emis = [1/6 1/6 1/6 1/6 1/6 1/6;
   1/10 1/10 1/10 1/10 1/10 1/2];

[seq,states] = hmmgenerate(100,trans,emis);
pStates = hmmdecode(seq,trans,emis);
[seq,states] = hmmgenerate(100,trans,emis,...
   'Symbols',{'one','two','three','four','five','six'})
pStates = hmmdecode(seq,trans,emis,...
   'Symbols',{'one','two','three','four','five','six'});
```

See Also

hmmgenerate | hmmestimate | hmmviterbi | hmmtrain

hmmestimate

Purpose

Hidden Markov model parameter estimates from emissions and states

Syntax

```
[TRANS,EMIS] = hmmestimate(seq,states)
hmmestimate(...,'Symbols',SYMBOLS)
hmmestimate(...,'Statenames',STATENAMES)
hmmestimate(...,'Pseudoemissions',PSEUDOE)
hmmestimate(...,'Pseudotransitions',PSEUDOTR)
```

Description

`[TRANS,EMIS] = hmmestimate(seq,states)` calculates the maximum likelihood estimate of the transition, `TRANS`, and emission, `EMIS`, probabilities of a hidden Markov model for sequence, `seq`, with known states, `states`.

`hmmestimate(...,'Symbols',SYMBOLS)` specifies the symbols that are emitted. `SYMBOLS` can be a numeric array or a cell array of the names of the symbols. The default symbols are integers 1 through N, where N is the number of possible emissions.

`hmmestimate(...,'Statenames',STATENAMES)` specifies the names of the states. `STATENAMES` can be a numeric array or a cell array of the names of the states. The default state names are 1 through `M`, where `M` is the number of states.

`hmmestimate(...,'Pseudoemissions',PSEUDOE)` specifies pseudocount emission values in the matrix `PSEUDO`. Use this argument to avoid zero probability estimates for emissions with very low probability that might not be represented in the sample sequence. `PSEUDOE` should be a matrix of size m-by-n, where m is the number of states in the hidden Markov model and n is the number of possible emissions. If the $i \to k$ emission does not occur in `seq`, you can set `PSEUDOE(i,k)` to be a positive number representing an estimate of the expected number of such emissions in the sequence `seq`.

`hmmestimate(...,'Pseudotransitions',PSEUDOTR)` specifies pseudocount transition values. You can use this argument to avoid zero probability estimates for transitions with very low probability that might not be represented in the sample sequence. `PSEUDOTR` should be a matrix of size m-by-m, where m is the number of states in the hidden

Markov model. If the $i \to j$ transition does not occur in `states`, you can set `PSEUDOTR(i,j)` to be a positive number representing an estimate of the expected number of such transitions in the sequence `states`.

Pseudotransitions and Pseudoemissions

If the probability of a specific transition or emission is very low, the transition might never occur in the sequence `states`, or the emission might never occur in the sequence `seq`. In either case, the algorithm returns a probability of 0 for the given transition or emission in `TRANS` or `EMIS`. You can compensate for the absence of transition with the `'Pseudotransitions'` and `'Pseudoemissions'` arguments. The simplest way to do this is to set the corresponding entry of `PSEUDO` or `PSEUDOTR` to `1`. For example, if the transition $i \to j$ does not occur in `states`, set `PSEUOTR(i,j) = 1`. This forces `TRANS(i,j)` to be positive.

If you have an estimate for the expected number of transitions $i \to j$ in a sequence of the same length as `states`, and the actual number of transitions $i \to j$ that occur in `seq` is substantially less than what you expect, you can set `PSEUOTR(i,j)` to the expected number. This increases the value of `TRANS(i,j)`. For transitions that do occur in states with the frequency you expect, set the corresponding entry of `PSEUDOTR` to `0`, which does not increase the corresponding entry of `TRANS`.

If you do not know the sequence of states, use `hmmtrain` to estimate the model parameters.

References

[1] Durbin, R., S. Eddy, A. Krogh, and G. Mitchison. *Biological Sequence Analysis*. Cambridge, UK: Cambridge University Press, 1998.

Examples

```
trans = [0.95,0.05; 0.10,0.90];
emis = [1/6 1/6 1/6 1/6 1/6 1/6;
   1/10 1/10 1/10 1/10 1/10 1/2];

[seq,states] = hmmgenerate(1000,trans,emis);
[estimateTR,estimateE] = hmmestimate(seq,states);
```

See Also hmmgenerate | hmmdecode | hmmviterbi | hmmtrain

Purpose

Hidden Markov model states and emissions

Syntax

```
[seq,states] = hmmgenerate(len,TRANS,EMIS)
hmmgenerate(...,'Symbols',SYMBOLS)
hmmgenerate(...,'Statenames',STATENAMES)
```

Description

`[seq,states] = hmmgenerate(len,TRANS,EMIS)` takes a known Markov model, specified by transition probability matrix `TRANS` and emission probability matrix `EMIS`, and uses it to generate

- A random sequence `seq` of emission symbols
- A random sequence `states` of states

The length of both `seq` and `states` is `len`. `TRANS(i,j)` is the probability of transition from state `i` to state `j`. `EMIS(k,l)` is the probability that symbol `l` is emitted from state `k`.

Note The function `hmmgenerate` begins with the model in state 1 at step 0, prior to the first emission. The model then makes a transition to state i_1, with probability T_{1i_1}, and generates an emission a_{k_1} with probability $E_{i_1k_{1_1}}$. `hmmgenerate` returns i_1 as the first entry of `states`, and a_{k_1} as the first entry of `seq`.

`hmmgenerate(...,'Symbols',SYMBOLS)` specifies the symbols that are emitted. `SYMBOLS` can be a numeric array or a cell array of the names of the symbols. The default symbols are integers `1` through `N`, where `N` is the number of possible emissions.

`hmmgenerate(...,'Statenames',STATENAMES)` specifies the names of the states. `STATENAMES` can be a numeric array or a cell array of the names of the states. The default state names are `1` through `M`, where `M` is the number of states.

Since the model always begins at state 1, whose transition probabilities are in the first row of `TRANS`, in the following example, the first entry of

the output `states` is be 1 with probability 0.95 and 2 with probability 0.05.

Examples

```
trans = [0.95,0.05;
         0.10,0.90];
emis = [1/6 1/6 1/6 1/6 1/6 1/6;
   1/10 1/10 1/10 1/10 1/10 1/2];

[seq,states] = hmmgenerate(100,trans,emis)
[seq,states] = hmmgenerate(100,trans,emis,...
    'Symbols',{'one','two','three','four','five','six'},...
    'Statenames',{'fair';'loaded'})
```

See Also

`hmmviterbi` | `hmmdecode` | `hmmestimate` | `hmmtrain`

Purpose

Hidden Markov model parameter estimates from emissions

Syntax

```
[ESTTR,ESTEMIT] = hmmtrain(seq,TRGUESS,EMITGUESS)
hmmtrain(...,'Algorithm',algorithm)
hmmtrain(...,'Symbols',SYMBOLS)
hmmtrain(...,'Tolerance',tol)
hmmtrain(...,'Maxiterations',maxiter)
hmmtrain(...,'Verbose',true)
hmmtrain(...,'Pseudoemissions',PSEUDOE)
hmmtrain(...,'Pseudotransitions',PSEUDOTR)
```

Description

`[ESTTR,ESTEMIT] = hmmtrain(seq,TRGUESS,EMITGUESS)` estimates the transition and emission probabilities for a hidden Markov model using the Baum-Welch algorithm. `seq` can be a row vector containing a single sequence, a matrix with one row per sequence, or a cell array with each cell containing a sequence. `TRGUESS` and `EMITGUESS` are initial estimates of the transition and emission probability matrices. `TRGUESS(i,j)` is the estimated probability of transition from state `i` to state `j`. `EMITGUESS(i,k)` is the estimated probability that symbol `k` is emitted from state `i`.

`hmmtrain(...,'Algorithm',algorithm)` specifies the training algorithm. *`algorithm`* can be either `'BaumWelch'` or `'Viterbi'`. The default algorithm is `'BaumWelch'`.

`hmmtrain(...,'Symbols',SYMBOLS)` specifies the symbols that are emitted. `SYMBOLS` can be a numeric array or a cell array of the names of the symbols. The default symbols are integers `1` through `N`, where `N` is the number of possible emissions.

`hmmtrain(...,'Tolerance',tol)` specifies the tolerance used for testing convergence of the iterative estimation process. The default tolerance is `1e-4`.

`hmmtrain(...,'Maxiterations',maxiter)` specifies the maximum number of iterations for the estimation process. The default maximum is `100`.

`hmmtrain(...,'Verbose',true)` returns the status of the algorithm at each iteration.

`hmmtrain(...,'Pseudoemissions',PSEUDOE)` specifies pseudocount emission values for the Viterbi training algorithm. Use this argument to avoid zero probability estimates for emissions with very low probability that might not be represented in the sample sequence. `PSEUDOE` should be a matrix of size m-by-n, where m is the number of states in the hidden Markov model and n is the number of possible emissions. If the $i \rightarrow k$ emission does not occur in `seq`, you can set `PSEUDOE(i,k)` to be a positive number representing an estimate of the expected number of such emissions in the sequence `seq`.

`hmmtrain(...,'Pseudotransitions',PSEUDOTR)` specifies pseudocount transition values for the Viterbi training algorithm. Use this argument to avoid zero probability estimates for transitions with very low probability that might not be represented in the sample sequence. `PSEUDOTR` should be a matrix of size m-by-m, where m is the number of states in the hidden Markov model. If the $i \rightarrow j$ transition does not occur in `states`, you can set `PSEUDOTR(i,j)` to be a positive number representing an estimate of the expected number of such transitions in the sequence `states`.

If you know the states corresponding to the sequences, use `hmmestimate` to estimate the model parameters.

Tolerance

The input argument '`tolerance`' controls how many steps the `hmmtrain` algorithm executes before the function returns an answer. The algorithm terminates when all of the following three quantities are less than the value that you specify for `tolerance`:

- The log likelihood that the input sequence `seq` is generated by the currently estimated values of the transition and emission matrices
- The change in the norm of the transition matrix, normalized by the size of the matrix

- The change in the norm of the emission matrix, normalized by the size of the matrix

The default value of `'tolerance'` is `.0001`. Increasing the tolerance decreases the number of steps the `hmmtrain` algorithm executes before it terminates.

`maxiterations`

The maximum number of iterations, `'maxiterations'`, controls the maximum number of steps the algorithm executes before it terminates. If the algorithm executes `maxiter` iterations before reaching the specified tolerance, the algorithm terminates and the function returns a warning. If this occurs, you can increase the value of `'maxiterations'` to make the algorithm reach the desired tolerance before terminating.

References

[1] Durbin, R., S. Eddy, A. Krogh, and G. Mitchison. *Biological Sequence Analysis*. Cambridge, UK: Cambridge University Press, 1998.

Examples

```
trans = [0.95,0.05;
      0.10,0.90];
emis = [1/6, 1/6, 1/6, 1/6, 1/6, 1/6;
   1/10, 1/10, 1/10, 1/10, 1/10, 1/2];

seq1 = hmmgenerate(100,trans,emis);
seq2 = hmmgenerate(200,trans,emis);
seqs = {seq1,seq2};
[estTR,estE] = hmmtrain(seqs,trans,emis);
```

See Also

`hmmgenerate` | `hmmdecode` | `hmmestimate` | `hmmviterbi`

hmmviterbi

Purpose

Hidden Markov model most probable state path

Syntax

```
STATES = hmmviterbi(seq,TRANS,EMIS)
hmmviterbi(...,'Symbols',SYMBOLS)
hmmviterbi(...,'Statenames',STATENAMES)
```

Description

`STATES = hmmviterbi(seq,TRANS,EMIS)` given a sequence, `seq`, calculates the most likely path through the hidden Markov model specified by transition probability matrix, `TRANS`, and emission probability matrix `EMIS`. `TRANS(i,j)` is the probability of transition from state `i` to state `j`. `EMIS(i,k)` is the probability that symbol `k` is emitted from state `i`.

Note The function `hmmviterbi` begins with the model in state 1 at step 0, prior to the first emission. `hmmviterbi` computes the most likely path based on the fact that the model begins in state 1.

`hmmviterbi(...,'Symbols',SYMBOLS)` specifies the symbols that are emitted. `SYMBOLS` can be a numeric array or a cell array of the names of the symbols. The default symbols are integers `1` through `N`, where `N` is the number of possible emissions.

`hmmviterbi(...,'Statenames',STATENAMES)` specifies the names of the states. `STATENAMES` can be a numeric array or a cell array of the names of the states. The default state names are 1 through `M`, where `M` is the number of states.

Examples

```
trans = [0.95,0.05;
         0.10,0.90];
emis = [1/6 1/6 1/6 1/6 1/6 1/6;
   1/10 1/10 1/10 1/10 1/10 1/2];

[seq,states] = hmmgenerate(100,trans,emis);
estimatedStates = hmmviterbi(seq,trans,emis);
```

```
[seq,states] = ...
   hmmgenerate(100,trans,emis,...
               'Statenames',{'fair';'loaded'});
estimatesStates = ...
   hmmviterbi(seq,trans,emis,...
              'Statenames',{'fair';'loaded'});
```

References

[1] Durbin, R., S. Eddy, A. Krogh, and G. Mitchison. *Biological Sequence Analysis*. Cambridge, UK: Cambridge University Press, 1998.

See Also

`hmmgenerate` | `hmmdecode` | `hmmestimate` | `hmmtrain`

categorical.horzcat

Purpose

Horizontal concatenation for categorical arrays

Syntax

```
C = horzcat(dim,A,B,...)
C = horzcat(A,B)
```

Description

`C = horzcat(dim,A,B,...)` horizontally concatenates the categorical arrays `A,B,...` . For matrices, all inputs must have the same number of rows. For n-D arrays, all inputs must have the same sizes except in the second dimension. The set of categorical levels for `C` is the sorted union of the sets of levels of the inputs, as determined by their labels.

`C = horzcat(A,B)` is called for the syntax `[A B]`.

See Also

`cat` | `vertcat`

Purpose

Horizontal concatenation for dataset arrays

Syntax

```
ds = horzcat(ds1, ds2, ...)
```

Description

`ds = horzcat(ds1, ds2, ...)` horizontally concatenates the dataset arrays `ds1, ds2, ...` . You may concatenate dataset arrays that have duplicate variable names, however, the variables must contain identical data, and `horzcat` includes only one copy of the variable in the output dataset.

Observation names for all dataset arrays that have them must be identical except for order. `horzcat` concatenates by matching observation names when present, or by position for datasets that do not have observation names.

See Also

`cat` | `vertcat`

hougen

Purpose

Hougen-Watson model

Syntax

```
yhat = hougen(beta,x)
```

Description

`yhat = hougen(beta,x)` returns the predicted values of the reaction rate, `yhat`, as a function of the vector of parameters, `beta`, and the matrix of data, `X`. `beta` must have 5 elements and `X` must have three columns.

`hougen` is a utility function for `rsmdemo`.

The model form is:

$$\hat{y} = \frac{\beta_1 x_2 - x_3 / \beta_5}{1 + \beta_2 x_1 + \beta_3 x_2 + \beta_4 x_3}$$

References

[1] Bates, D. M., and D. G. Watts. *Nonlinear Regression Analysis and Its Applications*. Hoboken, NJ: John Wiley & Sons, Inc., 1988.

See Also

`rsmdemo`

Purpose

Hypergeometric cumulative distribution function

Syntax

```
hygecdf(X,M,K,N)
```

Description

`hygecdf(X,M,K,N)` computes the hypergeometric cdf at each of the values in `X` using the corresponding size of the population, `M`, number of items with the desired characteristic in the population, `K`, and number of samples drawn, `N`. Vector or matrix inputs for `X`, `M`, `K`, and `N` must all have the same size. A scalar input is expanded to a constant matrix with the same dimensions as the other inputs.

The hypergeometric cdf is

$$p = F(x \mid M,K,N) = \sum_{i=0}^{x} \frac{\binom{K}{i}\binom{M-K}{N-i}}{\binom{M}{N}}$$

The result, p, is the probability of drawing up to x of a possible K items in N drawings without replacement from a group of M objects.

Examples

Suppose you have a lot of 100 floppy disks and you know that 20 of them are defective. What is the probability of drawing zero to two defective floppies if you select 10 at random?

```
p = hygecdf(2,100,20,10)
p =
  0.6812
```

See Also

`cdf` | `hygepdf` | `hygeinv` | `hygestat` | `hygernd`

hygeinv

Purpose

Hypergeometric inverse cumulative distribution function

Syntax

```
hygeinv(P,M,K,N)
```

Description

`hygeinv(P,M,K,N)` returns the smallest integer `X` such that the hypergeometric cdf evaluated at `X` equals or exceeds `P`. You can think of `P` as the probability of observing `X` defective items in `N` drawings without replacement from a group of `M` items where `K` are defective.

Examples

Suppose you are the Quality Assurance manager for a floppy disk manufacturer. The production line turns out floppy disks in batches of 1,000. You want to sample 50 disks from each batch to see if they have defects. You want to accept 99% of the batches if there are no more than 10 defective disks in the batch. What is the maximum number of defective disks should you allow in your sample of 50?

```
x = hygeinv(0.99,1000,10,50)
x =
   3
```

What is the median number of defective floppy disks in samples of 50 disks from batches with 10 defective disks?

```
x = hygeinv(0.50,1000,10,50)
x =
   0
```

See Also

`icdf` | `hygecdf` | `hygepdf` | `hygestat` | `hygernd`

Purpose

Hypergeometric probability density function

Syntax

```
Y = hygepdf(X,M,K,N)
```

Description

`Y = hygepdf(X,M,K,N)` computes the hypergeometric pdf at each of the values in `X` using the corresponding size of the population, `M`, number of items with the desired characteristic in the population, `K`, and number of samples drawn, `N`. `X`, `M`, `K`, and `N` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

The parameters in `M`, `K`, and `N` must all be positive integers, with $N \le M$. The values in `X` must be less than or equal to all the parameter values.

The hypergeometric pdf is

$$y = f(x \mid M,K,N) = \frac{\binom{K}{x}\binom{M-K}{N-x}}{\binom{M}{N}}$$

The result, y, is the probability of drawing exactly x of a possible K items in n drawings without replacement from a group of M objects.

Examples

Suppose you have a lot of 100 floppy disks and you know that 20 of them are defective. What is the probability of drawing 0 through 5 defective floppy disks if you select 10 at random?

```
p = hygepdf(0:5,100,20,10)
p =
  0.0951   0.2679   0.3182   0.2092   0.0841   0.0215
```

See Also

`pdf` | `hygecdf` | `hygeinv` | `hygestat` | `hygernd`

hygernd

Purpose

Hypergeometric random numbers

Syntax

```
R = hygernd(M,K,N)
R = hygernd(M,K,N,m,n,...)
R = hygernd(M,K,N,[m,n,...])
```

Description

`R = hygernd(M,K,N)` generates random numbers from the hypergeometric distribution with corresponding size of the population, `M`, number of items with the desired characteristic in the population, `K`, and number of samples drawn, `N`. `M`, `K`, and `N` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `R`. A scalar input for `M`, `K`, or `N` is expanded to a constant array with the same dimensions as the other inputs.

`R = hygernd(M,K,N,m,n,...)` or `R = hygernd(M,K,N,[m,n,...])` generates an `m`-by-`n`-by-... array. The `M`, `K`, `N` parameters can each be scalars or arrays of the same size as `R`.

Examples

```
numbers = hygernd(1000,40,50)
numbers =
   1
```

See Also

`random` | `hygepdf` | `hygecdf` | `hygeinv` | `hygestat`

Purpose

Hypergeometric mean and variance

Syntax

```
[MN,V] = hygestat(M,K,N)
```

Description

`[MN,V] = hygestat(M,K,N)` returns the mean of and variance for the hypergeometric distribution with corresponding size of the population, `M`, number of items with the desired characteristic in the population, `K`, and number of samples drawn, `N`. Vector or matrix inputs for `M`, `K`, and `N` must have the same size, which is also the size of `MN` and `V`. A scalar input for `M`, `K`, or `N` is expanded to a constant matrix with the same dimensions as the other inputs.

The mean of the hypergeometric distribution with parameters `M`, `K`, and `N` is `NK/M`, and the variance is `NK(M-K)(M-N)/[M^2(M-1)]`.

Examples

The hypergeometric distribution approaches the binomial distribution, where `p = K/M`, as `M` goes to infinity.

```
[m,v] = hygestat(10.^(1:4),10.^(0:3),9)
m =
  0.9000  0.9000  0.9000  0.9000
v =
  0.0900  0.7445  0.8035  0.8094

[m,v] = binostat(9,0.1)
m =
  0.9000
v =
  0.8100
```

See Also

`hygepdf` | `hygecdf` | `hygeinv` | `hygernd`

Purpose

Inverse cumulative distribution functions

Syntax

```
Y = icdf(name,X,A)
Y = icdf(name,X,A,B)
Y = icdf(name,X,A,B,C)
```

Description

`Y = icdf(name,X,A)` computes the inverse cumulative distribution function for the one-parameter family of distributions specified by `name`. Parameter values for the distribution are given in `A`. The inverse cumulative distribution function is evaluated at the values in `X` and its values are returned in `Y`.

If `X` and `A` are arrays, they must be the same size. If `X` is a scalar, it is expanded to a constant matrix the same size as `A`. If `A` is a scalar, it is expanded to a constant matrix the same size as `X`.

`Y` is the common size of `X` and `A` after any necessary scalar expansion.

`Y = icdf(name,X,A,B)` computes the inverse cumulative distribution function for two-parameter families of distributions, where parameter values are given in `A` and `B`.

If `X`, `A`, and `B` are arrays, they must be the same size. If `X` is a scalar, it is expanded to a constant matrix the same size as `A` and `B`. If either `A` or `B` are scalars, they are expanded to constant matrices the same size as `X`.

`Y` is the common size of `X`, `A`, and `B` after any necessary scalar expansion.

`Y = icdf(name,X,A,B,C)` computes the inverse cumulative distribution function for three-parameter families of distributions, where parameter values are given in `A`, `B`, and `C`.

If `X`, `A`, `B`, and `C` are arrays, they must be the same size. If `X` is a scalar, it is expanded to a constant matrix the same size as `A`, `B`, and `C`. If any of `A`, `B` or `C` are scalars, they are expanded to constant matrices the same size as `X`.

`Y` is the common size of `X`, `A`, `B` and `C` after any necessary scalar expansion.

Acceptable strings for `name` are:

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'beta' or 'Beta'	"Beta Distribution" on page B-4	a	b	—
'bino' or 'Binomial'	"Binomial Distribution" on page B-7	n: number of trials	p: probability of success for each trial	—
'chi2' or 'Chisquare'	"Chi-Square Distribution" on page B-12	ν: degrees of freedom	—	—
'exp' or 'Exponential'	"Exponential Distribution" on page B-16	μ: mean	—	—
'ev' or 'Extreme Value'	"Extreme Value Distribution" on page B-19	μ: location parameter	σ: scale parameter	—
'f' or 'F'	"F Distribution" on page B-25	$\nu 1$: numerator degrees of freedom	$\nu 2$: denominator degrees of freedom	—
'gam' or 'Gamma'	"Gamma Distribution" on page B-27	a: shape parameter	b: scale parameter	—
'gev' or 'Generalized Extreme Value'	"Generalized Extreme Value Distribution" on page B-32	k: shape parameter	σ: scale parameter	μ: location parameter

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'gp' or 'Generalized Pareto'	"Generalized Pareto Distribution" on page B-37	k: tail index (shape) parameter	σ: scale parameter	μ: threshold (location) parameter
'geo' or 'Geometric'	"Geometric Distribution" on page B-41	p: probability parameter	—	—
'hyge' or 'Hypergeometric'	"Hypergeometric Distribution" on page B-43	M: size of the population	K: number of items with the desired characteristic in the population	n: number of samples drawn
'logn' or 'Lognormal'	"Lognormal Distribution" on page B-51	μ	σ	—
'nbin' or 'Negative Binomial'	"Negative Binomial Distribution" on page B-72	r: number of successes	p: probability of success in a single trial	—
'ncf' or 'Noncentral F'	"Noncentral F Distribution" on page B-78	$\nu 1$: numerator degrees of freedom	$\nu 2$: denominator degrees of freedom	δ: noncentrality parameter
'nct' or 'Noncentral t'	"Noncentral t Distribution" on page B-80	ν: degrees of freedom	δ: noncentrality parameter	—
'ncx2' or 'Noncentral Chi-square'	"Noncentral Chi-Square Distribution" on page B-76	ν: degrees of freedom	δ: noncentrality parameter	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'norm' or 'Normal'	"Normal Distribution" on page B-83	μ: mean	σ: standard deviation	—
'poiss' or 'Poisson'	"Poisson Distribution" on page B-89	λ: mean	—	—
'rayl' or 'Rayleigh'	"Rayleigh Distribution" on page B-91	b: scale parameter	—	—
't' or 'T'	"Student's t Distribution" on page B-95	ν: degrees of freedom	—	—
'unif' or 'Uniform'	"Uniform Distribution (Continuous)" on page B-99	a: lower endpoint (minimum)	b: upper endpoint (maximum)	—
'unid' or 'Discrete Uniform'	"Uniform Distribution (Discrete)" on page B-101	N: maximum observable value	—	—
'wbl' or 'Weibull'	"Weibull Distribution" on page B-103	a: scale parameter	b: shape parameter	—

Examples

Compute the icdf of the normal distribution with mean 0 and standard deviation 1 at inputs 0.1, 0.3, ..., 0.9:

```
x1 = icdf('Normal',0.1:0.2:0.9,0,1)
x1 =
  -1.2816  -0.5244  0  0.5244  1.2816
```

The order of the parameters is the same as for `norminv`.

Compute the icdfs of Poisson distributions with rate parameters 0, 1, ..., 4 at inputs 0.1, 0.3, ..., 0.9, respectively:

```
x2 = icdf('Poisson',0.1:0.2:0.9,0:4)
x2 =
   NaN     0     2     4     7
```

The order of the parameters is the same as for `poissinv`.

See Also

`cdf` | `mle` | `pdf` | `random`

Purpose

Return inverse cumulative distribution function (ICDF) for ProbDistUnivKernel object

Syntax

```
Y = icdf(PD, P)
```

Description

`Y = icdf(PD, P)` returns `Y`, an array containing the inverse cumulative distribution function (ICDF) for the ProbDistUnivKernel object `PD`, evaluated at values in `P`.

Input Arguments

`PD`	An object of the class `ProbDistUnivKernel`.
`P`	A numeric array of values from `0` to `1` where you want to evaluate the ICDF.

Output Arguments

`Y`	An array containing the inverse cumulative distribution function (ICDF) for the ProbDistUnivKernel object `PD`.

See Also

`icdf`

ProbDistUnivParam.icdf

Purpose

Return inverse cumulative distribution function (ICDF) for ProbDistUnivParam object

Syntax

```
Y = icdf(PD, P)
```

Description

`Y = icdf(PD, P)` returns `Y`, an array containing the inverse cumulative distribution function (ICDF) for the ProbDistUnivParam object `PD`, evaluated at values in `P`.

Input Arguments

`PD`	An object of the class `ProbDistUnivParam`.
`P`	A numeric array of values from `0` to `1` where you want to evaluate the ICDF.

Output Arguments

`Y`	An array containing the inverse cumulative distribution function (ICDF) for the ProbDistUnivParam object `PD`.

See Also

`icdf`

Purpose

Inverse cumulative distribution function for piecewise distribution

Syntax

```
X = icdf(obj,P)
```

Description

`X = icdf(obj,P)` returns an array `X` of values of the inverse cumulative distribution function for the piecewise distribution object `obj`, evaluated at the values in the array `P`.

Examples

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);
[p,q] = boundary(obj)
p =
    0.1000
    0.9000
q =
   -1.7766
    1.8432

icdf(obj,p)
ans =
   -1.7766
    1.8432
```

See Also

`paretotails` | `cdf`

inconsistent

Purpose

Inconsistency coefficient

Syntax

```
Y = inconsistent(Z)
Y = inconsistent(Z,d)
```

Description

`Y = inconsistent(Z)` computes the inconsistency coefficient for each link of the hierarchical cluster tree `Z`, where `Z` is an (m-1)-by-3 matrix generated by the `linkage` function. The inconsistency coefficient characterizes each link in a cluster tree by comparing its height with the average height of other links at the same level of the hierarchy. The higher the value of this coefficient, the less similar the objects connected by the link.

`Y = inconsistent(Z,d)` computes the inconsistency coefficient for each link in the hierarchical cluster tree `Z` to depth `d`, where `d` is an integer denoting the number of levels of the cluster tree that are included in the calculation. By default, `d=2`.

The output, `Y`, is an (m-1)-by-4 matrix formatted as follows.

Column	Description
1	Mean of the heights of all the links included in the calculation.
2	Standard deviation of the heights of all the links included in the calculation.
3	Number of links included in the calculation.
4	Inconsistency coefficient.

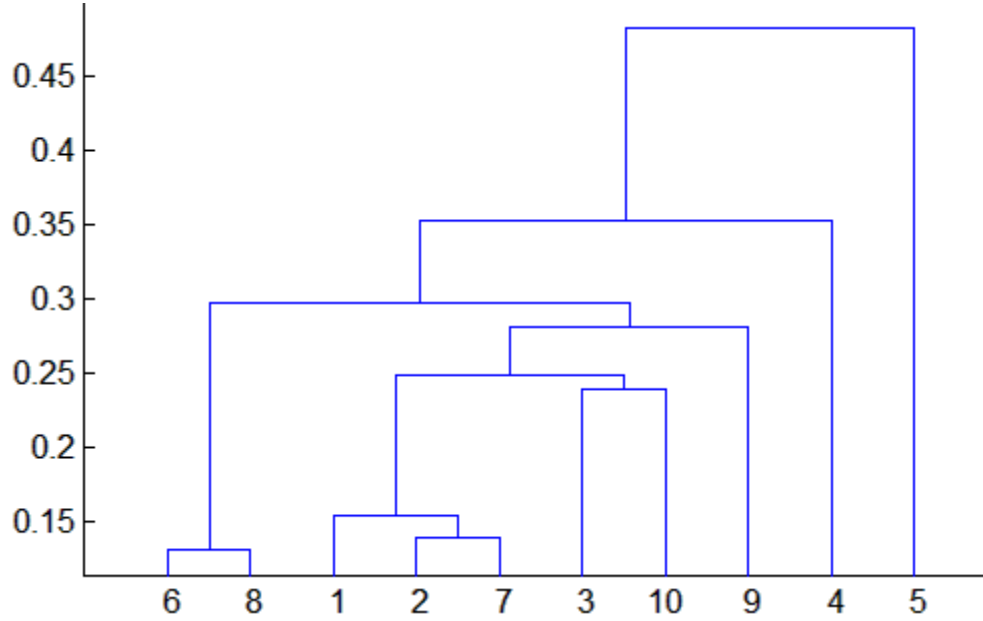
For each link, k, the inconsistency coefficient is calculated as:

$$Y(k,4) = (z(k,3) - Y(k,1)) / Y(k,2)$$

For leaf nodes, nodes that have no further nodes under them, the inconsistency coefficient is set to 0.

Examples

```
X = gallery('uniformdata',[10 2],12);
Y = pdist(X);
Z = linkage(Y,'single');
dendrogram(Z)
```




```
W = inconsistent(Z,3)
W =
    0.1313         0    1.0000         0
    0.1386         0    1.0000         0
    0.1463    0.0109    2.0000    0.7071
    0.2391         0    1.0000         0
    0.1951    0.0568    4.0000    0.9425
    0.2308    0.0543    4.0000    0.9320
    0.2395    0.0748    4.0000    0.7636
    0.2654    0.0945    4.0000    0.9203
    0.3769    0.0950    3.0000    1.1040
```

References

[1] Jain, A., and R. Dubes. *Algorithms for Clustering Data.* Upper Saddle River, NJ: Prentice-Hall, 1988.

[2] Zahn, C. T. "Graph-theoretical methods for detecting and describing Gestalt clusters." *IEEE Transactions on Computers*. Vol. C-20, Issue 1, 1971, pp. 68–86.

See Also

`cluster` | `cophenet` | `clusterdata` | `dendrogram` | `linkage` | `pdist` | `squareform`

Purpose

Read-only structure containing information about input data to ProbDist object

Description

`InputData` is a read-only property of the `ProbDist` class. `InputData` is a structure containing information about input data to a ProbDist object. It includes the following fields:

- `data`
- `cens`
- `freq`

Values

Possible values for the three fields in the structure are any data supplied to the `fitdist` function:

- `data` — Data passed to the `fitdist` function when creating the ProbDist object. This field is empty if the ProbDist object was created without fitting to data, that is by using the `ProbDistUnivParam.ProbDistUnivParam` constructor.
- `cens` — The vector supplied with the `'censoring'` parameter when creating the ProbDist object using the `fitdist` function. This field is empty if the ProbDist object was created without fitting to data, that is by using the `ProbDistUnivParam.ProbDistUnivParam` constructor.
- `freq` — The vector supplied with the `'frequency'` parameter when creating the ProbDist object using the `fitdist` function. This field is empty if the ProbDist object was created without fitting to data, that is by using the `ProbDistUnivParam.ProbDistUnivParam` constructor.

Use this information to view and compare the data supplied to create distributions.

categorical.int8

Purpose

Convert categorical array to signed 8-bit integer array

Syntax

```
B = int8(A)
```

Description

`B = int8(A)` converts the categorical array `A` to a signed 8-bit integer array. Each element of `B` contains the internal categorical level code for the corresponding element of `A`.

Undefined elements of `A` are assigned the value 0 in `B`. If `A` contains more than `intmax('int8')` levels, the internal codes will saturate to `intmax('int8')` when cast to `int8`.

See Also

`double` | `uint8`

How To

- "Integers"

Purpose

Convert categorical array to signed 16-bit integer array

Syntax

```
B = int16(A)
```

Description

`B = int16(A)` converts the categorical array `A` to a signed 16-bit integer array. Each element of `B` contains the internal categorical level code for the corresponding element of A.

Undefined elements of `A` are assigned the value 0 in `B`.

See Also

`double` | `uint16`

How To

- "Integers"

categorical.int32

Purpose

Convert categorical array to signed 32-bit integer array

Syntax

```
B = int32(A)
```

Description

`B = int32(A)` converts the categorical array `A` to a signed 32-bit integer array. Each element of `B` contains the internal categorical level code for the corresponding element of A.

Undefined elements of `A` are assigned the value 0 in `B`.

See Also

`double` | `uint32`

How To

- “Integers”

Purpose

Convert categorical array to signed 64-bit integer array

Syntax

```
B = int64(A)
```

Description

`B = int64(A)` converts the categorical array `A` to a signed 64-bit integer array. Each element of `B` contains the internal categorical level code for the corresponding element of A.

Undefined elements of `A` are assigned the value 0 in `B`.

See Also

`double` | `uint64`

How To

- "Integers"

interactionplot

Purpose

Interaction plot for grouped data

Syntax

```
interactionplot(Y,GROUP)
interactionplot(Y,GROUP,'varnames',VARNAMES)
[h,AX,bigax] = interactionplot(...)
```

Description

`interactionplot(Y,GROUP)` displays the two-factor interaction plot for the group means of matrix `Y` with groups defined by entries in the cell array `GROUP`. `Y` is a numeric matrix or vector. If `Y` is a matrix, the rows represent different observations and the columns represent replications of each observation. If `Y` is a vector, the rows give the means of each entry in the cell array `GROUP`. Each cell of `GROUP` must contain a grouping variable that can be a categorical variable, numeric vector, character matrix, or a single-column cell array of strings. (See "Grouped Data" on page 2-34.) `GROUP` can also be a matrix whose columns represent different grouping variables. Each grouping variable must have the same number of rows as `Y`. The number of grouping variables must be greater than 1.

The interaction plot is a matrix plot, with the number of rows and columns both equal to the number of grouping variables. The grouping variable names are printed on the diagonal of the plot matrix. The plot at off-diagonal position (*i*,*j*) is the interaction of the two variables whose names are given at row diagonal (*i*,*i*) and column diagonal (*j*,*j*), respectively.

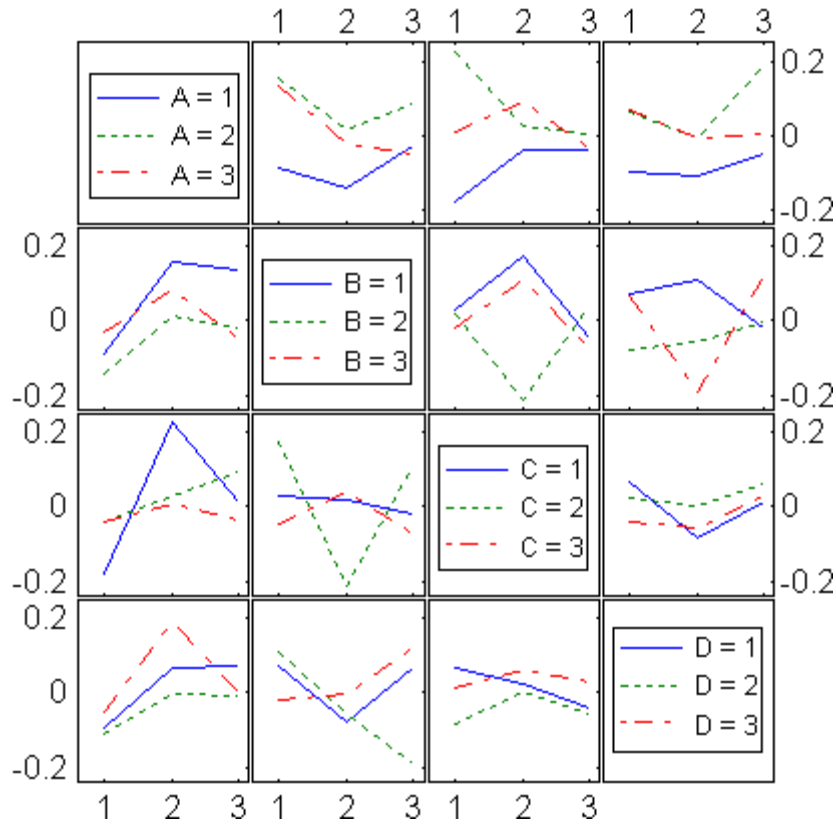
`interactionplot(Y,GROUP,'varnames',VARNAMES)` displays the interaction plot with user-specified grouping variable names `VARNAMES`. `VARNAMES` is a character matrix or a cell array of strings, one per grouping variable. Default names are `'X1'`, `'X2'`, ...

`[h,AX,bigax] = interactionplot(...)` returns a handle `h` to the figure window, a matrix `AX` of handles to the subplot axes, and a handle `bigax` to the big (invisible) axes framing the subplots.

Examples

Display interaction plots for data with four 3-level factors named `'A'`, `'B'`,`'C'`, and `'D'`:

```
y = randn(1000,1); % response
group = ceil(3*rand(1000,4)); % four 3-level factors
interactionplot(y,group,'varnames',{'A','B','C','D'})
```



See Also

`maineffectsplot` | `multivarichart`

How To

- “Grouped Data” on page 2-34

categorical.intersect

Purpose

Set intersection for categorical arrays

Syntax

```
C = intersect(A,B)
```

Description

`C = intersect(A,B)` when `A` and `B` are categorical arrays returns a categorical vector `C` containing the values common to both `A` and `B`. The result `C` is sorted. The set of categorical levels for `C` is the sorted union of the sets of levels of the inputs, as determined by their labels.

`[C,IA,IB] = UNION(A,B)` also returns index vectors `IA` and `IB` such that `C = A(IA)` and `C = B(IB)`.

See Also

`ismember` | `setdiff` | `setxor` | `union` | `unique`

Purpose

Inverse prediction

Syntax

```
X0 = invpred(X,Y,Y0)
[X0,DXLO,DXUP] = invpred(X,Y,Y0)
[X0,DXLO,DXUP] = invpred(X,Y,Y0,name1,val1,name2,val2,...)
```

Description

`X0 = invpred(X,Y,Y0)` accepts vectors `X` and `Y` of the same length, fits a simple regression, and returns the estimated value `X0` for which the height of the line is equal to `Y0`. The output, `X0`, has the same size as `Y0`, and `Y0` can be an array of any size.

`[X0,DXLO,DXUP] = invpred(X,Y,Y0)` also computes 95% inverse prediction intervals. `DXLO` and `DXUP` define intervals with lower bound `X0 DXLO` and upper bound `X0+DXUP`. Both `DXLO` and `DXUP` have the same size as `Y0`.

The intervals are not simultaneous and are not necessarily finite. Some intervals may extend from a finite value to `-Inf` or `+Inf`, and some may extend over the entire real line.

`[X0,DXLO,DXUP] = invpred(X,Y,Y0,name1,val1,name2,val2,...)` specifies optional argument name/value pairs chosen from the following list. Argument names are case insensitive and partial matches are allowed.

Name	Value
`'alpha'`	A value between 0 and 1 specifying a confidence level of `100*(1-alpha)`%. Default is `alpha=0.05` for 95% confidence.
`'predopt'`	Either `'observation'`, the default value to compute the intervals for `X0` at which a new observation could equal `Y0`, or `'curve'` to compute intervals for the `X0` value at which the curve is equal to `Y0`.

Examples

```
x = 4*rand(25,1);
y = 10 + 5*x + randn(size(x));
scatter(x,y)
x0 = invpred(x,y,20)
```

See Also

polyfit | polyval | polyconf | polytool

Purpose

Inverse permute dimensions of categorical array

Syntax

```
A = ipermute(B,order)
```

Description

`A = ipermute(B,order)` is the inverse of `permute`. `ipermute` rearranges the dimensions of the categorical array `B` so that `permute(A,order)` will produce `B`. The array produced has the same values of `A` but the order of the subscripts needed to access any particular element are rearranged as specified by `order`. The elements of `order` must be a rearrangement of the numbers from 1 to `n`.

See Also

`permute`

iqr

Purpose

Interquartile range

Syntax

```
y = iqr(X)
iqr(X,dim)
```

Description

`y = iqr(X)` returns the interquartile range of the values in X. For vector input, `y` is the difference between the 75th and the 25th percentiles of the sample in X. For matrix input, `y` is a row vector containing the interquartile range of each column of `X`. For N-dimensional arrays, `iqr` operates along the first nonsingleton dimension of `X`.

`iqr(X,dim)` calculates the interquartile range along the dimension `dim` of `X`.

Tips

The IQR is a robust estimate of the spread of the data, since changes in the upper and lower 25% of the data do not affect it. If there are outliers in the data, then the IQR is more representative than the standard deviation as an estimate of the spread of the body of the data. The IQR is less efficient than the standard deviation as an estimate of the spread when the data is all from the normal distribution.

Multiply the IQR by 0.7413 to estimate σ (the second parameter of the normal distribution.)

Examples

This Monte Carlo simulation shows the relative efficiency of the IQR to the sample standard deviation for normal data.

```
x = normrnd(0,1,100,100);
s = std(x);
s_IQR = 0.7413*iqr(x);
efficiency = (norm(s-1)./norm(s_IQR-1)).^2
efficiency =
  0.3297
```

See Also

`std` | `mad` | `range`

Purpose

Return interquartile range (IQR) for ProbDistUnivKernel object

Syntax

```
Y = iqr(PD)
```

Description

`Y = iqr(PD)` returns `Y`, the interquartile range for the ProbDistUnivKernel object `PD`. The interquartile range is the distance between the 75th and 25th percentiles.

Input Arguments

`PD`	An object of the class `ProbDistUnivKernel`.

Output Arguments

`Y`	The value of the interquartile range for the ProbDistUnivKernel object `PD`.

See Also

`iqr` | `ProbDistUnivKernel.icdf`

ProbDistUnivParam.iqr

Purpose

Return interquartile range (IQR) for ProbDistUnivParam object

Syntax

```
Y = iqr(PD)
```

Description

`Y = iqr(PD)` returns `Y`, the interquartile range for the ProbDistUnivParam object `PD`. The interquartile range is the distance between the 75th and 25th percentiles.

Input Arguments

`PD`	An object of the class `ProbDistUnivParam`.

Output Arguments

`Y`	The value of the interquartile range for the ProbDistUnivParam object `PD`.

See Also

`iqr` | `ProbDistUnivParam.icdf`

Purpose

Test node for branch

Syntax

```
ib = isbranch(t)
ib = isbranch(t,nodes)
```

Description

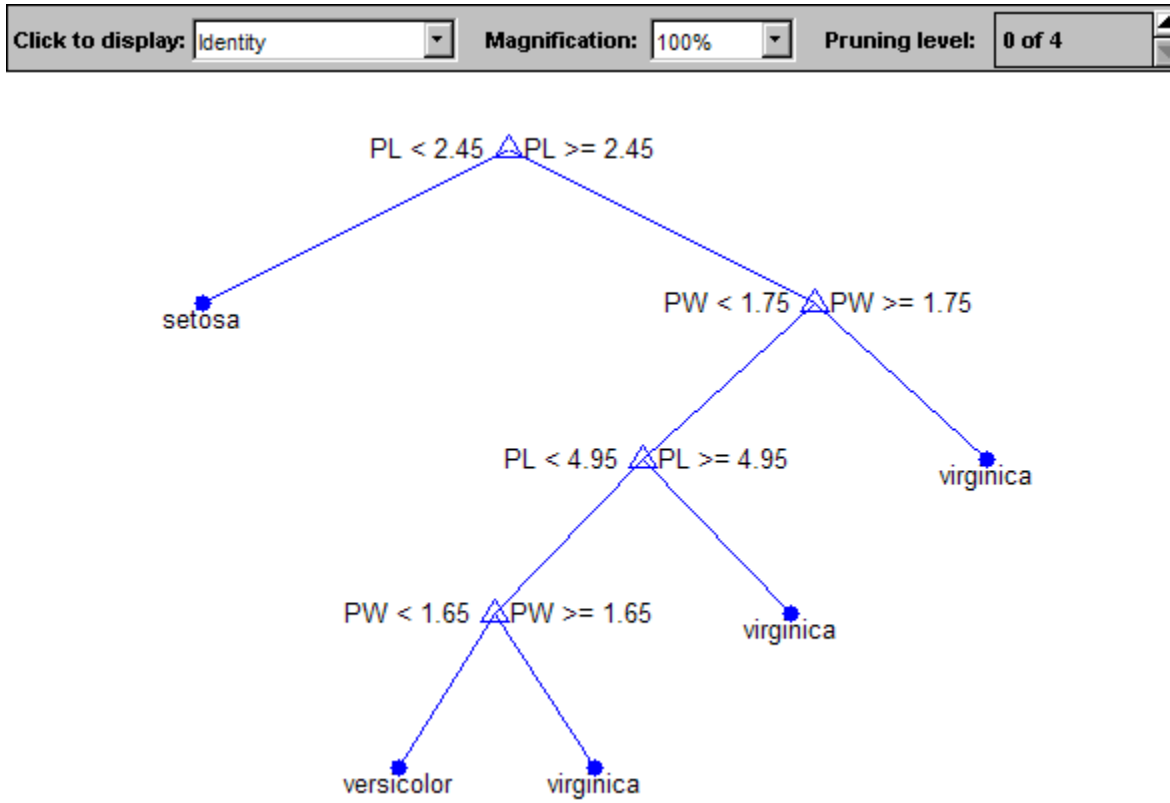
`ib = isbranch(t)` returns an n-element logical vector `ib` that is `true` for each branch node and `false` for each leaf node.

`ib = isbranch(t,nodes)` takes a vector `nodes` of node numbers and returns a vector of logical values for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
ib = isbranch(t)
ib =
     1
     0
     1
     1
     0
     1
     0
     0
```

```
0
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `cutvar` | `numnodes`

categorical.isempty

Purpose

True for empty categorical array

Syntax

```
TF = isempty(A)
```

Description

`TF = isempty(A)` returns true (`1`) if `A` is an empty categorical array and false (`0`) otherwise. An empty array has no elements, that is `numel(A)==0`.

See Also

`numel` | `size`

Purpose

True for empty dataset array

Syntax

```
tf = isempty(A)
```

Description

`tf = isempty(A)` returns true (`1`) if `A` is an empty dataset and false (`0`) otherwise. An empty array has no elements, that is `prod(size(A))==0`.

See Also

`size`

categorical.isequal

Purpose

True if categorical arrays are equal

Syntax

```
TF = isequal(A,B)
TF = isequal(A,B,C,...)
```

Description

`TF = isequal(A,B)` is true (`1`) if the categorical arrays `A` and `B` are the same class, have the same size and the same sets of levels, and contain the same values, and false (`0`) otherwise.

`TF = isequal(A,B,C,...)` is true (`1`) if all the input arguments are equal.

Elements with undefined levels are not considered equal to each other.

See Also

`getlabels`

Purpose

Test for levels

Syntax

```
I = islevel(levels,A)
```

Description

`I = islevel(levels,A)` returns a logical array `I` the same size as the string, cell array of strings, or 2-D character matrix `levels`. `I` is `true` (1) where the corresponding element of `levels` is the label of a level in the categorical array `A`, even if the level contains no elements. `I` is `false` (0) otherwise.

Examples

Display age levels in the data in `hospitl.mat`, before and after dropping occupied levels:

```
load hospital
edges = 0:10:100;
labels = strcat(num2str((0:10:90)','%d'),{'s'});
disp(labels')
 '0s' '10s' '20s' '30s' '40s' '50s' '60s' '70s' '80s' '90s'

AgeGroup = ordinal(hospital.Age,labels,[],edges);
I = islevel(labels,AgeGroup);
disp(I')
 1  1  1  1  1  1  1  1  1  1

AgeGroup = droplevels(AgeGroup);
I = islevel(labels,AgeGroup);
disp(I')
 0  0  1  1  1  1  0  0  0  0
```

See Also

`ismember` | `isundefined`

ordinal.ismember

Purpose

Test for membership

Syntax

```
I = ismember(A,levels)
[I,IDX] = ismember(A,levels)
```

Description

`I = ismember(A,levels)` returns a logical array `I` the same size as the categorical array `A`. `I` is `true` (`1`) where the corresponding element of `A` is one of the levels specified by the labels in the categorical array, cell array of strings, or 2-D character array `levels`. `I` is false (`0`) otherwise.

`[I,IDX] = ismember(A,levels)` also returns an array of indices `IDX` containing the highest absolute index in `levels` for each element in `A` whose level is a member of `levels`, and `0` if there is no such index.

Examples

Example 1

For nominal data:

```
load hospital
sex = hospital.Sex; % Nominal
smokers = hospital.Smoker; % Logical
I = ismember(sex(smokers),'Female');
I(1:5)
ans =
     0
     1
     0
     0
     0
```

The use of `ismember` above is equivalent to:

```
I = (sex(smokers) == 'Female');
```

Example 2

For ordinal data:

```
load hospital
edges = 0:10:100;
```

```
labels = strcat(num2str((0:10:90)','%d'),{'s'});
AgeGroup = ordinal(hospital.Age,labels,[],edges);
I = ismember(AgeGroup(1:5),{'20s','30s'})
I =
     1
     0
     1
     0
     0
```

See Also

`islevel` | `isundefined`

categorical.ismember

Purpose

True for elements of categorical array in set

Syntax

```
TF = ismember(A,levels)
[TF,LOC] = ismember(A,levels)
```

Description

`TF = ismember(A,levels)` returns a logical array the same size as the categorical array `A`, containing true (`1`) where the level of the corresponding element of `A` is equal to one of the levels specified in `levels`, and false (`0`) otherwise. `levels` is a categorical array, or a cell array of strings or 2-D character array containing level labels.

`[TF,LOC] = ismember(A,levels)` also returns an index array `LOC` containing the highest absolute index in `levels` for each element in `A` whose level is a member of `levels`, and 0 if there is no such index.

See Also

`intersect` | `islevel` | `setdiff` | `setxor` | `union` | `unique`

Purpose

True if categorical array is scalar

Syntax

```
TF = isscalar(A)
```

Description

`TF = isscalar(A)` returns true (`1`) if the categorical array `A` is a 1-by-1 matrix, and false (`0`) otherwise.

See Also

`isempty` | `isvector` | `size`

categorical.isundefined

Purpose

Test for undefined elements

Syntax

```
I = isundefined(A)
```

Description

`I = isundefined(A)` returns a logical array `I` the same size as the categorical array `A`. `I` is `true` (`1`) where the corresponding element of `A` is not assigned to any level. `I` is `false` (`0`) where the corresponding element of `A` is assigned to a level.

Examples

Create and display undefined levels in an ordinal array:

```
A = ordinal([1 2 3 2 1],{'lo','med','hi'})
A =
     lo      med      hi      med      lo

A = droplevels(A,{'med','hi'})
Warning: OLDLEVELS contains categorical levels that
were present in A, caused some array elements to
have undefined levels.
A =
     lo  <undefined>  <undefined>  <undefined>  lo

I = isundefined(A)
I =
     0     1     1     1     0
```

See Also

`islevel` | `ismember`

Purpose

Test handle validity

Syntax

```
tf = isvalid(h)
```

Description

`tf = isvalid(h)` performs an element-wise check for validity on the handle elements of `h`. The result is a logical array of the same dimensions as `h`, where each element is the element-wise validity result.

A handle is invalid if it has been deleted or if it is an element of a handle array and has not yet been initialized.

See Also

`delete` | `qrandstream`

categorical.isvector

Purpose

True if categorical array is vector

Syntax

```
TF = isvector(A)
```

Description

`TF = isvector(A)` returns true (`1`) if the categorical array `A` is a 1-by-`n` or `n`-by-1 vector, where `n >= 0`, and false (`0`) otherwise.

See Also

`isempty` | `isscalar` | `size`

Purpose

Number of iterations

Description

The number of iterations of the algorithm.

Note This property applies only to gmdistribution objects constructed with `fit`.

iwishrnd

Purpose

Inverse Wishart random numbers

Syntax

```
W = iwishrnd(Tau,df)
W = iwishrnd(Tau,df,DI)
[W,DI] = iwishrnd(Tau,df)
```

Description

`W = iwishrnd(Tau,df)` generates a random matrix `W` from the inverse Wishart distribution with parameters `Tau` and `df`. The inverse of `W` has the Wishart distribution with covariance matrix `Sigma = inv(Tau)` and with `df` degrees of freedom. `Tau` is a symmetric and positive definite matrix.

`W = iwishrnd(Tau,df,DI)` expects `DI` to be the transpose of the inverse of the Cholesky factor of `Tau`, so that `DI'*DI = inv(Tau)`, where `inv` is the MATLAB inverse function. `DI` is lower-triangular and the same size as `Tau`. If you call `iwishrnd` multiple times using the same value of `Tau`, it is more efficient to supply `DI` instead of computing it each time.

`[W,DI] = iwishrnd(Tau,df)` returns `DI` so you can use it as an input in future calls to `iwishrnd`.

Note that different sources use different parametrizations for the inverse Wishart distribution. This function defines the parameter `tau` so that the mean of the output matrix is `Tau/(df-d-1)` where `d` is the dimension of `Tau`.

See Also

`wishrnd`

How To

- "Inverse Wishart Distribution" on page B-46

Purpose

Jackknife sampling

Syntax

```
jackstat = jackknife(jackfun,X)
jackstat = jackknife(jackfun,X,Y,...)
jackstat = jackknife(jackfun,...,'Options',option)
```

Description

`jackstat = jackknife(jackfun,X)` draws jackknife data samples from the `n`-by-`p` data array `X`, computes statistics on each sample using the function `jackfun`, and returns the results in the matrix `jackstat`. `jackknife` regards each row of `X` as one data sample, so there are `n` data samples. Each of the `n` rows of `jackstat` contains the results of applying `jackfun` to one jackknife sample. `jackfun` is a function handle specified with `@`. Row `i` of `jackstat` contains the results for the sample consisting of `X` with the `i`th row omitted:

```
s = x;
s(i,:) = [];
jackstat(i,:) = jackfun(s);
```

If `jackfun` returns a matrix or array, then this output is converted to a row vector for storage in `jackstat`. If `X` is a row vector, it is converted to a column vector.

`jackstat = jackknife(jackfun,X,Y,...)` accepts additional arguments to be supplied as inputs to `jackfun`. They may be scalars, column vectors, or matrices. `jackknife` creates each jackknife sample by sampling with replacement from the rows of the non-scalar data arguments (these must have the same number of rows). Scalar data are passed to `jackfun` unchanged. Non-scalar arguments must have the same number of rows, and each jackknife sample omits the same row from these arguments.

`jackstat = jackknife(jackfun,...,'Options',option)` provides an option to perform jackknife iterations in parallel, if the Parallel Computing Toolbox is available. Set `'Options'` as a structure you create with `statset`. `jackknife` uses the following field in the structure:

`'UseParallel'` If `'always'` and if a `matlabpool` of the Parallel Computing Toolbox is open, use multiple processors to compute jackknife iterations. If the Parallel Computing Toolbox is not installed, or a `matlabpool` is not open, computation occurs in serial mode. Default is `'never'`, or serial computation.

For more information on using parallel computing, see Chapter 17, "Parallel Statistics".

Examples

Estimate the bias of the MLE variance estimator of random samples taken from the vector `y` using `jackknife`. The bias has a known formula in this problem, so you can compare the `jackknife` value to this formula.

```
sigma = 5;
y = normrnd(0,sigma,100,1);
m = jackknife(@var, y, 1);
n = length(y);
bias = -sigma^2 / n % known bias formula
jbias = (n - 1)*(mean(m)-var(y,1)) % jackknife bias estimate

bias =
   -0.2500

jbias =
   -0.3378
```

See Also

`bootstrp` | `random` | `randsample` | `hist` | `ksdensity`

Tutorials

- "The Jackknife" on page 3-12

Purpose

Jarque-Bera test

Syntax

```
h = jbtest(x)
h = jbtest(x,alpha)
[h,p] = jbtest(...)
[h,p,jbstat] = jbtest(...)
[h,p,jbstat,critval] = jbtest(...)
[h,p,...] = jbtest(x,alpha,mctol)
```

Description

`h = jbtest(x)` performs a Jarque-Bera test of the null hypothesis that the sample in vector `x` comes from a normal distribution with unknown mean and variance, against the alternative that it does not come from a normal distribution. The test is specifically designed for alternatives in "Generating Data Using the Pearson System" on page 6-26 of distributions. The test returns the logical value `h = 1` if it rejects the null hypothesis at the 5% significance level, and `h = 0` if it cannot. The test treats `NaN` values in `x` as missing values, and ignores them.

The Jarque-Bera test is a two-sided goodness-of-fit test suitable when a fully-specified null distribution is unknown and its parameters must be estimated. The test statistic is

$$JB = \frac{n}{6}\left(s^2 + \frac{(k-3)^2}{4} \right)$$

where n is the sample size, s is the sample skewness, and k is the sample kurtosis. For large sample sizes, the test statistic has a chi-square distribution with two degrees of freedom.

Jarque-Bera tests often use the chi-square distribution to estimate critical values for large samples, deferring to the Lilliefors test (see `lillietest`) for small samples. `jbtest`, by contrast, uses a table of critical values computed using Monte-Carlo simulation for sample sizes less than 2000 and significance levels between 0.001 and 0.50. Critical values for a test are computed by interpolating into the table, using the analytic chi-square approximation only when extrapolating for larger sample sizes.

`h = jbtest(x,alpha)` performs the test at significance level `alpha`. `alpha` is a scalar in the range [0.001, 0.50]. To perform the test at a significance level outside of this range, use the `mctol` input argument.

`[h,p] = jbtest(...)` returns the *p* value `p`, computed using inverse interpolation into the table of critical values. Small values of `p` cast doubt on the validity of the null hypothesis. `jbtest` warns when `p` is not found within the tabulated range of [0.001, 0.50], and returns either the smallest or largest tabulated value. In this case, you can use the `mctol` input argument to compute a more accurate *p* value.

`[h,p,jbstat] = jbtest(...)` returns the test statistic `jbstat`.

`[h,p,jbstat,critval] = jbtest(...)` returns the critical value `critval` for the test. When `jbstat > critval`, the null hypothesis is rejected at significance level `alpha`.

`[h,p,...] = jbtest(x,alpha,mctol)` computes a Monte-Carlo approximation for `p` directly, rather than interpolating into the table of pre-computed values. This is useful when `alpha` or `p` lie outside the range of the table. `jbtest` chooses the number of Monte Carlo replications, `mcreps`, large enough to make the Monte Carlo standard error for `p`, `sqrt(p*(1-p)/mcreps)`, less than `mctol`.

Examples

Use `jbtest` to determine if car mileage, in miles per gallon (MPG), follows a normal distribution across different makes of cars:

```
load carbig
[h,p] = jbtest(MPG)
h =
     1
p =
    0.0022
```

The *p* value is below the default significance level of 5%, and the test rejects the null hypothesis that the distribution is normal.

With a log transformation, the distribution becomes closer to normal, but the *p* value is still well below 5%:

```
[h,p] = jbtest(log(MPG))
h =
     1
p =
    0.0078
```

Decreasing the significance level makes it harder to reject the null hypothesis:

```
[h,p] = jbtest(log(MPG),0.0075)
h =
     0
p =
    0.0078
```

References

[1] Jarque, C. M., and A. K. Bera. "A test for normality of observations and regression residuals." *International Statistical Review*. Vol. 55, No. 2, 1987, pp. 163–172.

[2] Deb, P., and M. Sefton. "The Distribution of a Lagrange Multiplier Test of Normality." *Economics Letters*. Vol. 51, 1996, pp. 123–130. This paper proposed a Monte Carlo simulation for determining the distribution of the test statistic. The results of this function are based on an independent Monte Carlo simulation, not the results in this paper.

johnsrnd

Purpose

Johnson system random numbers

Syntax

```
r = johnsrnd(quantiles,m,n)
r = johnsrnd(quantiles)
[r,type] = johnsrnd(...)
[r,type,coefs] = johnsrnd(...)
```

Description

`r = johnsrnd(quantiles,m,n)` returns an `m`-by-`n` matrix of random numbers drawn from the distribution in the Johnson system that satisfies the quantile specification given by `quantiles`. `quantiles` is a four-element vector of quantiles for the desired distribution that correspond to the standard normal quantiles [–1.5 –0.5 0.5 1.5]. In other words, you specify a distribution from which to draw random values by designating quantiles that correspond to the cumulative probabilities [0.067 0.309 0.691 0.933]. `quantiles` may also be a `2`-by-`4` matrix whose first row contains four standard normal quantiles, and whose second row contains the corresponding quantiles of the desired distribution. The standard normal quantiles must be spaced evenly.

Note Because `r` is a random sample, its sample quantiles typically differ somewhat from the specified distribution quantiles.

`r = johnsrnd(quantiles)` returns a scalar value.

`r = johnsrnd(quantiles,m,n,...)` or `r = johnsrnd(quantiles,[m,n,...])` returns an `m`-by-`n`-by-... array.

`[r,type] = johnsrnd(...)` returns the type of the specified distribution within the Johnson system. `type` is `'SN'`, `'SL'`, `'SB'`, or `'SU'`. Set `m` and `n` to zero to identify the distribution type without generating any random values.

The four distribution types in the Johnson system correspond to the following transformations of a normal random variate:

- `'SN'` — Identity transformation (normal distribution)

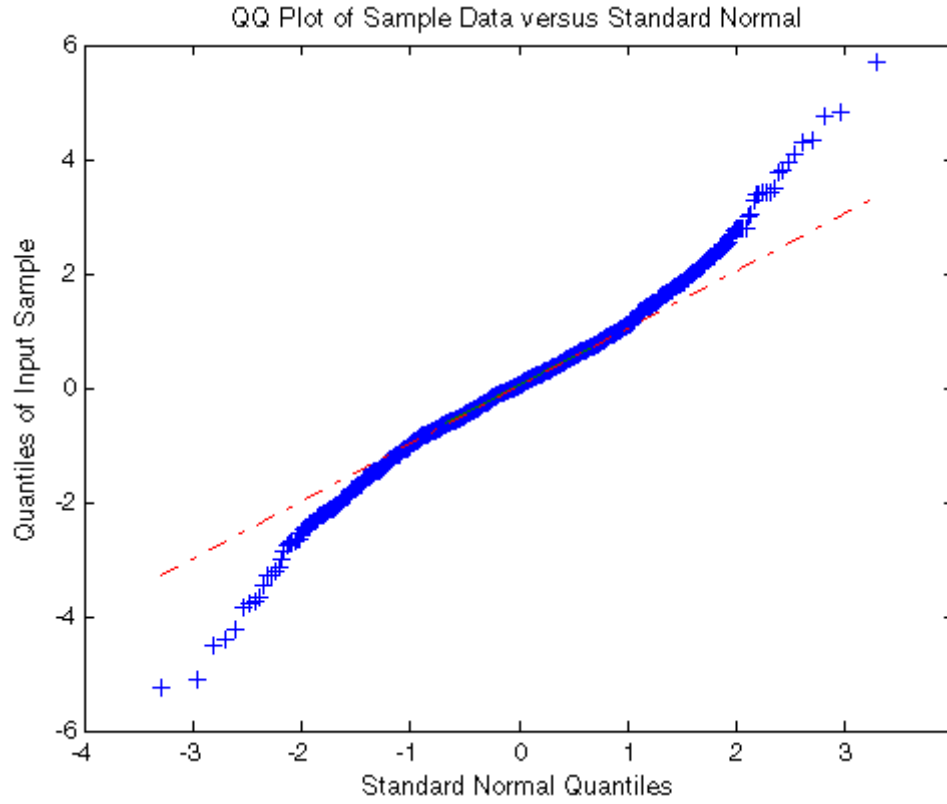
- `'SL'` — Exponential transformation (lognormal distribution)
- `'SB'` — Logistic transformation (bounded)
- `'SU'` — Hyperbolic sine transformation (unbounded)

`[r,type,coefs] = johnsrnd(...)` returns coefficients `coefs` of the transformation that defines the distribution. `coefs` is `[gamma, eta, epsilon, lambda]`. If `z` is a standard normal random variable and `h` is one of the transformations defined above, `r = lambda*h((z-gamma)/eta)+epsilon` is a random variate from the distribution type corresponding to `h`.

Examples

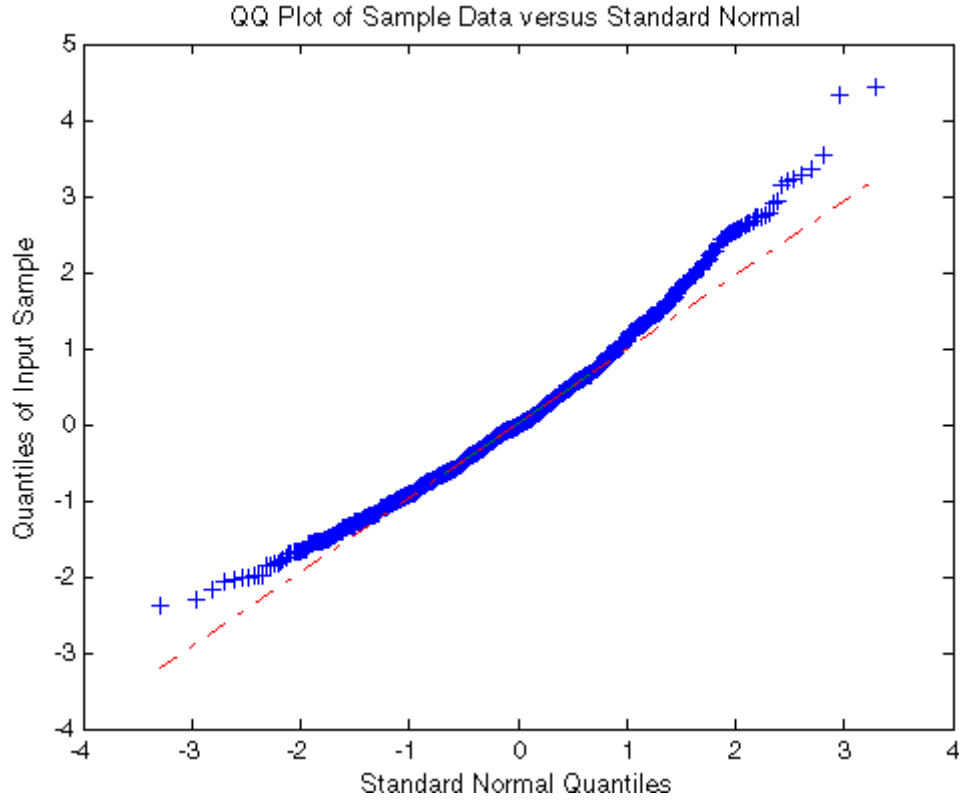
Generate random values with longer tails than a standard normal:

```
r = johnsrnd([-1.7 -.5 .5 1.7],1000,1);
qqplot(r);
```



Generate random values skewed to the right:

```
r = johnsrnd([-1.3 -.5 .5 1.7],1000,1);
qqplot(r);
```



Generate random values that match some sample data well in the right-hand tail:

```
load carbig;
qnorm = [.5 1 1.5 2];
q = quantile(Acceleration, normcdf(qnorm));
r = johnsrnd([qnorm;q],1000,1);
[q;quantile(r,normcdf(qnorm))]
ans =
   16.7000   18.2086   19.5376   21.7263
   16.8190   18.2474   19.4492   22.4156
```

Determine the distribution type and the coefficients:

```
[r,type,coefs] = johnsrnd([qnorm;q],0)
r =
    []
type =
    SU
coefs =
    1.0920    0.5829   18.4382    1.4494
```

See Also

`random` | `pearsrnd`

How To

- "Johnson System" on page B-48

Purpose

Merge observations

Syntax

```
C = join(A,B)
C = join(A,B,key)
C = join(A,B,param1,val1,param2,val2,...)
[C,IB] = join(...)
C = join(A,B,'Type',TYPE,...)
C = join(A,B,'Type',TYPE,'MergeKeys',true,...)
[C,IA,IB] = join(A,B,'Type',TYPE,...)
```

Description

`C = join(A,B)` creates a dataset array `C` by merging observations from the two dataset arrays `A` and `B`. `join` performs the merge by first finding *key variables*, that is, a pair of dataset variables, one in `A` and one in `B`, that share the same name. The key from `B` must contain unique values, and must contain all the values that are present in the key from `A`. `join` then uses these key variables to define a many-to-one correspondence between observations in `A` and those in `B`. `join` uses this correspondence to replicate the observations in `B` and combine them with the observations in `A` to create `C`.

`C = join(A,B,key)` performs the merge using the variable specified by `key` as the key variable in both `A` and `B`. `key` is a positive integer, a variable name, a cell array containing a variable name, or a logical vector with one `true` entry.

`C` contains one observation for each observation in `A`. Variables in `C` include all of the variables from `A`, as well as one variable corresponding to each variable in `B` (except for the key from `B`). If `A` and `B` contain variables with identical names, `join` adds the suffix `'_left'` and `'_right'` to the corresponding variables in `C`.

`C = join(A,B,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs to control how the dataset variables in `A` and `B` are used in the merge. Parameters are:

- `'Keys'` — Specifies the variable to use as a keys in both `A` and `B`.
- `'LeftKeys'` — Specifies the variable to use as a keys in `A`.

- 'RightKeys' — Specifies the variable to use as a keys in B.

You may provide either the 'Keys' parameter, or both the 'LeftKeys' and 'RightKeys' parameters. The value for these parameters is a positive integer, a variable name, a cell array containing a variable name, or a logical vector with one true entry. 'LeftKeys' or 'RightKeys' must both specify the same number of key variables, and join pairs the left and right keys are paired in the order specified.

- 'LeftVars' — Specifies the variables from A to include in C. By default, join includes all variables from A.
- 'RightVars' — Specifies the variables from B to include in C. By default, join includes all variables from B except the key variable.

You can use 'LeftVars' or 'RightVars' to include or exclude key variables as well as data variables. The value for these parameters is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

[C,IB] = join(...) returns an index vector IB, where join constructs C by horizontally concatenating A(:,LeftVars) and B(IB,RightVars). join can also perform more complicated inner and outer join operations that allow a many-to-many correspondence between A and B, and allow unmatched observations in either A or B.

C = join(A,B,'Type',TYPE,...) performs the join operation specified by TYPE. TYPE is one of 'inner', 'leftouter', 'rightouter', 'fullouter', or 'outer' (which is a synonym for 'fullouter'). For an inner join, C only contains observations corresponding to a combination of key values that occurred in both A and B. For a left (or right) outer join, C also contains observations corresponding to keys in A (or B) that did not match any in B (or A). Variables in C taken from A (or B) contain null values in those observations. A full outer join is equivalent to a left and right outer join. C contains variables corresponding to the key variables from both A and B, and join sorts the observations in C by the key values.

For inner and outer joins, C contains variables corresponding to the key variables from both A and B by default, as well as all the remaining variables. join sorts the observations in the result C by the key values.

C = join(A,B,'Type',TYPE,'MergeKeys',true,...) includes a single variable in C for each key variable pair from A and B, rather than including two separate variables. For outer joins, join creates the single variable by merging the key values from A and B, taking values from A where a corresponding observation exists in A, and from B otherwise. Setting the 'MergeKeys' parameter to true overrides inclusion or exclusion of any key variables specified via the 'LeftVars' or 'RightVars' parameter. Setting the 'MergeKeys' parameter to false is equivalent to not passing in the 'MergeKeys' parameter.

[C,IA,IB] = join(A,B,'Type',TYPE,...) returns index vectors IA and IB indicating the correspondence between observations in C and those in A and B. For an inner join, join constructs C by horizontally concatenating A(IA,LeftVars) and B(IB,RightVars). For an outer join, IA or IB may also contain zeros, indicating the observations in C that do not correspond to observations in A or B, respectively.

Examples

Create a dataset array from Fisher's iris data:

```
load fisheriris
NumObs = size(meas,1);
NameObs = strcat({'Obs'},num2str((1:NumObs)','%-d'));
iris = dataset({nominal(species),'species'},...
               {meas,'SL','SW','PL','PW'},...
               'ObsNames',NameObs);
```

Create a separate dataset array with the diploid chromosome counts for each species of iris:

```
snames = nominal({'setosa';'versicolor';'virginica'});
CC = dataset({snames,'species'},{[38;108;70],'cc'})
CC =
    species       cc
```

```
    setosa         38
    versicolor    108
    virginica      70
```

Broadcast the data in `CC` to the rows of `iris` using the key variable `species` in each dataset:

```
iris2 = join(iris,CC);
iris2([1 2 51 52 101 102],:)
ans =
           species       SL     SW     PL     PW     cc
 Obs1      setosa        5.1    3.5    1.4    0.2     38
 Obs2      setosa        4.9      3    1.4    0.2     38
 Obs51     versicolor      7    3.2    4.7    1.4    108
 Obs52     versicolor    6.4    3.2    4.5    1.5    108
 Obs101    virginica     6.3    3.3      6    2.5     70
 Obs102    virginica     5.8    2.7    5.1    1.9     70
```

Create two datasets and join them using the `'MergeKeys'` flag:

```
% Create two data sets that both contain the key variable
% 'Key1'. The two arrays contain observations with common
% values of Key1, but each array also contains observations
% with values of Key1 not present in the other.
a = dataset({'a' 'b' 'c' 'e' 'h'}',[1 2 3 11 17]',...
   'VarNames',{'Key1' 'Var1'})
b = dataset({'a' 'b' 'd' 'e'}',[4 5 6 7]',...
   'VarNames',{'Key1' 'Var2'})

% Combine a and b with an outer join, which matches up
% observations with common key values, but also retains
% observations whose key values don't have a match.
% Keep the key values as separate variables in the result.
couter = join(a,b,'key','Key1','Type','outer')
```

```
% Join a and b, merging the key values as a single variable
% in the result.
coutermerge = join(a,b,'key','Key1','Type','outer',...
   'MergeKeys',true)

% Join a and b, retaining only observations whose key
% values match.
cinner = join(a,b,'key','Key1','Type','inner',...
   'MergeKeys',true)

a =

    Key1       Var1
    'a'         1
    'b'         2
    'c'         3
    'e'        11
    'h'        17


b =

    Key1       Var2
    'a'        4
    'b'        5
    'd'        6
    'e'        7


couter =

    Key1_left    Var1    Key1_right    Var2
    'a'            1     'a'             4
    'b'            2     'b'             5
    'c'            3     ''            NaN
    ''           NaN     'd'             6
    'e'           11     'e'             7
```

```
    'h'          17     ''           NaN


coutermerge =

    Key1       Var1    Var2
    'a'          1       4
    'b'          2       5
    'c'          3     NaN
    'd'        NaN       6
    'e'         11       7
    'h'         17     NaN


cinner =

    Key1       Var1    Var2
    'a'         1      4
    'b'         2      5
    'e'        11      7
```

See Also

sortrows

Superclasses

NeighborSearcher

Purpose

Nearest neighbors search using *k*d-tree

Description

A `KDTreeSearcher` object represents *k*NN (*k*-nearest neighbor) search using a *k*d-tree. Search objects store information about the data used, the distance metric and parameters, and the maximal number of data points in each leaf node. You cannot create this object for sparse input data. The search performance for this object, compared with the `ExhaustiveSearcher` object, tends to be better for smaller dimensions (10 or fewer) and worse for larger dimensions. For more information on search objects, see "What Are Search Objects?" on page 13-17.

Construction

`NS = KDTreeSearcher(X,'Name',Value)` constructs a *k*d-tree based on `X` and saves the information in a `KDTreeSearcher` object where rows of `X` correspond to observations and columns correspond to variables. You can use this tree to find neighbors in `X` nearest to the query points. See the following section for optional name/value pairs.

`NS = createns(X,'NSMethod','kdtree','Name',Value)` creates a *k*d-tree based on `X` using `createns` and saves the information in a `KDTreeSearcher` object where rows of `X` correspond to observations and columns correspond to variables. You can use this tree to find neighbors in `X` nearest to the query points. See the following section for optional name/value pairs.

Name-Value Pair Arguments

`KDTreeSearcher` and `createns` accept one or more of the following optional name/value pairs as input:

`Distance`

A string specifying the default distance metric used when you call the `knnsearch` method.

- `'euclidean'` — Euclidean distance (default).
- `'cityblock'` — City block distance.

- `'chebychev'` — Chebychev distance (maximum coordinate difference).
- `'minkowski'` — Minkowski distance.

For more information on these distance metrics, see "Distance Metrics" on page 13-9.

`P`

A positive scalar indicating the exponent of the Minkowski distance. This parameter is only valid when `Distance` is `'minkowski'`. Default is 2.

`BucketSize`

A positive integer, indicating the maximum number of data points in each leaf node of the *k*d-tree. Default is 50.

Properties

`X`

A matrix used to create the object

`Distance`

A string specifying a built-in distance metric that you provide when you create the object. This property is the default distance metric used when you call the `knnsearch` method to find nearest neighbors for future query points.

`DistParameter`

Specifies the additional parameter for the chosen distance metric. The value is:

- If `'Distance'` is `'minkowski'`: A positive scalar indicating the exponent of the Minkowski distance.
- Otherwise: Empty.

Methods

knnsearch	Find k-nearest neighbors using `KDTreeSearcher` object
rangesearch	Find all neighbors within specified distance using object

Examples

Create a `KDTreeSearcher` object using the constructor:

```
load fisheriris
x = meas(:,3:4);
kdtreeobj = kdtreesearcher(x,'distance','minkowski')

kdtreeobj =

  KDTreeSearcher

  Properties:
       BucketSize: 50
                X: [150x2 double]
         Distance: 'minkowski'
    DistParameter: 2
```

Create a `KDTreeSearcher` object using `createns`:

```
load fisheriris
x = meas(:,3:4);
kdtreeobj = createns(x,'NsMethod','kdtree',...
   'distance','minkowski')

kdtreeobj =

  KDTreeSearcher

  Properties:
       BucketSize: 50
```

```
                X: [150x2 double]
         Distance: 'minkowski'
    DistParameter: 2
```

For more in-depth examples using the `knnsearch` method, see the method reference page or see "Example: Classifying Query Data Using knnsearch" on page 13-18.

References

[1] Friedman, J. H., Bentely, J., and Finkel, R. A. (1977). *An Algorithm for Finding Best Matches in Logarithmic Expected Time*, ACM Transactions on Mathematical Software 3, 209.

See Also

`createns` | `ExhaustiveSearcher` | `NeighborSearcher`

How To

- "*k*-Nearest Neighbor Search and Radius Search" on page 13-12

Purpose

Read-only string specifying name of kernel smoothing function for ProbDistKernel object

Description

`Kernel` is a read-only property of the `ProbDistKernel` class. `Kernel` is a string specifying the name of the kernel smoothing function used to create a ProbDistKernel object.

Values

```
'normal'
'box'
'triangle'
'epanechnikov'
```

Use this information to view and compare the kernel smoothing function used to create distributions.

See Also

`ksdensity`

ClassificationPartitionedEnsemble.kfoldEdge

Purpose

Classification edge for observations not used for training

Syntax

```
E = kfoldEdge(obj)
E = kfoldEdge(obj,Name,Value)
```

Description

`E = kfoldEdge(obj)` returns classification edge (average classification margin) obtained by cross-validated classification ensemble `obj`. For every fold, this method computes classification edge for in-fold observations using an ensemble trained on out-of-fold observations.

`E = kfoldEdge(obj,Name,Value)` calculates edge with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

Object of class `ClassificationPartitionedEnsemble`. Create `ens` with `fitensemble` along with one of the cross-validation options: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Alternatively, create `ens` from a classification ensemble with `crossval`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`folds`

Indices of folds ranging from `1` to `ens.KFold`. Use only these folds for predictions.

Default: `1:ens.KFold`

`mode`

String representing the meaning of the output `edge`:

- `'average'` — `edge` is a scalar value, the average over all folds.
- `'individual'` — `edge` is a vector of length `ens.KFold` with one element per fold.
- `'cumulative'` — `edge` is a vector of length `min(ens.NTrainedPerFold)` in which element `J` is obtained by averaging values across all folds for weak learners `1:J` in each fold.

Default: `'average'`

Output Arguments

`E`

The average classification margin. `E` is a scalar or vector, depending on the setting of the `mode` name-value pair.

Definitions

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in `obj.Prior`.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `obj.X`.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Compute the k-fold edge for an ensemble trained on the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
cvens = crossval(ens);
E = kfoldEdge(cvens)

E =
    3.2078
```

See Also

`kfoldPredict` | `kfoldLoss` | `kfoldMargin` | `kfoldfun` | `crossval`

How To

- Chapter 13, "Nonparametric Supervised Learning"

Purpose

Classification edge for observations not used for training

Syntax

```
E = kfoldEdge(obj)
E = kfoldEdge(obj,Name,Value)
```

Description

`E = kfoldEdge(obj)` returns classification edge (average classification margin) obtained by cross-validated classification model `obj`. For every fold, this method computes classification edge for in-fold observations using an ensemble trained on out-of-fold observations.

`E = kfoldEdge(obj,Name,Value)` calculates edge with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`obj`

Object of class `ClassificationPartitionedModel`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`folds`

Indices of folds ranging from `1` to `obj.KFold`. Use only these folds for predictions.

Default: `1:obj.KFold`

`mode`

String representing the meaning of the output `edge`:

- `'average'` — `edge` is a scalar value, the average over all folds.

- `'individual'` — `edge` is a vector of length `obj.KFold` with one element per fold.

Default: `'average'`

Output Arguments

`E`

The average classification margin. `E` is a scalar or vector, depending on the setting of the `mode` name-value pair.

Definitions

Edge

The *edge* is the weighted mean value of the classification *margin*. The weights are the class probabilities in `obj.Prior`. If you supply weights in the `weights` name-value pair, those weights are normalized to sum to the prior probabilities in the respective classes, and are then used to compute the weighted average.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `obj.X`. A high value of margin indicates a more reliable prediction than a low value.

Score (discriminant analysis)

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see “Posterior Probability” on page 12-7.

Score (tree)

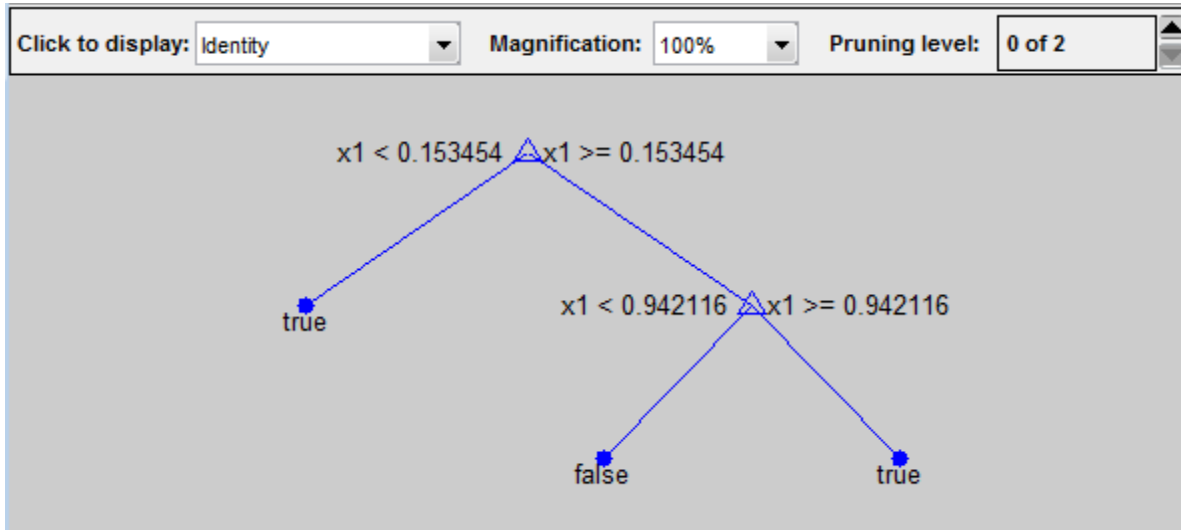
For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

1

Generate 100 random points and classify them:

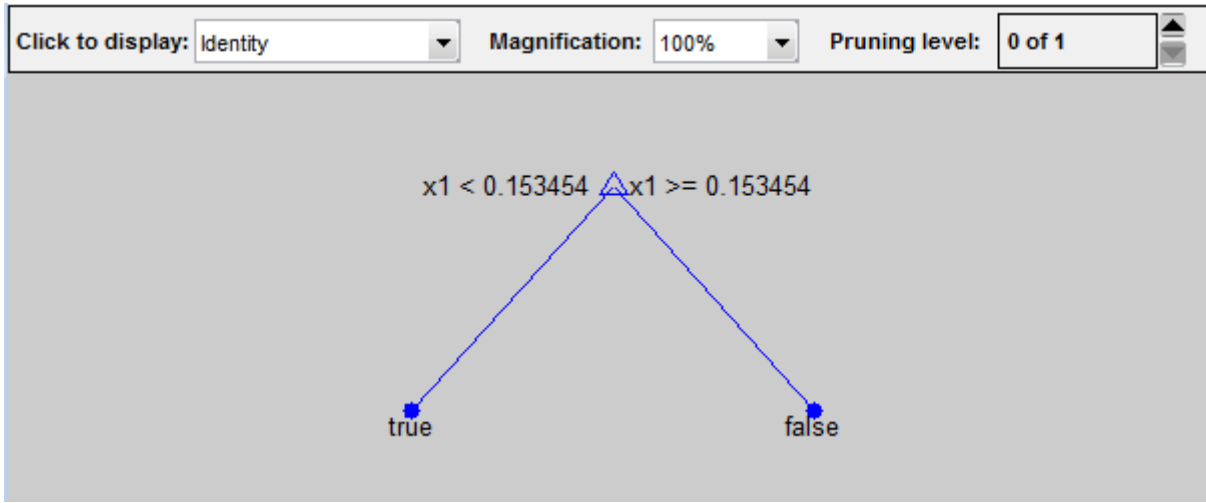
```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = ClassificationTree.fit(X,Y);
view(tree,'mode','graph')
```



2

Prune the tree:

```
tree1 = prune(tree,'level',1);
view(tree1,'mode','graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

3

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]

ans =
    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
```

```
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the rightmost column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Compute the k-fold edge for a model trained on the Fisher iris data:

```
load fisheriris
tree = ClassificationTree.fit(meas,species);
cvtree = crossval(tree);
E = kfoldEdge(cvtree)

E =
    0.8711
```

See Also

`kfoldPredict` | `kfoldMargin` | `kfoldLoss` | `kfoldfun` | `crossval` | `ClassificationPartitionedEnsemble` | `ClassificationPartitionedModel`

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- Chapter 13, “Nonparametric Supervised Learning”

ClassificationPartitionedModel.kfoldfun

Purpose

Cross validate function

Syntax

```
vals = kfoldfun(obj,fun)
```

Description

`vals = kfoldfun(obj,fun)` cross validates the function `fun` by applying `fun` to the data stored in the cross-validated model `obj`. You must pass `fun` as a function handle.

Input Arguments

`obj`

Object of class `ClassificationPartitionedModel` or `ClassificationPartitionedEnsemble`.

`fun`

A function handle for a cross-validation function. `fun` has the syntax

```
testvals = fun(CMP,Xtrain,Ytrain,Wtrain,Xtest,Ytest,Wtest)
```

- `CMP` is a compact model stored in one element of the `obj.Trained` property.
- `Xtrain` is the training matrix of predictor values.
- `Ytrain` is the training array of response values.
- `Wtrain` are the training weights for observations.
- `Xtest` and `Ytest` are the test data, with associated weights `Wtest`.
- The returned value `testvals` must have the same size across all folds.

Output Arguments

`vals`

The arrays of `testvals` output, concatenated vertically over all folds. For example, if `testvals` from every fold is a numeric vector of length `N`, `kfoldfun` returns a `KFold`-by-`N` numeric matrix with one row per fold.

Examples

Cross validate a classification tree, and obtain the classification error (see `kfoldLoss`):

```
load fisheriris
t = ClassificationTree.fit(meas,species);
rng(0,'twister') % for reproducibility
cv = crossval(t);
L = kfoldLoss(cv)

L =
    0.0467
```

Examine the result when the error of misclassifying a flower as `'versicolor'` is `10`, and any other error is `1`:

1. Write a function file that gives a cost of `1` for misclassification, but `10` for misclassifying a flower as `versicolor`.

```
function averageCost = noversicolor(CMP,Xtrain,Ytrain,Wtrain,Xtest,Ytest,Wtest)

Ypredict = predict(CMP,Xtest);
misclassified = not(strcmp(Ypredict,Ytest)); % different result
classifiedAsVersicolor = strcmp(Ypredict,'versicolor'); % index of bad decisions
cost = sum(misclassified) + ...
    9*sum(misclassified & classifiedAsVersicolor); % total differences
averageCost = cost/numel(Ytest); % average error
```

2. Save the file as `noversicolor.m` on your MATLAB path.

3. Compute the mean misclassification error with the `noversicolor` cost:

```
mean(kfoldfun(cv,@noversicolor))

ans =
    0.1667
```

See Also `kfoldPredict` | `kfoldEdge` | `kfoldMargin` | `kfoldLoss` | `crossval`

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Purpose

Cross validate function

Syntax

```
vals = kfoldfun(obj,fun)
```

Description

`vals = kfoldfun(obj,fun)` cross validates the function `fun` by applying `fun` to the data stored in the cross-validated model `obj`. You must pass `fun` as a function handle.

Input Arguments

`obj`

Object of class `RegressionPartitionedModel` or `RegressionPartitionedEnsemble`. Create `obj` with `RegressionTree.fit` or `fitensemble` along with one of the cross-validation options: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Alternatively, create `obj` from a regression tree or regression ensemble with `crossval`.

`fun`

A function handle for a cross-validation function. `fun` has the syntax

```
testvals = fun(CMP,Xtrain,Ytrain,Wtrain,Xtest,Ytest,Wtest)
```

- `CMP` is a compact model stored in one element of the `obj.Trained` property.
- `Xtrain` is the training matrix of predictor values.
- `Ytrain` is the training array of response values.
- `Wtrain` are the training weights for observations.
- `Xtest` and `Ytest` are the test data, with associated weights `Wtest`.
- The returned value `testvals` must have the same size across all folds.

Output Arguments

`vals`

The arrays of `testvals` output, concatenated vertically over all folds. For example, if `testvals` from every fold is a numeric vector of length `N`, `kfoldfun` returns a `KFold`-by-`N` numeric matrix with one row per fold.

Examples

Cross validate a regression tree, and obtain the mean squared error (see `kfoldLoss`):

```
load imports-85
t = RegressionTree.fit(X(:,[4 5]),X(:,16),...
    'predictornames',{'length' 'width'},...
    'responsename','price');
cv = crossval(t);
L = kfoldLoss(cv)

L =
  1.5489e+007
```

Examine the result of simple averaging of responses instead of using predictions:

```
f = @(cmp,Xtrain,Ytrain,Wtrain,Xtest,Ytest,Wtest)...
    mean((Ytest-mean(Ytrain)).^2)
mean(kfoldfun(cv,f))

ans =
  6.3497e+007
```

See Also

`RegressionPartitionedEnsemble` | `kfoldPredict` | `kfoldLoss` | `RegressionPartitionedModel` | `crossval`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Classification loss for observations not used for training

Syntax

```
L = kfoldLoss(ens)
L = kfoldLoss(ens,Name,Value)
```

Description

`L = kfoldLoss(ens)` returns loss obtained by cross-validated classification model `ens`. For every fold, this method computes classification loss for in-fold observations using a model trained on out-of-fold observations.

`L = kfoldLoss(ens,Name,Value)` calculates loss with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

Object of class `ClassificationPartitionedEnsemble`. Create `ens` with `fitensemble` along with one of the cross-validation options: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Alternatively, create `ens` from a classification ensemble with `crossval`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`folds`

Indices of folds ranging from `1` to `ens.KFold`. Use only these folds for predictions.

Default: `1:ens.KFold`

`lossfun`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 20-826
- `'classiferror'` — Fraction of misclassified data
- `'exponential'` — See "Loss Functions" on page 20-826

You can write your own loss function in the syntax described in "Loss Functions" on page 20-826.

Default: `'classiferror'`

`mode`

A string for determining the output of `kfoldLoss`:

- `'average'` — `L` is a scalar, the loss averaged over all folds.
- `'individual'` — `L` is a vector of length `ens.KFold`, where each entry is the loss for a fold.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'average'`

Output Arguments

`L`

Loss, by default the fraction of misclassified data. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Definitions

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.
- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of `ens.X`.
- `K` is the number of classes in `ens`, represented in `ens.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `tree.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `score` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` gives a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Find the average cross-validated classification error for an ensemble model of the `ionosphere` data:

```
load ionosphere
ens = fitensemble(X,Y,'AdaBoostM1',100,'Tree');
cvens = crossval(ens);
L = kfoldLoss(cvens)

L =
    0.0826
```

See Also

`kfoldPredict` | `kfoldEdge` | `kfoldMargin` | `kfoldfun` | `crossval`

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Purpose

Classification loss for observations not used for training

Syntax

```
L = kfoldLoss(obj)
L = kfoldLoss(obj,Name,Value)
```

Description

`L = kfoldLoss(obj)` returns loss obtained by cross-validated classification model `obj`. For every fold, this method computes classification loss for in-fold observations using a model trained on out-of-fold observations.

`L = kfoldLoss(obj,Name,Value)` calculates loss with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`obj`

Object of class `ClassificationPartitionedModel`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`folds`

Indices of folds ranging from `1` to `obj.KFold`. Use only these folds for predictions.

Default: `1:obj.KFold`

`lossfun`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 20-830

- `'classiferror'` — Fraction of misclassified data
- `'exponential'` — See "Loss Functions" on page 20-830

You can write your own loss function in the syntax described in "Loss Functions" on page 20-830.

Default: `'classiferror'`

`mode`

A string for determining the output of `kfoldLoss`:

- `'average'` — `L` is a scalar, the loss averaged over all folds.
- `'individual'` — `L` is a vector of length `obj.KFold`, where each entry is the loss for a fold.

Default: `'average'`

Output Arguments

`L`

Loss, by default the fraction of misclassified data. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Definitions

Classification Error

The default classification error is the fraction of the data `X` that `obj` misclassifies, where `Y` are the true classifications.

Weighted classification error is the sum of weight *i* times the Boolean value that is `1` when `obj` misclassifies the *i*th row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.
- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of `obj.X`.
- `K` is the number of classes in `obj`, represented in `obj.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `obj.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `score` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` gives a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Find the average cross-validated classification error for a model of the `ionosphere` data:

```
load ionosphere
tree = ClassificationTree.fit(X,Y);
cvtree = crossval(tree);
L = kfoldLoss(cvtree)

L =
    0.1197
```

See Also

`kfoldPredict` | `kfoldEdge` | `kfoldMargin` | `kfoldfun` | `crossval`

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Purpose

Cross-validation loss of partitioned regression ensemble

Syntax

```
L = kfoldLoss(cvens)
L = kfoldLoss(cvens,Name,Value)
```

Description

`L = kfoldLoss(cvens)` returns the cross-validation loss of `cvens`.

`L = kfoldLoss(cvens,Name,Value)` returns cross-validation loss with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`cvens`

Object of class `RegressionPartitionedEnsemble`. Create `obj` with `fitensemble` along with one of the cross-validation options: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Alternatively, create `obj` from a regression ensemble with `crossval`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`folds`

Indices of folds ranging from `1` to `cvens.KFold`. Use only these folds for predictions.

Default: `1:cvens.KFold`

`lossfun`

Function handle for loss function, or the string `'mse'`, meaning mean squared error. If you pass a function handle `fun`, `loss` calls it as

```
fun(Y,Yfit,W)
```

where `Y`, `Yfit`, and `W` are numeric vectors of the same length.

- `Y` is the observed response.
- `Yfit` is the predicted response.
- `W` is the observation weights.

The returned value `fun(Y,Yfit,W)` should be a scalar.

Default: `'mse'`

`mode`

String representing the meaning of the output `L`:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`L`

The loss (mean squared error) between the observations in a fold when compared against predictions made with an ensemble trained on the out-of-fold data. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Examples

Find the cross-validation loss for a regression ensemble of the `carsmall` data:

```
load carsmall
```

```
X = [Displacement Horsepower Weight];
rens = fitensemble(X,MPG,'LSboost',100,'Tree');
cvrens = crossval(rens);
L = kfoldLoss(cvrens)

L =
   25.6935
```

See Also

`RegressionPartitionedEnsemble` | `loss` | `kfoldPredict`

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- Chapter 13, “Nonparametric Supervised Learning”

RegressionPartitionedModel.kfoldLoss

Purpose

Cross-validation loss of partitioned regression model

Syntax

```
L = kfoldLoss(cvmodel)
L = kfoldLoss(cvmodel,Name,Value)
```

Description

`L = kfoldLoss(cvmodel)` returns the cross-validation loss of `cvmodel`.

`L = kfoldLoss(cvmodel,Name,Value)` returns cross-validation loss with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`cvmodel`

Object of class `RegressionPartitionedModel`. Create `obj` with `RegressionTree.fit` along with one of the cross-validation options: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Alternatively, create `obj` from a regression tree with `crossval`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`folds`

Indices of folds ranging from `1` to `obj.KFold`. Use only these folds for predictions.

Default: `1:obj.KFold`

`lossfun`

Function handle for loss function, or the string `'mse'`, meaning mean squared error. If you pass a function handle `fun`, `kfoldLoss` calls it as

```
fun(Y,Yfit,W)
```

where `Y`, `Yfit`, and `W` are numeric vectors of the same length.

- `Y` is the observed response.
- `Yfit` is the predicted response.
- `W` is the observation weights.

The returned value `fun(Y,Yfit,W)` should be a scalar.

Default: `'mse'`

`mode`

One of the following strings:

- `'average'` — `L` is the average loss over all folds.
- `'individual'` — `L` is a vector of the individual losses of in-fold observations trained on out-of-fold data.

Default: `'average'`

Output Arguments

`L`

The loss (mean squared error) between the observations in a fold when compared against predictions made with a tree trained on the out-of-fold data. If `mode` is `'individual'`, `L` is a vector of the losses. If `mode` is `'average'`, `L` is the average loss.

Examples

Construct a partitioned regression model, and examine the cross-validation losses for the folds:

```
load carsmall
XX = [Cylinders Displacement Horsepower Weight];
YY = MPG;
cvmodel = RegressionTree.fit(XX,YY,'crossval','on');
```

```
L = kfoldLoss(cvmodel,'mode','individual')

L =
   44.9635
   11.8525
   18.2046
    9.2965
   29.4329
   54.8659
   24.6446
    8.2085
   19.7593
   16.7394
```

Alternatives

You can avoid constructing a cross-validated tree model by calling `cvLoss` instead of `kfoldLoss`. The cross-validated tree can save time if you are going to examine it more than once.

See Also

`loss` | `kfoldPredict`

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Purpose

Classification margins for observations not used for training

Syntax

```
M = kfoldMargin(obj)
```

Description

`M = kfoldMargin(obj)` returns classification margins obtained by cross-validated classification model `obj`. For every fold, this method computes classification margins for in-fold observations using a model trained on out-of-fold observations.

Input Arguments

`obj`

A partitioned classification model of type `ClassificationPartitionedModel` or `ClassificationPartitionedEnsemble`.

Output Arguments

`M`

The classification margin.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `obj.X`. A high value of margin indicates a more reliable prediction than a low value.

Score (discriminant analysis)

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see "Posterior Probability" on page 12-7.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Score (tree)

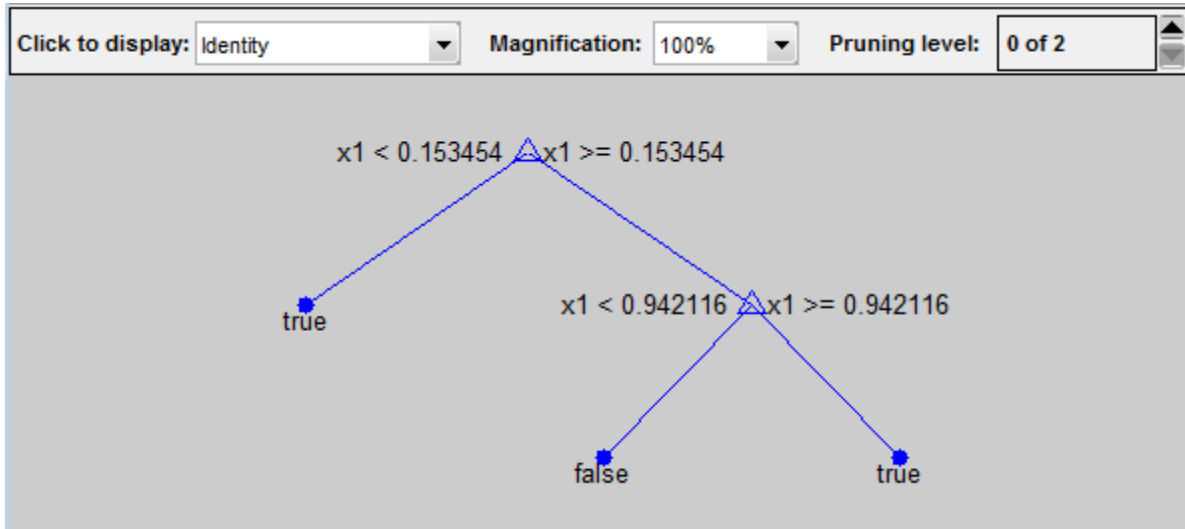
For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

1

Generate 100 random points and classify them:

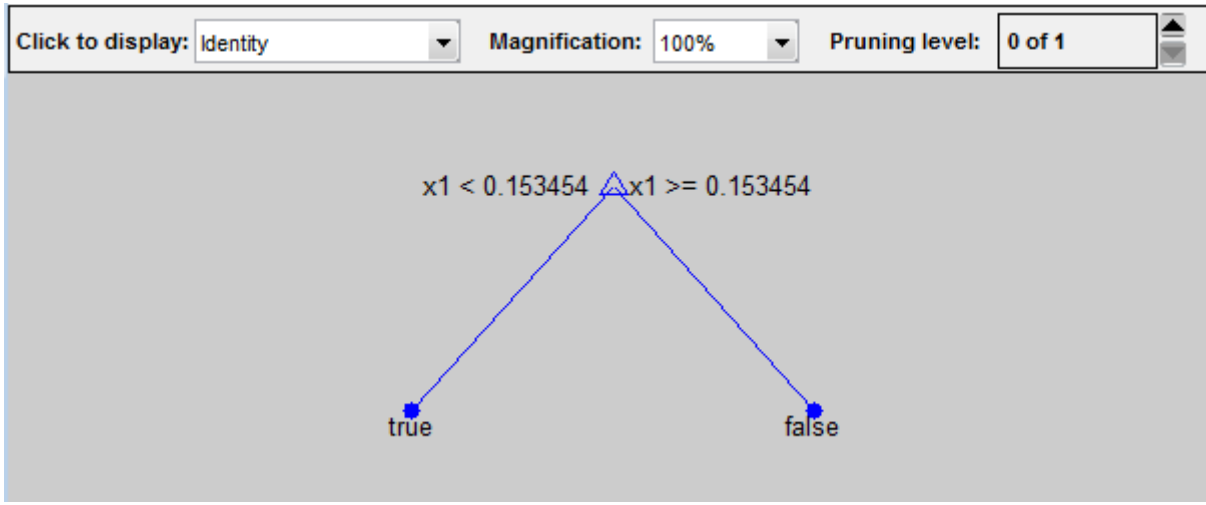
```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = ClassificationTree.fit(X,Y);
view(tree,'mode','graph')
```



2

Prune the tree:

```
tree1 = prune(tree,'level',1);
view(tree1,'mode','graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

3

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]

ans =
    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
```

```
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the rightmost column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Find the k-fold margins for an ensemble that classifies the `ionosphere` data:

```
load ionosphere
ens = fitensemble(X,Y,'AdaBoostM1',100,'Tree');
cvens = crossval(ens);
M = kfoldMargin(cvens);
[min(M) mean(M) max(M)]

ans =
   -7.6394    7.3469   22.4833
```

See Also

`kfoldPredict` | `kfoldEdge` | `kfoldLoss` | `kfoldfun` | `crossval`

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ClassificationPartitionedModel.kfoldPredict

Purpose

Predict response for observations not used for training

Syntax

```
label = kfoldPredict(obj)
[label,score] = kfoldPredict(obj)
[label,score,cost] = kfoldPredict(obj)
```

Description

`label = kfoldPredict(obj)` returns class labels predicted by `obj`, a cross-validated classification. For every fold, `kfoldPredict` predicts class labels for in-fold observations using a model trained on out-of-fold observations.

`[label,score] = kfoldPredict(obj)` returns the predicted classification scores for in-fold observations using a model trained on out-of-fold observations.

`[label,score,cost] = kfoldPredict(obj)` returns misclassification costs when `obj` is a cross-validated discriminant analysis classifier.

Input Arguments

`obj`

Object of class `ClassificationPartitionedModel` or `ClassificationPartitionedEnsemble`.

Output Arguments

`label`

Vector of class labels of the same type as the response data used in training `obj`. Each entry of `label` corresponds to a predicted class label for the corresponding row of `X`.

`score`

Numeric matrix of size `N`-by-`K`, where `N` is the number of observations (rows) in `obj.X`, and `K` is the number of classes (in `obj.ClassNames`). `score(i,j)` represents the confidence that row `i` of `obj.X` is of class `j`. For details, see "Definitions" on page 20-845.

`cost`

Numeric matrix of misclassification costs of size `N`-by-`K`. `cost(i,j)` is the average misclassification cost of predicting that row `i` of `obj.X` is of class `j`. Applies only to discriminant analysis classification.

Definitions

Cost (discriminant analysis)

The *average misclassification cost* is the mean misclassification cost for predictions made by the cross-validated classifiers trained on out-of-fold observations. The matrix of expected costs per observation is defined in "Cost" on page 12-8.

Score (discriminant analysis)

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see "Posterior Probability" on page 12-7.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Score (tree)

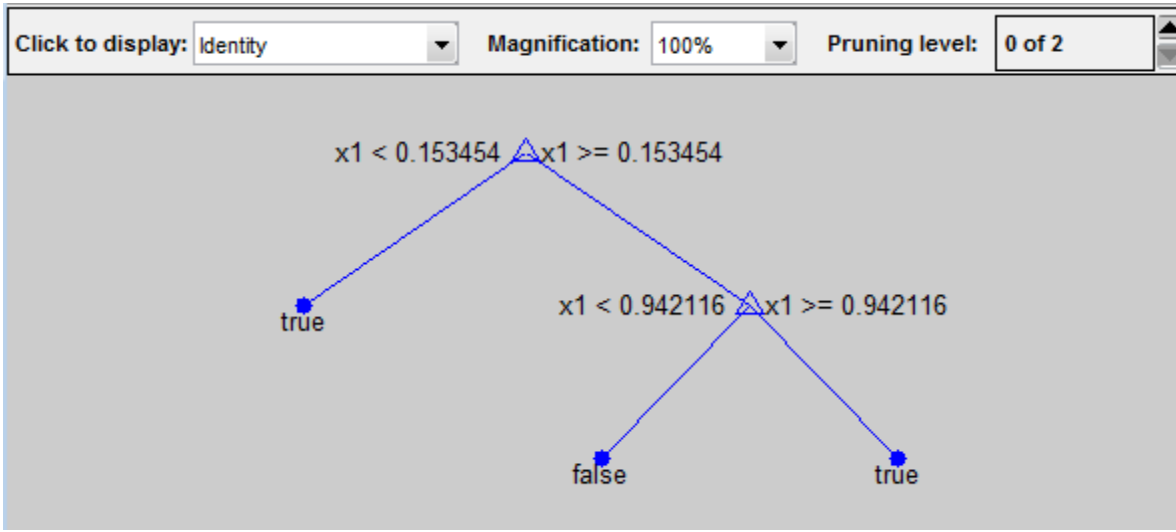
For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

1

Generate 100 random points and classify them:

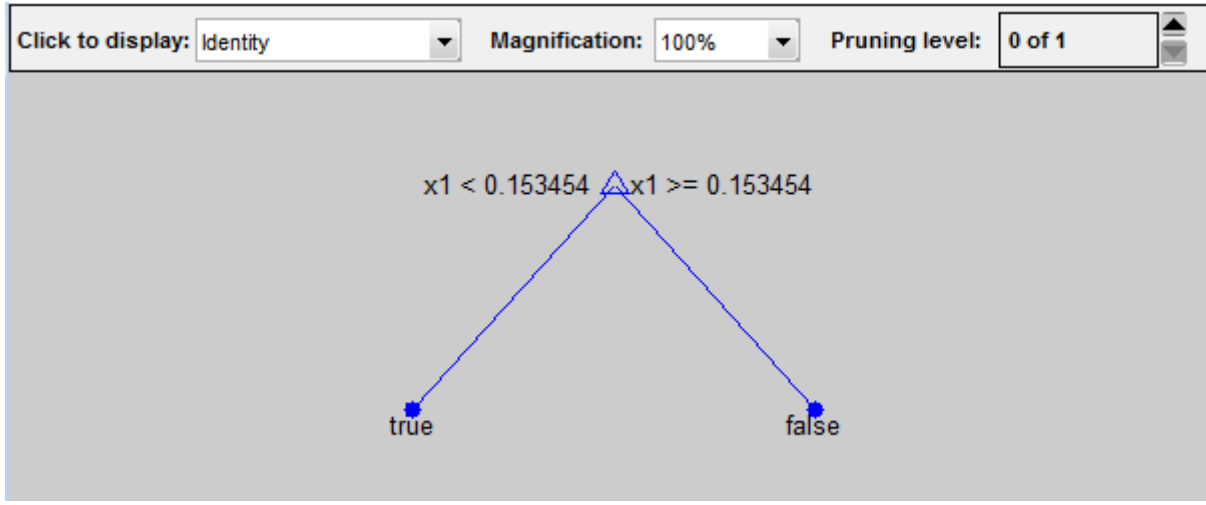
```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = ClassificationTree.fit(X,Y);
view(tree,'mode','graph')
```



2

Prune the tree:

```
tree1 = prune(tree,'level',1);
view(tree1,'mode','graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

3

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]

ans =
    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
```

```
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the rightmost column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Find the cross-validation predictions for a model based on the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
cvens = crossval(ens);
[elabel escore] = kfoldPredict(cvens);
max(escore)

ans =
    9.3634    8.5624    9.3981

min(escore)

ans =
    0.0017    3.7518    0.8911
```

See Also

`kfoldEdge` | `kfoldMargin` | `kfoldLoss` | `crossval`

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Purpose

Predict response for observations not used for training.

Syntax

```
yfit = kfoldPredict(obj)
```

Description

`yfit = kfoldPredict(obj)` returns the predicted values for the responses of the training data based on `obj`, an object trained on out-of-fold observations.

Input Arguments

`obj`

Object of class `RegressionPartitionedModel`. Create `obj` with `RegressionTree.fit` or `fitensemble` along with one of the cross-validation options: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Alternatively, create `obj` from a regression tree or regression ensemble with `crossval`.

Output Arguments

`yfit`

A vector of predicted values for the response data based on a model trained on out-of-fold observations.

Examples

Construct a partitioned regression model, and examine the cross-validation loss. The cross-validation loss is the mean squared error between `yfit` and the true response data:

```
load carsmall
XX = [Cylinders Displacement Horsepower Weight];
YY = MPG;
tree = RegressionTree.fit(XX,YY);
cvmodel = crossval(tree);
L = kfoldLoss(cvmodel)

L =
   26.5271

yfit = kfoldPredict(cvmodel);
mean( (yfit - tree.Y).^2 )
```

```
ans =
   26.5271
```

See Also

`kfoldLoss`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

K-means clustering

Syntax

```
IDX = kmeans(X,k)
[IDX,C] = kmeans(X,k)
[IDX,C,sumd] = kmeans(X,k)
[IDX,C,sumd,D] = kmeans(X,k)
[...] = kmeans(...,param1,val1,param2,val2,...)
```

Description

`IDX = kmeans(X,k)` partitions the points in the `n`-by-`p` data matrix `X` into `k` clusters. This iterative partitioning minimizes the sum, over all clusters, of the within-cluster sums of point-to-cluster-centroid distances. Rows of `X` correspond to points, columns correspond to variables. `kmeans` returns an `n`-by-`1` vector `IDX` containing the cluster indices of each point. By default, `kmeans` uses squared Euclidean distances. When `X` is a vector, `kmeans` treats it as an *n*-by-1 data matrix, regardless of its orientation.

`[IDX,C] = kmeans(X,k)` returns the `k` cluster centroid locations in the `k`-by-`p` matrix `C`.

`[IDX,C,sumd] = kmeans(X,k)` returns the within-cluster sums of point-to-centroid distances in the `1`-by-`k` vector `sumd`.

`[IDX,C,sumd,D] = kmeans(X,k)` returns distances from each point to every centroid in the `n`-by-`k` matrix `D`.

`[...] = kmeans(...,param1,val1,param2,val2,...)` enables you to specify optional parameter/value pairs to control the iterative algorithm used by `kmeans`. Valid parameter strings are listed in the following table.

Parameter	Value	
'distance'	Distance measure, in p-dimensional space. kmeans minimizes with respect to this parameter. kmeans computes centroid clusters differently for the different supported distance measures.	
	'sqEuclidean'	Squared Euclidean distance (default). Each centroid is the mean of the points in that cluster.
	'cityblock'	Sum of absolute differences, i.e., the L1 distance. Each centroid is the component-wise median of the points in that cluster.
	'cosine'	One minus the cosine of the included angle between points (treated as vectors). Each centroid is the mean of the points in that cluster, after normalizing those points to unit Euclidean length.
	'correlation'	One minus the sample correlation between points (treated as sequences of values). Each centroid is the component-wise mean of the points in that cluster, after centering and normalizing those points to zero mean and unit standard deviation.
	'Hamming'	Percentage of bits that differ (only suitable for binary data). Each centroid is the component-wise median of points in that cluster.

Parameter	Value	
'emptyaction'	Action to take if a cluster loses all its member observations.	
	'error'	Treat an empty cluster as an error (default).
	'drop'	Remove any clusters that become empty. kmeans sets the corresponding return values in C and D to NaN.
	'singleton'	Create a new cluster consisting of the one point furthest from its centroid.
'onlinephase'	Flag indicating whether kmeans should perform an online update phase in addition to a batch update phase. The online phase can be time consuming for large data sets, but guarantees a solution that is a local minimum of the distance criterion, that is, a partition of the data where moving any single point to a different cluster increases the total sum of distances.	
	'on'	Perform online update (default).
	'off'	Do not perform online update.
'options'	Options for the iterative algorithm used to minimize the fitting criterion, as created by statset.	
'replicates'	Number of times to repeat the clustering, each with a new set of initial cluster centroid positions. kmeans returns the solution with the lowest value for sumd. You can supply 'replicates' implicitly by supplying a 3D array as the value for the 'start' parameter.	

Parameter	Value	
'start'	Method used to choose the initial cluster centroid positions, sometimes known as *seeds*.	
	'sample'	Select k observations from X at random (default).
	'uniform'	Select k points uniformly at random from the range of X. Not valid with Hamming distance.
	'cluster'	Perform a preliminary clustering phase on a random 10% subsample of X. This preliminary phase is itself initialized using 'sample'.
	Matrix	k-by-p matrix of centroid starting locations. In this case, you can pass in [] for k, and kmeans infers k from the first dimension of the matrix. You can also supply a 3-D array, implying a value for the 'replicates' parameter from the array's third dimension.

Algorithms

kmeans uses a two-phase iterative algorithm to minimize the sum of point-to-centroid distances, summed over all k clusters:

1. The first phase uses *batch updates*, where each iteration consists of reassigning points to their nearest cluster centroid, all at once, followed by recalculation of cluster centroids. This phase occasionally does not converge to solution that is a local minimum, that is, a partition of the data where moving any single point to a different cluster increases the total sum of distances. This is more likely for small data sets. The batch phase is fast, but potentially only approximates a solution as a starting point for the second phase.

2 The second phase uses *online updates*, where points are individually reassigned if doing so will reduce the sum of distances, and cluster centroids are recomputed after each reassignment. Each iteration during the second phase consists of one pass though all the points. The second phase will converge to a local minimum, although there may be other local minima with lower total sum of distances. The problem of finding the global minimum can only be solved in general by an exhaustive (or clever, or lucky) choice of starting points, but using several replicates with random starting points typically results in a solution that is a global minimum.

References

[1] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

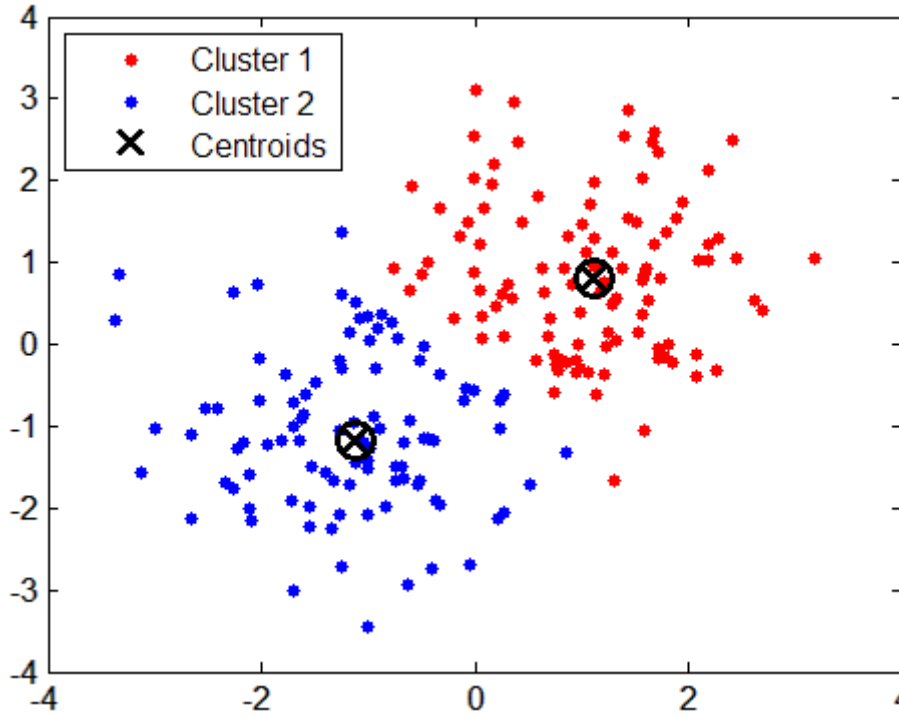
[2] Spath, H. *Cluster Dissection and Analysis: Theory, FORTRAN Programs, Examples*. Translated by J. Goldschmidt. New York: Halsted Press, 1985.

Examples

The following creates two clusters from separated random data:

```
X = [randn(100,2)+ones(100,2);...
     randn(100,2)-ones(100,2)];
opts = statset('Display','final');

[idx,ctrs] = kmeans(X,2,...
                    'Distance','city',...
                    'Replicates',5,...
                    'Options',opts);
5 iterations, total sum of distances = 284.671
4 iterations, total sum of distances = 284.671
4 iterations, total sum of distances = 284.671
3 iterations, total sum of distances = 284.671
3 iterations, total sum of distances = 284.671

plot(X(idx==1,1),X(idx==1,2),'r.','MarkerSize',12)
hold on
plot(X(idx==2,1),X(idx==2,2),'b.','MarkerSize',12)
```

```
plot(ctrs(:,1),ctrs(:,2),'kx',...
     'MarkerSize',12,'LineWidth',2)
plot(ctrs(:,1),ctrs(:,2),'ko',...
     'MarkerSize',12,'LineWidth',2)
legend('Cluster 1','Cluster 2','Centroids',...
       'Location','NW')
```



See Also

`linkage` | `clusterdata` | `silhouette`

Purpose

Find k-nearest neighbors using `ExhaustiveSearcher` object

Syntax

```
IDX = knnsearch(NS,Y)
[IDX,D] = knnsearch(NS,Y)
[IDX,D] = knnsearch(NS,Y,'Name',Value)
```

Description

`IDX = knnsearch(NS,Y)` finds the nearest neighbor (closest point) in `NS.X` for each point in `Y`. Rows of `Y` correspond to observations and columns correspond to features. `Y` must have the same number of columns as `NS.X`. `IDX` is a column vector with ny rows, where ny is the number of rows in `Y`. Each row in `IDX` contains the index of observation in `NS.X` which has the smallest distance to the corresponding observation in `Y`.

`[IDX,D] = knnsearch(NS,Y)` returns a column vector `D` containing the distances between each observation in `Y` and the corresponding closest observation in `NS.X`. That is, `D(i)` is the distance between `NS.X(IDX(i),:)` and `Y(i,:)`.

`[IDX,D] = knnsearch(NS,Y,'Name',Value)` accepts one or more comma-separated argument name/value pairs. Specify *`Name`* inside single quotes.

Input Arguments

Name-Value Pair Arguments

`K`

A positive integer, k, specifying the number of nearest neighbors in `NS.X` for each point in `Y`. Default is 1. `IDX` and `D` are ny-by-k matrices. `D` sorts the distances in each row in ascending order. Each row in `IDX` contains the indices of the k closest neighbors in `NS.X` corresponding to the k smallest distances in `D`.

`IncludeTies`

A logical value indicating whether `knnsearch` includes all the neighbors whose distance values are equal to the `K`th smallest distance. If `IncludeTies` is `true`, `knnsearch` includes all these neighbors. In this case, `IDX` and `D` are ny-by-`1` cell arrays. Each

row in `IDX` and `D` contains a vector with at least `K` numeric numbers. `D` sorts the distances in each vector in ascending order. Each row in `IDX` contains the indices of the closest neighbors corresponding to these smallest distances in `D`.

Default: `false`

`Distance`

- `'euclidean'` — Euclidean distance (default).
- `'seuclidean'` — Standardized Euclidean distance. Each coordinate difference between `X` and each query point is scaled by dividing by a scale value `S`. The default value of `S` is `NS.DistParameter` if `NS.Distance` is `'seuclidean'`, otherwise the default is the standard deviation computed from `X`, `S=nanstd(X)`. To specify another value for `S`, use the `'Scale'` argument.
- `'cityblock'` — City block distance.
- `'chebychev'` — Chebychev distance (maximum coordinate difference).
- `'minkowski'` — Minkowski distance.
- `'mahalanobis'` — Mahalanobis distance, which is computed using a positive definite covariance matrix `C`. The default value of `C` is `nancov(X)`. To change the value of `C`, use the `Cov` parameter.
- `'cosine'` — One minus the cosine of the included angle between observations (treated as vectors).
- `'correlation'` — One minus the sample linear correlation between observations (treated as sequences of values).
- `'spearman'` — One minus the sample Spearman's rank correlation between observations (treated as sequences of values).

- `'hamming'` — Hamming distance, which is the percentage of coordinates that differ.
- `'jaccard'` — One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.
- custom distance function — A distance function specified using `@` (for example, `@distfun`). A distance function must be of the form `function D2 = distfun(ZI, ZJ)`, taking as arguments a 1-by-n vector `ZI` containing a single row of from `X` or from the query points `Y`, an m2-by-n matrix `ZJ` containing multiple rows of `X` or `Y`, and returning an m2-by-1 vector of distances `D2`, whose jth element is the distance between the observations `ZI` and `ZJ`(j,:).

Default is `NS.Distance`. For more information on these distance metrics, see “Distance Metrics” on page 13-9.

`P`

A positive scalar, p, indicating the exponent of the Minkowski distance. This parameter is only valid if `knnsearch` uses the `'minkowski'` distance metric. Default is `NS.DistParameter` if `NS.Distance` is `'minkowski'` and 2 otherwise.

`Cov`

A positive definite matrix indicating the covariance matrix when computing the Mahalanobis distance. This parameter is only valid when `knnsearch` uses the `'mahalanobis'` distance metric. Default is `NS.DistParameter` if `NS.Distance` is `'mahalanobis'`, or `nancov(X)` otherwise.

`Scale`

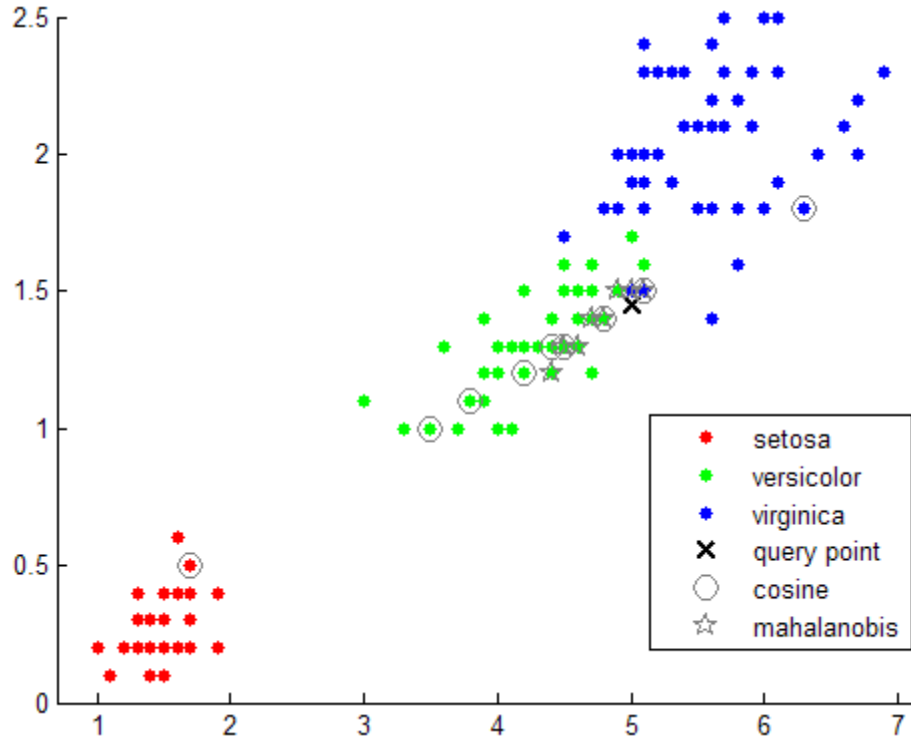
A vector `S` with the length equal to the number of columns in `X`. Each coordinate of `X` and each query point is scaled by the corresponding element of `S` when computing the standardized Euclidean distance. This parameter is only valid when `Distance` is `'seuclidean'`. Default is `nanstd(X)`.

Examples

Create an `ExhaustiveSearcher` object specifying `'cosine'` as the distance metric. Perform a *k*-nearest neighbors search on the object using the `mahalanobis` metric and compare the results:

```
load fisheriris
x = meas(:,3:4);
exhaustiveobj = ExhaustiveSearcher(x,'Distance','cosine')

exhaustiveobj =

  ExhaustiveSearcher

  Properties:
               X: [150x2 double]
        Distance: 'cosine'
    DistParameter: []

% Perform a knnsearch between x and a query point, using
% first cosine then mahalanobis distance metrics:
newpoint = [5 1.45];
[n,d]=knnsearch(exhaustiveobj,newpoint,'k',10);
[nmah,dmah] = knnsearch(exhaustiveobj,newpoint,'k',10,...
   'distance','mahalanobis');

% Visualize the results of the two different nearest
% neighbors searches:

% First plot the training data:
gscatter(x(:,1),x(:,2),species)
% Plot an X for the query point:
line(newpoint(1),newpoint(2),'marker','x','color','k',...
   'markersize',10,'linewidth',2,'linestyle','none')
% Use circles to denote the cosine nearest neighbors:
line(x(n,1),x(n,2),'color',[.5 .5 .5],'marker','o',...
   'linestyle','none','markersize',10)
% Use pentagrams to denote the mahalanobis nearest neighbors:
line(x(nmah,1),x(nmah,2),'color',[.5 .5 .5],'marker','p',...
```

```
    'linestyle','none','markersize',10)
legend('setosa','versicolor','virginica','query point',...
    'cosine','mahalanobis')
set(legend,'location','best')
```



Algorithms

For information on a specific search algorithm, see “Distance Metrics” on page 13-9.

See Also

`createns` | `ExhaustiveSearcher` | `KDTreeSearcher.knnsearch` | `knnsearch` | `rangesearch`

How To

- “*k*-Nearest Neighbor Search and Radius Search” on page 13-12

- “Distance Metrics” on page 13-9

Purpose

Find k-nearest neighbors using `KDTreeSearcher` object

Syntax

```
IDX = knnsearch(NS,Y)
[IDX,D] = knnsearch(NS,Y)
[IDX,D] = knnsearch(NS,Y,'Name',Value)
```

Description

`IDX = knnsearch(NS,Y)` finds the nearest neighbor (closest point) in `NS.X` for each point in `Y`. Rows of `Y` correspond to observations and columns correspond to features. `Y` must have the same number of columns as `NS.X`. `IDX` is a column vector with ny rows, where ny is the number of rows in `Y`. Each row in `IDX` contains the index of observation in `NS.X` which has the smallest distance to the corresponding observation in `Y`.

`[IDX,D] = knnsearch(NS,Y)` returns a column vector `D` containing the distances between each observation in `Y` and the corresponding closest observation in `NS.X`. That is, `D(i)` is the distance between `NS.X(IDX(i),:)` and `Y(i,:)`.

`[IDX,D] = knnsearch(NS,Y,'Name',Value)` accepts one or more comma-separated name/value pairs. Specify *`Name`* inside single quotes.

Input Arguments

Name-Value Pair Arguments

`K`

A positive integer, k, specifying the number of nearest neighbors in `NS.X` for each point in `Y`. Default is 1. `IDX` and `D` are ny-by-k matrices. `D` sorts the distances in each row in ascending order. Each row in `IDX` contains the indices of the k closest neighbors in `NS.X` corresponding to the k smallest distances in `D`.

`Distance`

Select one of the following distance algorithms.

- `'euclidean'` — Euclidean distance (default).
- `'cityblock'` — City block distance.

- `'chebychev'` — Chebychev distance (maximum coordinate difference).
- `'minkowski'` — Minkowski distance.

Default is `NS.Distance`. For more information on these distance metrics, see "Distance Metrics" on page 13-9.

`IncludeTies`

A logical value indicating whether `knnsearch` includes all the neighbors whose distance values are equal to the `K`th smallest distance. If `IncludeTies` is `true`, `knnsearch` includes all these neighbors. In this case, `IDX` and `D` are *ny*-by-`1` cell arrays. Each row in `IDX` and `D` contains a vector with at least `K` numeric numbers. `D` sorts the distances in each vector in ascending order. Each row in `IDX` contains the indices of the closest neighbors corresponding to these smallest distances in `D`.

Default: `false`

`P`

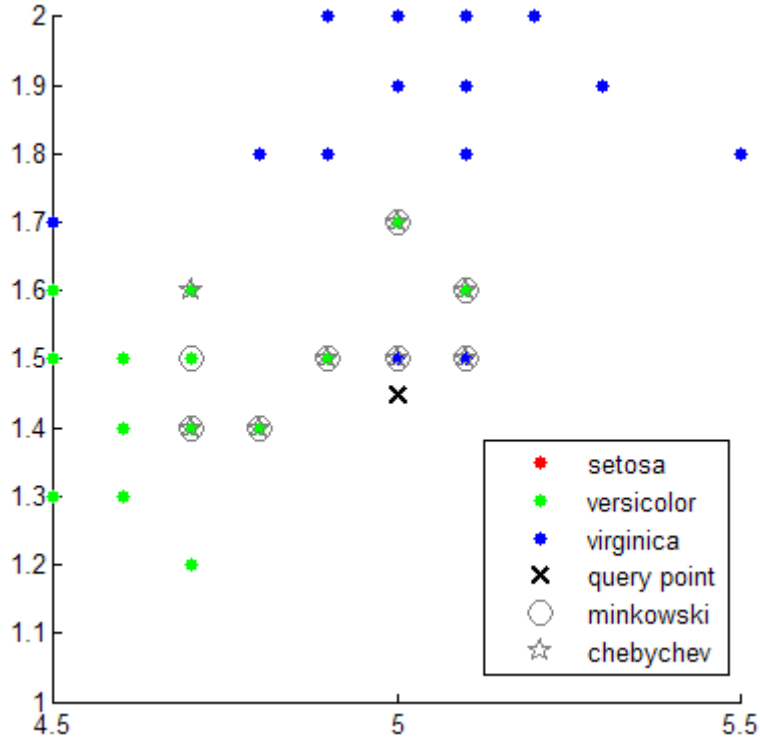
A positive scalar, *p*, indicating the exponent of the Minkowski distance. This parameter is only valid whenthe `Distance` is `'minkowski'`. Default is `NS.DistParameter` if `NS.Distance` is `'minkowski'` and 2 otherwise.

Examples

Create a `KDTreeSearcher` object specifying `'minkowski'` as the distance metric with an exponent of 5. Perform a *k*-nearest neighbors search on the object using the `chebychev` metric and compare the results:

```
load fisheriris
x = meas(:,3:4);
kdtreeNS = KDTreeSearcher(x,'Distance','minkowski','P',5)

kdtreeNS =

  KDTreeSearcher
```

```
  Properties:
       BucketSize: 50
                X: [150x2 double]
         Distance: 'minkowski'
    DistParameter: 5

% Perform a knnsearch between X and a query point, using
% first Minkowski then Chebychev distance metrics:
newpoint = [5 1.45];
[n,d]=knnsearch(kdtreeNS,newpoint,'k',10);
[ncb,dcb] = knnsearch(kdtreeNS,newpoint,'k',10,...
   'distance','chebychev');

% Visualize the results of the two different nearest
% neighbors searches:

% First plot the training data:
gscatter(x(:,1),x(:,2),species)
% Zoom in on the points of interest:
set(gca,'xlim',[4.5 5.5],'ylim',[1 2]); axis square
% Plot an X for the query point:
line(newpoint(1),newpoint(2),'marker','x','color','k',...
   'markersize',10,'linewidth',2,'linestyle','none')
% Use circles to denote the Minkowski nearest neighbors:
line(x(n,1),x(n,2),'color',[.5 .5 .5],'marker','o',...
   'linestyle','none','markersize',10)
% Use pentagrams to denote the Chebychev nearest neighbors:
line(x(ncb,1),x(ncb,2),'color',[.5 .5 .5],'marker','p',...
   'linestyle','none','markersize',10)
legend('setosa','versicolor','virginica','query point',...
   'minkowski','chebychev')
set(legend,'location','best')
```



Algorithms

For information on a specific search algorithm, see “Distance Metrics” on page 13-9.

References

[1] Friedman, J. H., Bentely, J., and Finkel, R. A. (1977). *An Algorithm for Finding Best Matches in Logarithmic Expected Time*, ACM Transactions on Mathematical Software 3, 209.

See Also

`createns` | `ExhaustiveSearcher` | `ExhaustiveSearcher.knnsearch` | `knnsearch` | `rangesearch`

How To

- “*k*-Nearest Neighbor Search and Radius Search” on page 13-12

- “Distance Metrics” on page 13-9

knnsearch

Purpose

Find *k*-nearest neighbors using data

Syntax

```
IDX = knnsearch(X,Y)
[IDX,D] = knnsearch(X,Y)
[IDX,D] = knnsearch(X,Y,'Name',Value)
```

Description

`IDX = knnsearch(X,Y)` finds the nearest neighbor in `X` for each point in `Y`. `X` is an *mx*-by-*n* matrix and `Y` is an *my*-by-*n* matrix. Rows of `X` and `Y` correspond to observations and columns correspond to variables. `IDX` is a column vector with *my* rows. Each row in `IDX` contains the index of nearest neighbor in `X` for the corresponding row in `Y`.

`[IDX,D] = knnsearch(X,Y)` returns an *my*-by-1 vector `D` containing the distances between each observation in `Y` and the corresponding closest observation in `X`. That is, `D(i)` is the distance between `X(IDX(i),:)` and `Y(i,:)`.

`[IDX,D] = knnsearch(X,Y,'Name',Value)` accepts one or more optional comma-separated name/value pairs. Specify *`Name`* inside single quotes.

`knnsearch` does not save a search object. To create a search object, use `createns`.

Tips

- For a fixed positive integer `K`, `knnsearch` finds the `K` points in `X` that are nearest each point in `Y`. In contrast, for a fixed positive real value `r`, `rangesearch` finds all the points in `X` that are within a distance `r` of each point in `Y`.

Input Arguments

Name-Value Pair Arguments

`K`

Positive integer specifying the number of nearest neighbors in `X` for each point in `Y`. Default is 1. `IDX` and `D` are *my*-by-`K` matrices. `D` sorts the distances in each row in ascending order. Each row in `IDX` contains the indices of the `K` closest neighbors in `X` corresponding to the `K` smallest distances in `D`.

`IncludeTies`

A logical value indicating whether `knnsearch` includes all the neighbors whose distance values are equal to the `K`th smallest distance. If `IncludeTies` is `true`, `knnsearch` includes all these neighbors. In this case, `IDX` and `D` are *my*-by-`1` cell arrays. Each row in `IDX` and `D` contains a vector with at least `K` numeric numbers. `D` sorts the distances in each vector in ascending order. Each row in `IDX` contains the indices of the closest neighbors corresponding to these smallest distances in `D`.

Default: `false`

`NSMethod`

Nearest neighbors search method. Value is either:

- `'kdtree'` — Creates and uses a `K`d-tree to find nearest neighbors. This is the default value when the number of columns of `X` is less than 10, `X` is not sparse, and the distance measure is one of the following measures. `'kdtree'` is only valid when the distance measure is one of the following:
  - `'euclidean'`
  - `'cityblock'`
  - `'minkowski'`
  - `'chebychev'`
- `'exhaustive'` — Uses the exhaustive search algorithm by computing the distance values from all the points in `X` to each point in `Y` to find nearest neighbors.

`Distance`

A string or a function handle specifying the distance metric. The value can be one of the following:

- `'euclidean'` — Euclidean distance (default).

- `'seuclidean'` — Standardized Euclidean distance. Each coordinate difference between rows in `X` and the query matrix is scaled by dividing by the corresponding element of the standard deviation computed from `X`, `S=nanstd(X)`. To specify another value for `S`, use the `Scale` argument.
- `'cityblock'` — City block distance.
- `'chebychev'` — Chebychev distance (maximum coordinate difference).
- `'minkowski'` — Minkowski distance. The default exponent is 2. To specify a different exponent, use the `'P'` argument.
- `'mahalanobis'` — Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is `nancov(X)`. To change the value of `C`, use the `Cov` parameter.
- `'cosine'` — 1 minus the cosine of the included angle between observations (treated as vectors).
- `'correlation'` — One minus the sample linear correlation between observations (treated as sequences of values).
- `'spearman'` — One minus the sample Spearman's rank correlation between observations (treated as sequences of values).
- `'hamming'` — Hamming distance, which is the percentage of coordinates that differ.
- `'jaccard'` — One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.
- custom distance function — A distance function specified using `@` (for example, `@distfun`). A distance function must be of the form `function D2 = distfun(ZI, ZJ)`, taking as arguments a 1-by-*n* vector `ZI` containing a single row of `X` or `Y`, an *m2*-by-*n* matrix `ZJ` containing multiple rows of `X` or `Y`, and returning an *m2*-by-1 vector of distances `D2`, whose *j*th element is the distance between the observations `ZI` and `ZJ`(*j*,:).

For more information on these distance metrics, see "Distance Metrics" on page 13-9.

`P`

A positive scalar, *p*, indicating the exponent of the Minkowski distance. This parameter is only valid if the `Distance` is `'minkowski'`. Default is 2.

`Cov`

A positive definite matrix indicating the covariance matrix when computing the Mahalanobis distance. This parameter is only valid when `Distance` is `'mahalanobis'`. Default is `nancov(X)`.

`Scale`

A vector `S` containing nonnegative values, with length equal to the number of columns in `X`. Each coordinate of `X` and each query point is scaled by the corresponding element of `S` when computing the standardized Euclidean distance. This argument is only valid when `Distance` is `'seuclidean'`. Default is `nanstd(X)`.

`BucketSize`

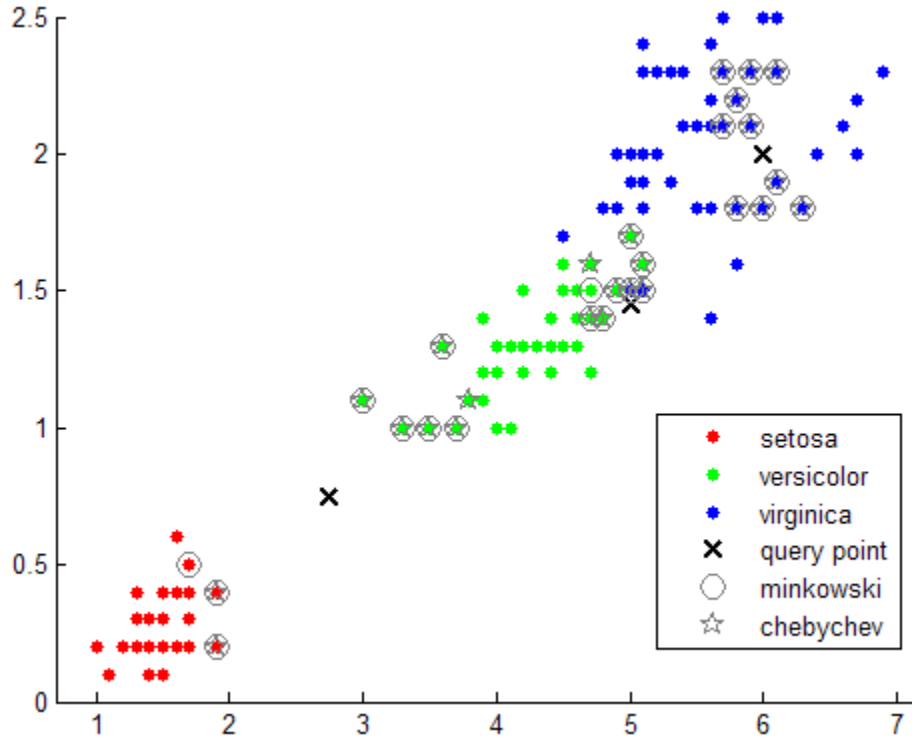
The maximum number of data points in the leaf node of the *k*d-tree. This argument is only meaningful when using the *k*d-tree search method. Default is 50.

Examples

Find the 10 nearest neighbors in `x` to each point in `y` using first the `'minkowski'` distance metric with a `p` value of 5, and then using the `'chebychev'` distance metric. Visually compare the results:

```
load fisheriris
x = meas(:,3:4);
y = [5 1.45;6 2;2.75 .75];

% Perform a knnsearch between x and the query points in y,
% using first Minkowski then Chebychev distance metrics.
[n,d]=knnsearch(x,y,'k',10,'distance','minkowski','p',5);
[ncb,dcb] = knnsearch(x,y,'k',10,...
```

```
   'distance','chebychev');

% Visualize the results of the two different nearest
% neighbors searches.

% First plot the training data.
gscatter(x(:,1),x(:,2),species)

% Plot an X for the query points.
line(y(:,1),y(:,2),'marker','x','color','k',...
   'markersize',10,'linewidth',2,'linestyle','none')

% Use circles to denote the Minkowski nearest neighbors.
line(x(n,1),x(n,2),'color',[.5 .5 .5],'marker','o',...
   'linestyle','none','markersize',10)

% Use pentagrams to denote the Chebychev nearest neighbors.
line(x(ncb,1),x(ncb,2),'color',[.5 .5 .5],'marker','p',...
   'linestyle','none','markersize',10)
legend('setosa','versicolor','virginica','query point',...
'minkowski','chebychev')
set(legend,'location','best')
```



Algorithms

For information on a specific search algorithm, see “Distance Metrics” on page 13-9.

References

[1] Friedman, J. H., Bentely, J., and Finkel, R. A. (1977) An Algorithm for Finding Best Matches in Logarithmic Expected Time, ACM Transactions on Mathematical Software 3, 209.

See Also

`createns` | `KDTreeSearcher.knnsearch` | `ExhaustiveSearcher.knnsearch` | `rangesearch`

How To

- “*k*-Nearest Neighbor Search and Radius Search” on page 13-12

kruskalwallis

Purpose

Kruskal-Wallis test

Syntax

```
p = kruskalwallis(X)
p = kruskalwallis(X,group)
p = kruskalwallis(X,group,displayopt)
[p,table] = kruskalwallis(...)
[p,table,stats] = kruskalwallis(...)
```

Description

`p = kruskalwallis(X)` performs a Kruskal-Wallis test to compare samples from two or more groups. Each column of the m-by-n matrix `X` represents an independent sample containing m mutually independent observations. The function compares the medians of the samples in `X`, and returns the p value for the null hypothesis that all samples are drawn from the same population (or equivalently, from different populations with the same distribution). Note that the Kruskal-Wallis test is a nonparametric version of the classical one-way ANOVA, and an extension of the Wilcoxon rank sum test to more than two groups.

If the p value is near zero, this casts doubt on the null hypothesis and suggests that at least one sample median is significantly different from the others. The choice of a critical p value to determine whether the result is judged statistically significant is left to the researcher. It is common to declare a result significant if the p value is less than 0.05 or 0.01.

The `kruskalwallis` function displays two figures. The first figure is a standard ANOVA table, calculated using the ranks of the data rather than their numeric values. Ranks are found by ordering the data from smallest to largest across all groups, and taking the numeric index of this ordering. The rank for a tied observation is equal to the average rank of all observations tied with it. For example, the following table shows the ranks for a small sample.

X value	1.4	2.7	1.6	1.6	3.3	0.9	1.1
Rank	3	6	4.5	4.5	7	1	2

The entries in the ANOVA table are the usual sums of squares, degrees of freedom, and other quantities calculated on the ranks. The usual *F* statistic is replaced by a chi-square statistic. The *p* value measures the significance of the chi-square statistic.

The second figure displays box plots of each column of `X` (not the ranks of `X`).

`p = kruskalwallis(X,group)` uses the values in `group` (a character array or cell array) as labels for the box plot of the samples in `X`, when `X` is a matrix. Each row of `group` contains the label for the data in the corresponding column of `X`, so `group` must have length equal to the number of columns in `X`.

When `X` is a vector, `kruskalwallis` performs a Kruskal-Wallis test on the samples contained in `X`, as indexed by input `group` (a categorical variable, vector, character array, or cell array). Each element in `group` identifies the group (i.e., sample) to which the corresponding element in vector `X` belongs, so `group` must have the same length as `X`. The labels contained in `group` are also used to annotate the box plot. (See "Grouped Data" on page 2-34.)

It is not necessary to label samples sequentially (`1`, `2`, `3`, ...). For example, if `X` contains measurements taken at three different temperatures, -27°, 65°, and 110°, you could use these numbers as the sample labels in `group`. If a row of `group` contains an empty cell or empty string, that row and the corresponding observation in `X` are disregarded. `NaN`s in either input are similarly ignored.

`p = kruskalwallis(X,group,`*`displayopt`*`)` enables the table and box plot displays when *`displayopt`* is `'on'` (default) and suppresses the displays when *`displayopt`* is `'off'`.

`[p,table] = kruskalwallis(...)` returns the ANOVA table (including column and row labels) in cell array `table`.

`[p,table,stats] = kruskalwallis(...)` returns a `stats` structure that you can use to perform a follow-up multiple comparison test. The `kruskalwallis` test evaluates the hypothesis that all samples come from populations that have the same median, against the alternative

that the medians are not all the same. Sometimes it is preferable to perform a test to determine which pairs are significantly different, and which are not. You can use the `multcompare` function to perform such tests by supplying the `stats` structure as input.

Assumptions

The Kruskal-Wallis test makes the following assumptions about the data in `X`:

- All samples come from populations having the same continuous distribution, apart from possibly different locations due to group effects.
- All observations are mutually independent.

The classical one-way ANOVA test replaces the first assumption with the stronger assumption that the populations have normal distributions.

Examples

This example compares the material strength study used with the `anova1` function, to see if the nonparametric Kruskal-Wallis procedure leads to the same conclusion. The example studies the strength of beams made from three alloys:

```
strength = [82 86 79 83 84 85 86 87 74 82 ...
            78 75 76 77 79 79 77 78 82 79];

alloy = {'st','st','st','st','st','st','st','st',...
         'al1','al1','al1','al1','al1','al1',...
         'al2','al2','al2','al2','al2','al2'};
```

This example uses both classical and Kruskal-Wallis ANOVA, omitting displays:

```
anova1(strength,alloy,'off')
ans =
 1.5264e-004

kruskalwallis(strength,alloy,'off')
```

```
ans =
  0.0018
```

Both tests find that the three alloys are significantly different, though the result is less significant according to the Kruskal-Wallis test. It is typical that when a data set has a reasonable fit to the normal distribution, the classical ANOVA test is more sensitive to differences between groups.

To understand when a nonparametric test may be more appropriate, let's see how the tests behave when the distribution is not normal. You can simulate this by replacing one of the values by an extreme value (an outlier).

```
strength(20)=120;
anova1(strength,alloy,'off')
ans =
  0.2501

kruskalwallis(strength,alloy,'off')
ans =
  0.0060
```

Now the classical ANOVA test does not find a significant difference, but the nonparametric procedure does. This illustrates one of the properties of nonparametric procedures - they are often not severely affected by changes in a small portion of the data.

References

[1] Gibbons, J. D. *Nonparametric Statistical Inference*. New York: Marcel Dekker, 1985.

[2] Hollander, M., and D. A. Wolfe. *Nonparametric Statistical Methods*. Hoboken, NJ: John Wiley & Sons, Inc., 1999.

See Also

`anova1` | `boxplot` | `friedman`

How To

- "Grouped Data" on page 2-34

- multcompare
- ranksum

Purpose

Kernel smoothing density estimate

Syntax

```
[f,xi] = ksdensity(x)
f = ksdensity(x,xi)
ksdensity(...)
ksdensity(ax,...)
[f,xi,u] = ksdensity(...)
[...] = ksdensity(...,'Name',value)
```

Description

`[f,xi] = ksdensity(x)` computes a probability density estimate of the sample in the vector `x`. `f` is the vector of density values evaluated at the points in `xi`. The estimate is based on a normal kernel function, using a window parameter (`width`) that is a function of the number of points in `x`. The density is evaluated at 100 equally spaced points that cover the range of the data in `x`. `ksdensity` works best with continuously distributed samples.

`f = ksdensity(x,xi)` specifies the vector `xi` of values, where the density estimate is to be evaluated.

`ksdensity(...)` without output arguments produces a plot of the results.

`ksdensity(ax,...)` plots into axes `ax` instead of `gca`.

`[f,xi,u] = ksdensity(...)` also returns the width of the kernel-smoothing window.

`[...] = ksdensity(...,'Name',value)` specifies one or more optional parameter name/value pairs to control the density estimation. Specify *`Name`* inside single quotes. Valid parameter strings and their possible values are as follows:

Name	Value
`censoring`	A logical vector of the same length as `x`, indicating which entries are censoring times. Default is no censoring.
`kernel`	The type of kernel smoother to use. Choose the value as • `'normal'` (default) • `'box'` • `'triangle'` • `'epanechnikov'` Alternatively, you can specify some other function, as a function handle or as a string, e.g., `@normpdf` or `'normpdf'`. The function must take a single argument that is an array of distances between data values and places where the density is evaluated. It must return an array of the same size containing corresponding values of the kernel function.
`npoints`	The number of equally spaced points in `xi`. Default is `100`.
`support`	• `'unbounded'` allows the density to extend over the whole real line (default). • `'positive'` restricts the density to positive values. • A two-element vector gives finite lower and upper bounds for the support of the density.
`weights`	Vector of the same length as `x`, assigning weight to each `x` value.

Name	Value
`width`	The bandwidth of the kernel-smoothing window. The default is optimal for estimating normal densities, but you may want to choose a smaller value to reveal features such as multiple modes.
`function`	The function type to estimate, chosen from among • `'pdf'` — density • `'cdf'` — cumulative probability • `'icdf'` — inverse cumulative probability • `'survivor'` — survivor • `'cumhazard'` — cumulative hazard functions For `'icdf'`, `f=ksdensity(x,yi,...,'function','icdf')` computes the estimated inverse CDF of the values in `x`, and evaluates it at the probability values specified in `yi`.

In place of the kernel functions listed above, you can specify another kernel function by using `@` (such as `@normpdf`) or quotes (such as `'normpdf'`). `ksdensity` calls the function with a single argument that is an array containing distances between data values in `x` and locations in `xi` where the density is evaluated. The function must return an array of the same size containing corresponding values of the kernel function. When the `function` parameter value is `'pdf'`, this kernel function returns density values, otherwise it returns cumulative probability values. Specifying a custom kernel when the `function` parameter value is `'icdf'` returns an error.

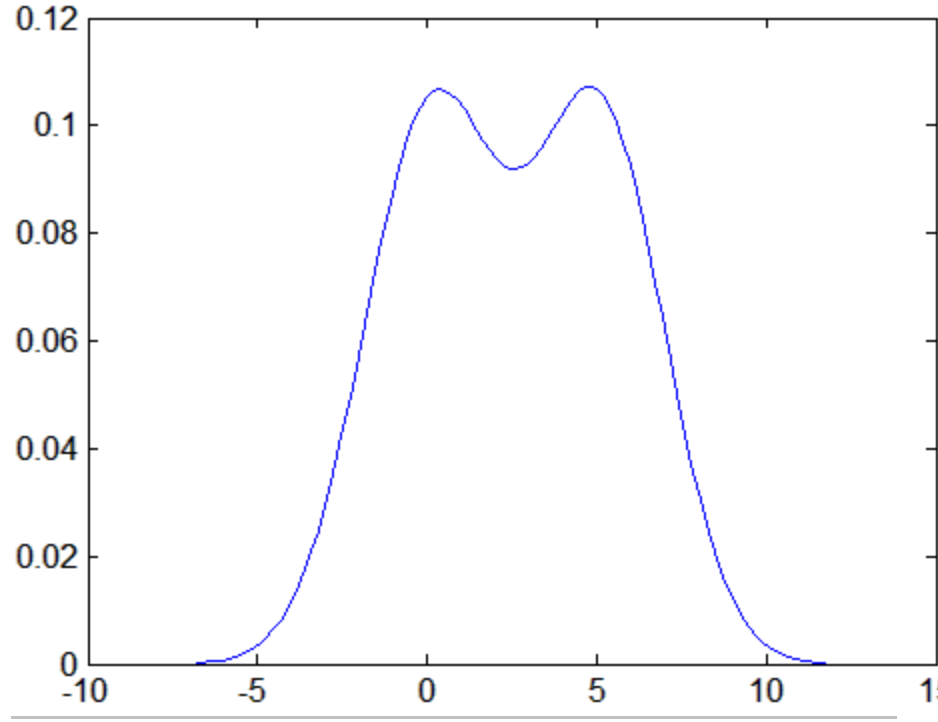
If the `support` parameter is `'positive'`, `ksdensity` transforms `x` using a log function, estimates the density of the transformed values, and transforms back to the original scale. If `support` is a vector `[L U]`,

`ksdensity` uses the transformation `log((X-L)/(U-X))`. The `width` parameter and `u` outputs are on the scale of the transformed values.

Examples

Generate a mixture of two normal distributions and plots the estimated density:

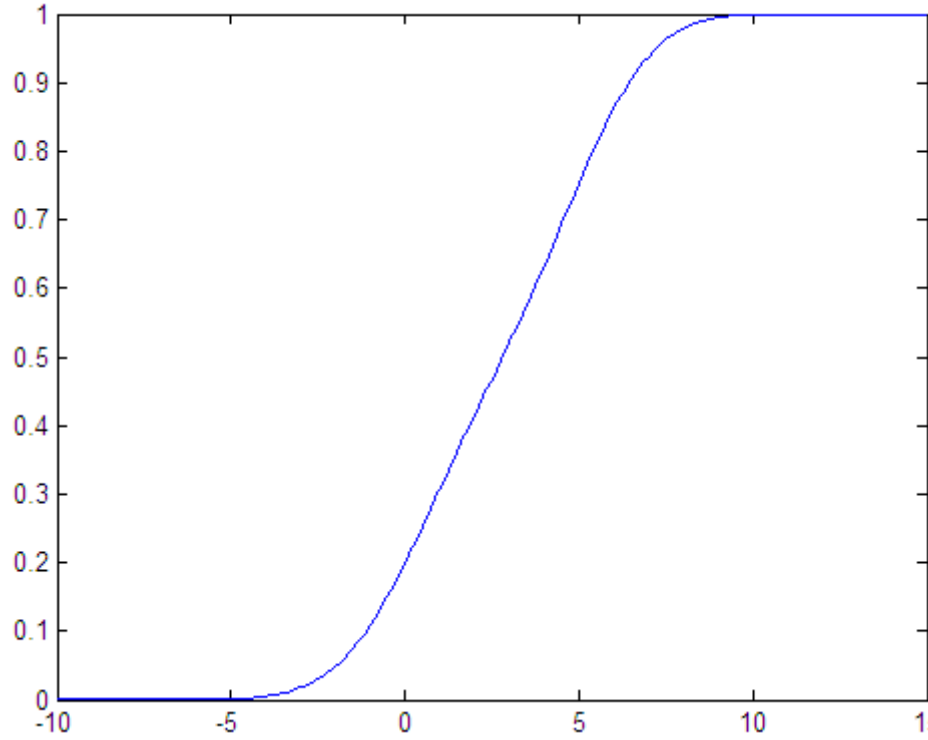
```
x = [randn(30,1); 5+randn(30,1)];
[f,xi] = ksdensity(x);
plot(xi,f);
```



Generate a mixture of two normal distributions, and plot the estimated cumulative distribution at a specified set of values:

```
x = [randn(30,1); 5+randn(30,1)];
```

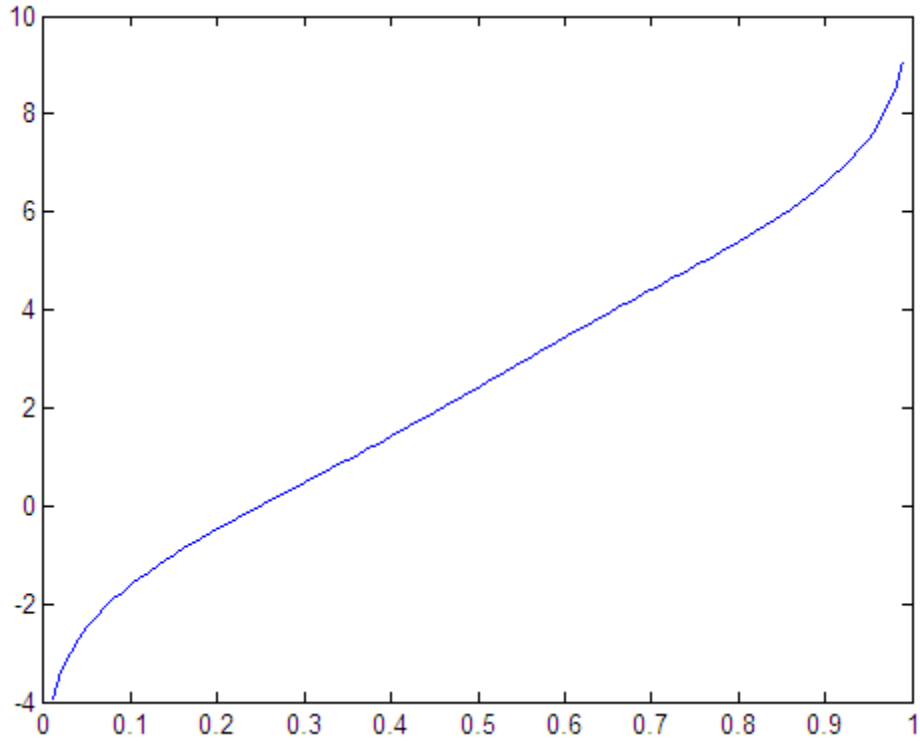
```
xi = linspace(-10,15,201);
f = ksdensity(x,xi,'function','cdf');
plot(xi,f);
```



Generate a mixture of two normal distributions, and plot the estimated inverse cumulative distribution function at a specified set of values:

```
x = [randn(30,1); 5+randn(30,1)];
yi = linspace(.01,.99,99);
g = ksdensity(x,yi,'function','icdf');
```

```
plot(yi,g);
```



References

[1] Bowman, A. W., and A. Azzalini. *Applied Smoothing Techniques for Data Analysis*. New York: Oxford University Press, 1997.

See Also

`hist` | `@`

Purpose

One-sample Kolmogorov-Smirnov test

Syntax

```
h = kstest(x)
h = kstest(x,CDF)
h = kstest(x,CDF,alpha)
h = kstest(x,CDF,alpha,type)
[h,p,ksstat,cv] = kstest(...)
```

Description

`h = kstest(x)` performs a Kolmogorov-Smirnov test to compare the values in the data vector `x` to a standard normal distribution. The null hypothesis is that `x` has a standard normal distribution. The alternative hypothesis is that `x` does not have that distribution. The result `h` is `1` if the test rejects the null hypothesis at the 5% significance level, `0` otherwise.

The test statistic is:

$$\max(|F(x) - G(x)|)$$

where $F(x)$ is the empirical cdf and $G(x)$ is the standard normal cdf.

`h = kstest(x,CDF)` compares the distribution of `x` to the hypothesized continuous distribution defined by `CDF`, which is either a two-column matrix or a ProbDist object of the `ProbDistUnivParam` class or `ProbDistUnivKernel` class. When `CDF` is a matrix, column 1 contains a set of possible x values, and column 2 contains the corresponding hypothesized cumulative distribution function values $G(x)$. If possible, define `CDF` so that column 1 contains the values in `x`. If there are values in `x` not found in column 1 of `CDF`, `kstest` approximates $G(x)$ by interpolation. All values in `x` must lie in the interval between the smallest and largest values in the first column of `CDF`. If the second argument is empty (`[]`), `kstest` uses the standard normal distribution.

The Kolmogorov-Smirnov test requires that `CDF` be predetermined. It is not accurate if `CDF` is estimated from the data. To test `x` against a normal distribution without specifying the parameters, use `lillietest` instead.

`h = kstest(x,CDF,alpha)` specifies the significance level `alpha` for the test. The default is `0.05`.

`h = kstest(x,CDF,alpha,type)` specifies the type of test using one of the following values for the string *`type`*:

- `'unequal'` — Tests the alternative hypothesis that the population cdf is unequal to the specified `CDF`. This is the default.
- `'larger'` — Tests the alternative hypothesis that the population cdf is larger than the specified `CDF`. The test statistic does not use the absolute value.
- `'smaller'` — Tests the alternative hypothesis that the population cdf is smaller than the specified `CDF`. The test statistic does not use the absolute value.

`[h,p,ksstat,cv] = kstest(...)` also returns the *p* value `p`, the test statistic `ksstat`, and the cutoff value `cv` for determining if `ksstat` is significant.

Examples

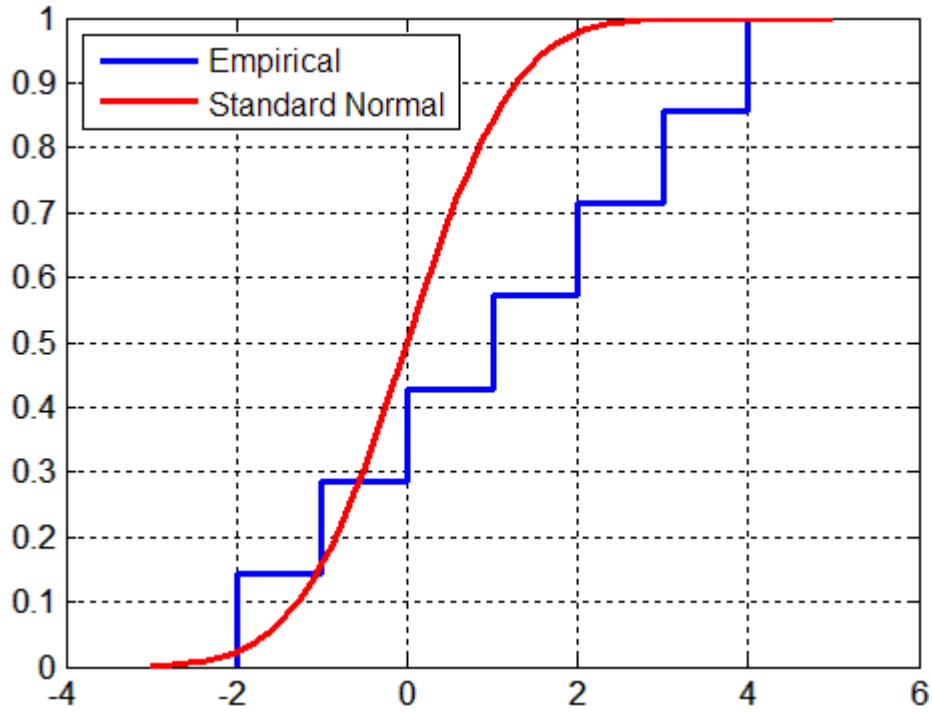
Generate evenly spaced numbers and perform a Kolmogorov-Smirnov test to see if they come from a standard normal distribution:

```
x = -2:1:4
x =
  -2  -1   0   1   2   3   4

[h,p,k,c] = kstest(x,[],0.05,0)
h =
   0
p =
   0.13632
k =
   0.41277
c =
   0.48342
```

The test fails to reject the null hypothesis that the values come from a standard normal distribution. This illustrates the difficulty of testing normality in small samples. (The Lilliefors test, implemented by the Statistics Toolbox function `lillietest`, may be more appropriate.)

The following figure illustrates the test statistic:

```
xx = -3:.1:5;
F = cdfplot(x);
hold on
G = plot(xx,normcdf(xx),'r-');
set(F,'LineWidth',2)
set(G,'LineWidth',2)
legend([F G],...
       'Empirical','Standard Normal',...
       'Location','NW')
```



The test statistic `k` is the maximum difference between the curves.

Setting *`type`* to `'smaller'` tests the alternative that the population cdf is smaller than the normal cdf:

```
[h,p,ksstat] = kstest(x,[],0.05,'smaller')
h =
   0
p =
   0.068181
k =
   0.41277
```

The test statistic is the same as before, but the *p* value is smaller.

Setting *type* to `'larger'` changes the test statistic:

```
[h,p,k] = kstest(x,[],0.05,'larger')
h =
   0
p =
   0.77533
k =
   0.12706
```

References

[1] Massey, F. J. "The Kolmogorov-Smirnov Test for Goodness of Fit." *Journal of the American Statistical Association*. Vol. 46, No. 253, 1951, pp. 68–78.

[2] Miller, L. H. "Table of Percentage Points of Kolmogorov Statistics." *Journal of the American Statistical Association*. Vol. 51, No. 273, 1956, pp. 111–121.

[3] Marsaglia, G., W. Tsang, and J. Wang. "Evaluating Kolmogorov's Distribution." *Journal of Statistical Software*. Vol. 8, Issue 18, 2003.

How To

- `kstest2`
- `lillietest`

kstest2

Purpose

Two-sample Kolmogorov-Smirnov test

Syntax

```
h = kstest2(x1,x2)
h = kstest2(x1,x2,alpha,type)
[h,p] = kstest2(...)
[h,p,ks2stat] = kstest2(...)
```

Description

`h = kstest2(x1,x2)` performs a two-sample Kolmogorov-Smirnov test to compare the distributions of the values in the two data vectors `x1` and `x2`. The null hypothesis is that `x1` and `x2` are from the same continuous distribution. The alternative hypothesis is that they are from different continuous distributions. The result `h` is `1` if the test rejects the null hypothesis at the 5% significance level; `0` otherwise.

The test statistic is:

$$\max(|F1(x) - F2(x)|)$$

where $F1(x)$ is the proportion of `x1` values less than or equal to x and $F1(x)$ is the proportion of `x2` values less than or equal to x.

`h = kstest2(x1,x2,alpha)` specifies the significance level `alpha` for the test. The default is `0.05`.

`h = kstest2(x1,x2,alpha,type)` specifies the type of test using one of the following values for the string *`type`*:

- `'unequal'` — Tests the alternative hypothesis that the population cdfs are unequal. This is the default.
- `'larger'` — Tests the alternative hypothesis that the first population cdf is larger than the second population cdf. The test statistic does not use the absolute value.
- `'smaller'` — Tests the alternative hypothesis that the first population cdf is smaller than the second population cdf. The test statistic does not use the absolute value.

`[h,p] = kstest2(...)` also returns the asymptotic *p* value `p`. The asymptotic `p` value becomes very accurate for large sample sizes, and is believed to be reasonably accurate for sample sizes `n1` and `n2` such that `(n1*n2)/(n1 + n2) >= 4`.

`[h,p,ks2stat] = kstest2(...)` also returns the *p* value `p` and the test statistic `ks2stat`.

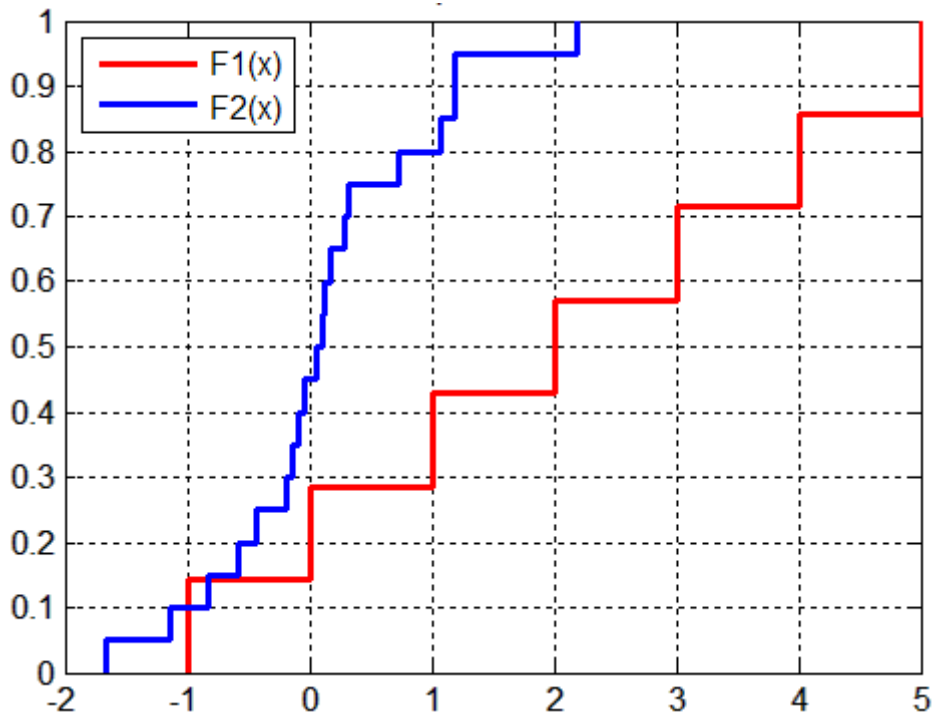
Examples

The following test compares the distributions of a small evenly-spaced sample and a larger normal sample:

```
x = -1:1:5
y = randn(20,1);
[h,p,k] = kstest2(x,y)
h =
     0
p =
    0.0774
k =
    0.5214
```

The following figure illustrates the test statistic:

```
F1 = cdfplot(x);
hold on
F2 = cdfplot(y)
set(F1,'LineWidth',2,'Color','r')
set(F2,'LineWidth',2)
legend([F1 F2],'F1(x)','F2(x)','Location','NW')
```



The test statistic `k` is the maximum difference between the curves.

References

[1] Massey, F. J. "The Kolmogorov-Smirnov Test for Goodness of Fit." *Journal of the American Statistical Association*. Vol. 46, No. 253, 1951, pp. 68–78.

[2] Miller, L. H. "Table of Percentage Points of Kolmogorov Statistics." *Journal of the American Statistical Association*. Vol. 51, No. 273, 1956, pp. 111–121.

[3] Marsaglia, G., W. Tsang, and J. Wang. "Evaluating Kolmogorov's Distribution." *Journal of Statistical Software*. Vol. 8, Issue 18, 2003.

[4] Stephens, M. A. “Use of the Kolmogorov-Smirnov, Cramer-Von Mises and Related Statistics Without Extensive Tables.” *Journal of the Royal Statistical Society*. Series B, Vol. 32, No. 1, 1970, pp. 115–122.

How To

- `kstest`
- `lillietest`

kurtosis

Purpose

Kurtosis

Syntax

```
k = kurtosis(X)
k = kurtosis(X,flag)
k = kurtosis(X,flag,dim)
```

Description

`k = kurtosis(X)` returns the sample kurtosis of `X`. For vectors, `kurtosis(x)` is the kurtosis of the elements in the vector `x`. For matrices `kurtosis(X)` returns the sample kurtosis for each column of `X`. For N-dimensional arrays, `kurtosis` operates along the first nonsingleton dimension of `X`.

`k = kurtosis(X,flag)` specifies whether to correct for bias (`flag` is `0`) or not (`flag` is `1`, the default). When `X` represents a sample from a population, the kurtosis of `X` is biased, that is, it will tend to differ from the population kurtosis by a systematic amount that depends on the size of the sample. You can set `flag` to `0` to correct for this systematic bias.

`k = kurtosis(X,flag,dim)` takes the kurtosis along dimension `dim` of `X`.

`kurtosis` treats `NaN`s as missing values and removes them.

Algorithms

Kurtosis is a measure of how outlier-prone a distribution is. The kurtosis of the normal distribution is 3. Distributions that are more outlier-prone than the normal distribution have kurtosis greater than 3; distributions that are less outlier-prone have kurtosis less than 3.

The kurtosis of a distribution is defined as

$$k = \frac{E(x-\mu)^4}{\sigma^4}$$

where μ is the mean of x, σ is the standard deviation of x, and $E(t)$ represents the expected value of the quantity t. `kurtosis` computes a sample version of this population value.

Note Some definitions of kurtosis subtract 3 from the computed value, so that the normal distribution has kurtosis of 0. The `kurtosis` function does not use this convention.

When you set `flag` to 1, the following equation applies:

$$k_1 = \frac{\frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^4}{\left(\frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^2\right)^2}$$

When you set `flag` to 0, the following equation applies:

$$k_0 = \frac{n-1}{(n-2)(n-3)}\left((n+1)k_1 - 3(n-1)\right) + 3$$

This bias-corrected formula requires that `X` contain at least four elements.

Examples

```
X = randn([5 4])
X =
  1.1650  1.6961  -1.4462  -0.3600
  0.6268  0.0591  -0.7012  -0.1356
  0.0751  1.7971  1.2460  -1.3493
  0.3516  0.2641  -0.6390  -1.2704
  -0.6965  0.8717  0.5774  0.9846

k = kurtosis(X)
k =
  2.1658  1.2967  1.6378  1.9589
```

See Also

`mean` | `moment` | `skewness` | `std` | `var`

categorical.labels property

Purpose Text labels for levels

Description Text labels for levels. Access labels with `getlabels`.

Purpose

Regularized least-squares regression using lasso or elastic net algorithms

Syntax

```
B = lasso(X,Y)
[B,FitInfo] = lasso(X,Y)
[B,FitInfo] = lasso(X,Y,Name,Value)
```

Description

`B = lasso(X,Y)` returns fitted least-squares regression coefficients for a set of regularization coefficients `Lambda`.

`[B,FitInfo] = lasso(X,Y)` returns a structure containing information about the fits.

`[B,FitInfo] = lasso(X,Y,Name,Value)` fits regularized regressions with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`X`

Numeric matrix with `n` rows and `p` columns. Each row represents one observation, and each column represents one predictor (variable).

`Y`

Numeric vector of length `n`, where `n` is the number of rows of `X`. `Y(i)` is the response to row `i` of `X`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`Alpha`

Scalar value from `0` to `1` (excluding `0`) representing the weight of lasso (L^1) versus ridge (L^2) optimization. `Alpha = 1` represents lasso regression, `Alpha` close to `0` approaches ridge regression, and

other values represent elastic net optimization. See "Definitions" on page 20-902.

Default: `1`

`CV`

Method `lasso` uses to estimate mean squared error:

- `K`, a positive integer — `lasso` uses `K`-fold cross validation.
- `cvp`, a `cvpartition` object — `lasso` uses the cross-validation method expressed in `cvp`. You cannot use a `'leaveout'` partition with `lasso`.
- `'resubstitution'` — `lasso` uses `X` and `Y` to fit the model and to estimate the mean squared error, without cross validation.

Default: `'resubstitution'`

`DFmax`

Maximum number of nonzero coefficients in the model. `lasso` returns results only for `Lambda` values that satisfy this criterion.

Default: `Inf`

`Lambda`

Vector of nonnegative `Lambda` values. See "Definitions" on page 20-902.

- If you do not supply `Lambda`, `lasso` calculates the largest value of `Lambda` that gives a nonnull model. In this case, `LambdaRatio` gives the ratio of the smallest to the largest value of the sequence, and `NumLambda` gives the length of the vector.
- If you supply `Lambda`, `lasso` ignores `LambdaRatio` and `NumLambda`.

Default: Geometric sequence of `NumLambda` values, the largest just sufficient to produce `B = 0`

`LambdaRatio`

Positive scalar, the ratio of the smallest to the largest `Lambda` value when you do not set `Lambda`.

If you set `LambdaRatio = 0`, `lasso` generates a default sequence of `Lambda` values, and replaces the smallest one with `0`.

Default: `1e-4`

`MCReps`

Positive integer, the number of Monte Carlo repetitions for cross validation.

- If `CV` is `'resubstitution'` or a `cvpartition` of type `'resubstitution'`, `MCReps` must be `1`.
- If `CV` is a `cvpartition` of type `'holdout'`, `MCReps` must be greater than `1`.

Default: `1`

`NumLambda`

Positive integer, the number of `Lambda` values `lasso` uses when you do not set `Lambda`.

Default: `100`

`Options`

Structure that specifies whether to cross validate in parallel, and specifies the random stream or streams. Create the `Options` structure with `statset`. Option fields:

- `UseParallel` — Set to `'always'` to compute in parallel. Default is `'never'`.
- `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. Default is `'never'`.
- `Streams` — A `RandStream` object or cell array consisting of one such object. If you do not specify `Streams`, `lasso` uses the default stream.

For details on using parallel computing, see Chapter 17, "Parallel Statistics".

`PredictorNames`

Cell array of strings representing names of the predictor variables, in the order in which they appear in `X`.

Default: `{}`

`RelTol`

Convergence threshold for the coordinate descent algorithm (see Friedman, Tibshirani, and Hastie [3]). The algorithm terminates when successive estimates of the coefficient vector differ in the L^2 norm by a relative amount less than `RelTol`.

Default: `1e-4`

`Standardize`

Boolean value specifying whether `lasso` scales `X` and `Y` before fitting the models. `lasso` always centers the data before fitting.

Default: `true`

`Weights`

Observation weights, a nonnegative vector of length `n`, where `n` is the number of rows of `X`. `lasso` scales `Weights` to sum to `1`.

Default: `1/n * ones(n,1)`

Output Arguments

`B`

Fitted coefficients, a `p`-by-`L` matrix, where `p` is the number of predictors (columns) in `X`, and `L` is the number of `Lambda` values.

`FitInfo`

Structure containing information about the model fits.

Field in FitInfo	Description
`Intercept`	Intercept term β_0 for each linear model, a `1`-by-`L` vector
`Lambda`	Lambda parameters in ascending order, a `1`-by-`L` vector
`Alpha`	Value of `Alpha` parameter, a scalar
`DF`	Number of nonzero coefficients in `B` for each value of `Lambda`, a `1`-by-`L` vector
`MSE`	Mean squared error (MSE), a `1`-by-`L` vector

If you set the `CV` name-value pair to cross validate, the `FitInfo` structure contains additional fields.

Field in FitInfo	Description
`SE`	The standard error of MSE for each `Lambda`, as calculated during cross validation, a `1`-by-`L` vector
`LambdaMinMSE`	The `Lambda` value with minimum MSE, a scalar

Field in FitInfo	Description
`IndexMinMSE`	The largest `Lambda` such that MSE is within one standard error of the minimum, a scalar
`IndexMinMSE`	The index of `Lambda` with value `LambdaMinMSE`, a scalar
`Index1SE`	The index of `Lambda` with value `Lambda1SE`, a scalar

Definitions

Lasso

For a given value of λ, a nonnegative parameter, `lasso` solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{2N}\sum_{i=1}^{N}\left(y_i-\beta_0-x_i^T\beta\right)+\lambda\sum_{j=1}^{p}\left|\beta_j\right|\right),$$

where

- N is the number of observations.
- y_i is the response at observation i.
- x_i is data, a vector of p values at observation i.
- λ is a nonnegative regularization parameter corresponding to one value of `Lambda`.
- The parameters β_0 and β are scalar and p-vector respectively.

As λ increases, the number of nonzero components of β decreases.

The lasso problem involves the L^1 norm of β, as contrasted with the elastic net algorithm.

Elastic Net

For an α strictly between 0 and 1, and a nonnegative λ, elastic net solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{2N}\sum_{i=1}^{N}\left(y_i-\beta_0-x_i^T\beta\right)+\lambda P_\alpha(\beta)\right),$$

where

$$P_\alpha(\beta)=\frac{(1-\alpha)}{2}\|\beta\|_2^2+\alpha\|\beta\|_1=\sum_{j=1}^{p}\left(\frac{(1-\alpha)}{2}\beta_j^2+\alpha\left|\beta_j\right|\right).$$

Elastic net is the same as lasso when $\alpha = 1$. As α shrinks toward 0, elastic net approaches `ridge` regression. For other values of α, the penalty term $P_\alpha(\beta)$ interpolates between the L^1 norm of β and the squared L^2 norm of β.

Examples

Construct a data set with redundant predictors, and identify those predictors using cross-validated `lasso`:

```
X = randn(100,5);
r = [0;2;0;-3;0]; % only two nonzero coefficients
Y = X*r + randn(100,1)*.1; % small added noise
[b fitinfo] = lasso(X,Y,'CV',10);
lam = fitinfo.Index1SE; % find index of suggested lambda
b(:,lam)

ans =
         0
    1.9642
         0
   -2.9636
         0
```

`lasso` identifies and removes the redundant predictors.

References

[1] Tibshirani, R. *Regression shrinkage and selection via the lasso.* Journal of the Royal Statistical Society, Series B, Vol 58, No. 1, pp. 267–288, 1996.

[2] Zou, H. and T. Hastie. *Regularization and variable selection via the elastic net.* Journal of the Royal Statistical Society, Series B, Vol. 67, No. 2, pp. 301–320, 2005.

[3] Friedman, J., R. Tibshirani, and T. Hastie. *Regularization paths for generalized linear models via coordinate descent.* Journal of Statistical Software, Vol 33, No. 1, 2010. `http://www.jstatsoft.org/v33/i01`

[4] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning,* 2nd edition. Springer, New York, 2008.

See Also

`lassoPlot | ridge`

How To

- "Lasso and Elastic Net" on page 9-32

Purpose

Trace plot of lasso fit

Syntax

```
ax = lassoPlot(B)
ax = lassoPlot(B,FitInfo)
ax = lassoPlot(B,FitInfo,Name,Value)
[ax,figh] = lassoPlot(B,...)
```

Description

`ax = lassoPlot(B)` creates a trace plot of the values in `B` against the L^1 norm of `B`. `ax` is a handle to the plot axis.

`ax = lassoPlot(B,FitInfo)` creates a plot with type depending on the data type of `FitInfo` and the value, if any, of the `plotType` name-value pair.

`ax = lassoPlot(B,FitInfo,Name,Value)` creates a plot with additional options specified by one or more `Name,Value` pair arguments.

`[ax,figh] = lassoPlot(B,...)` returns a handle to the figure window.

Input Arguments

`B`

Coefficients of a sequence of regression fits, as returned from the `lasso` function. `B` is a `p`-by-`NLambda` matrix, where `p` is the number of predictors, and each column of `B` is a set of coefficients `lasso` calculates using one `Lambda` penalty value.

`FitInfo`

Information controlling the plot:

- `FitInfo` is a structure, especially as returned from `lasso` — `lassoPlot` creates a plot based on the `PlotType` name-value pair.
- `FitInfo` is a vector — `lassoPlot` forms the x-axis of the plot from the values in `FitInfo`. The length of `FitInfo` must equal the number of columns of `B`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`Parent`

Axis in which to draw the plot.

Default: New plot

`PlotType`

Choose the plot type when you give a `FitInfo` vector or structure:

FitInfo Type	PlotType	Plot
Vector or Structure	`'L1'`	`plotLasso` creates the x-axis from the L^1 norm of the coefficients in `B`. The x-axis at the top of the plot contains the degrees of freedom (`df`), meaning the number of nonzero coefficients of `B`.
Structure	`'Lambda'`	`plotLasso` creates the x-axis from the `Lambda` field of `FitInfo`. The x-axis at the top of the plot contains the degrees of freedom (`df`), meaning the number of nonzero coefficients of `B`.
Cross-Validated Structure	`'CV'`	• For each `Lambda`, plots an estimate of the mean squared prediction error on new data for the model fitted by `lasso` with that value of `Lambda`. • Plots error bars for the estimates. • Plots the value of `Lambda` with minimum cross-validated MSE. • Plots the greatest `Lambda` that is within one standard error of minimum MSE (so makes the sparsest model within that region).

Default: `'L1'`

`PredictorNames`

Cell array of strings to label each coefficient of `B`. If the length of `PredictorNames` is less than the number of rows of `B`, the remaining labels are padded with default values.

`lassoPlot` uses the predictor names in `FitInfo` only if:

- You created `FitInfo` with a call to `lasso` that included a `PredictorNames` name-value pair.
- You call `lassoPlot` *without* a `PredictorNames` name-value pair.
- You include `FitInfo` in your `lassoPlot` call.

Default: `{'B1','B2',...}`

`XScale`

- `'linear'` for linear x-axis
- `'log'` for logarithmic scaled x-axis

Default: `'linear'`, except `'log'` for the `'CV'` plot type

Output Arguments

`ax`

Handle to the axis of the plot (see "Setting Axis Parameters").

`figh`

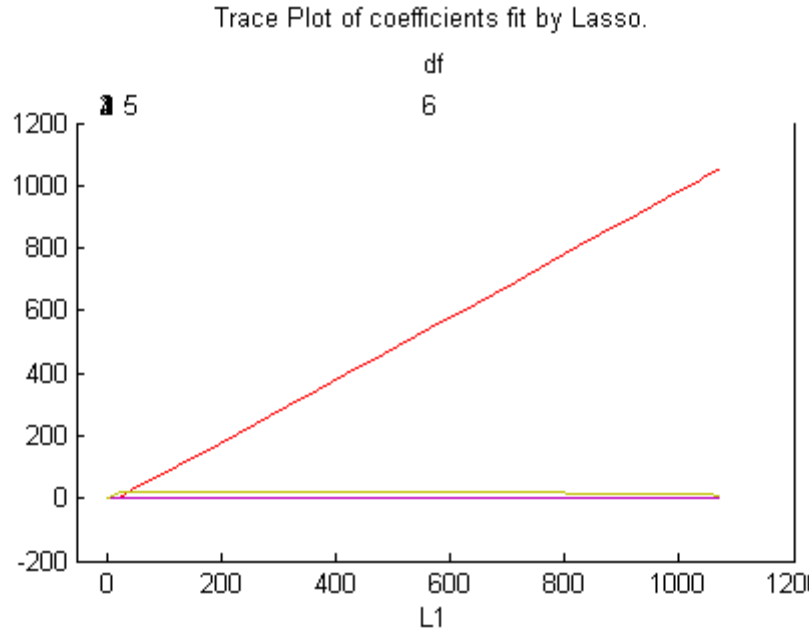
Handle to the figure window (see "Graphics Windows — the Figure").

Examples

Fit a regularized model of the `acetylene` data with `lasso`, and plot the fits with the default plot type:

```
load acetylene
```

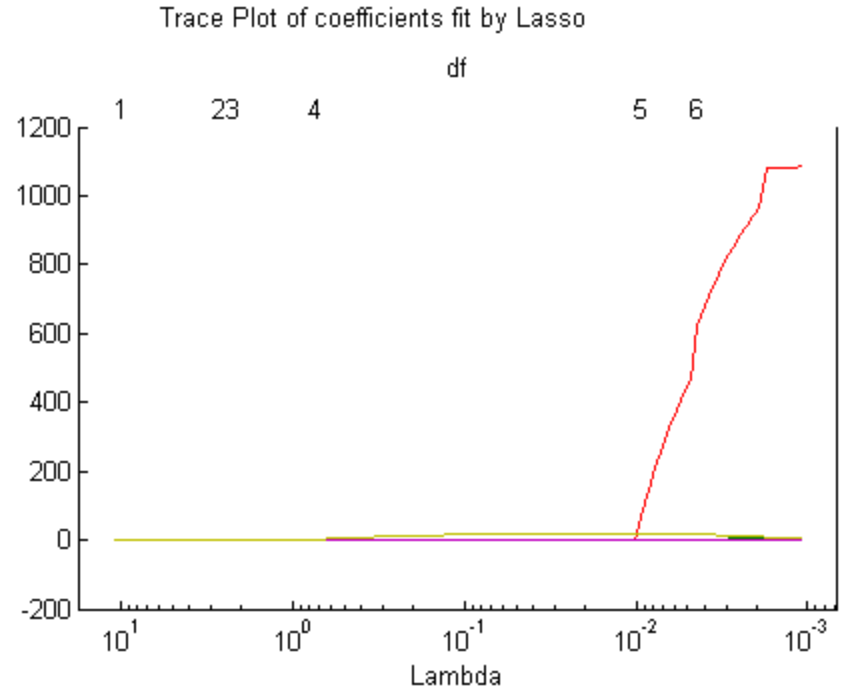
```
X = [x1 x2 x3];
D = x2fx(X,'interaction');
D(:,1) = []; % No constant term
B = lasso(D,y);
lassoPlot(B);
```



Fit a regularized model of the `acetylene` data with `lasso`, and plot the fits with the `Lambda` plot type and logarithmic scaling:

```
load acetylene
X = [x1 x2 x3];
D = x2fx(X,'interaction');
D(:,1) = []; % No constant term
```

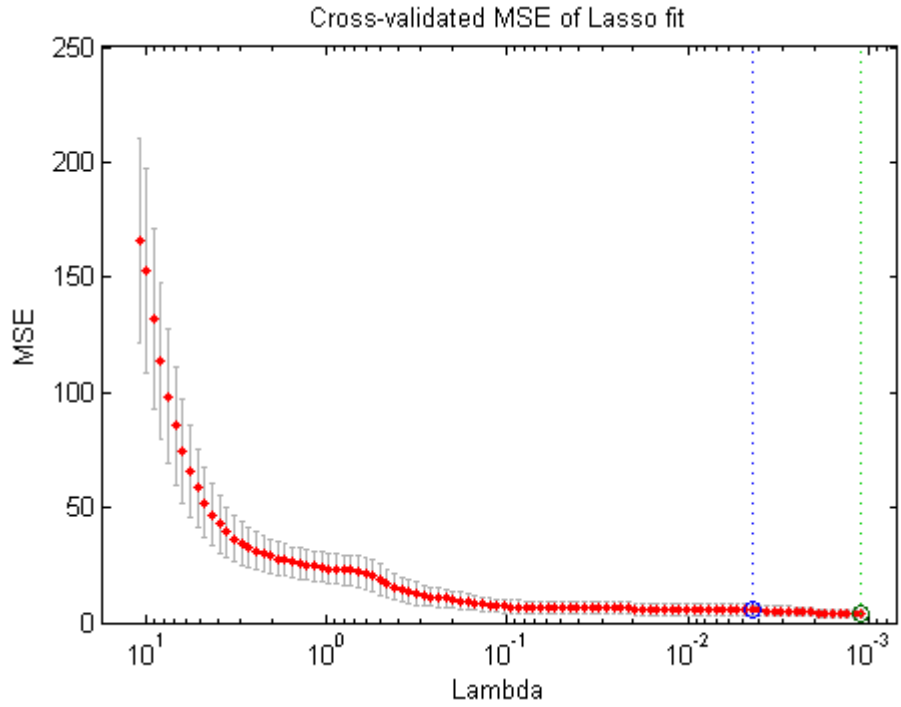
```
[B FitInfo] = lasso(D,y);
lassoPlot(B,FitInfo,'PlotType','Lambda','XScale','log');
```



Fit a regularized model of the `acetylene` data with `lasso` and cross validation, and plot the cross-validated fits:

```
load acetylene
X = [x1 x2 x3];
D = x2fx(X,'interaction');
D(:,1) = []; % No constant term
[B FitInfo] = lasso(D,y,'CV',10);
```

```
lassoPlot(B,FitInfo,'PlotType','CV');
```



See Also

`lasso`

How To

- “Lasso and Elastic Net” on page 9-32

Purpose

Less than or equal relation for handles

Syntax

```
h1 <= h2
```

Description

Handles are equal if they are handles for the same object. All comparisons use a number associated with each handle object. Nothing can be assumed about the result of a handle comparison except that the repeated comparison of two handles in the same MATLAB session will yield the same result. The order of handle values is purely arbitrary and has no connection to the state of the handle objects being compared.

`h1 <= h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise `<=` result.

If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = le(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `eq` | `ge` | `gt` | `lt` | `ne`

qrandset.Leap property

Purpose

Interval between points

Description

Number of points to leap over and omit for each point taken from the sequence. The `Leap` property of a point set contains a positive integer which specifies the number of points in the sequence to leap over and omit for every point taken. The default `Leap` value is 0, which corresponds to taking every point from the sequence.

Leaping is a technique used to improve the quality of a point set. However, you must choose the `Leap` values with care; many `Leap` values create sequences that fail to touch on large sub-hyper-rectangles of the unit hypercube, and so fail to be a uniform quasi-random point set.

Choosing Leap Values for Halton Sets

A known rule for choosing `Leap` values for Halton sets is to set it to (`P`-1) where `P` is a prime number that has not been used to generate one of the dimensions, i.e. for a `k`-dimensional point set `P` would be the (`k`+1)th or greater prime.

Examples

Experiment with different leap values:

```
% No leaping produces the standard Halton sequence.
P = haltonset(5);
P(1:5,:)

% Set a leap of 1.  The point set now includes every other
% point from the sequence.
P.Leap = 1;
P(1:5,:)
```

See Also

`net` | `qrandset` | `Skip` | `subsref` | `haltonset`

Purpose

Length of dataset array

Syntax

```
n = length(A)
```

Description

`n = length(A)` returns the number of observations in the dataset `A`. `length` is equivalent to `size(A,1)`.

See Also

`size`

qrandset.length

Purpose

Length of point set

Syntax

```
length(p)
```

Description

`length(p)` returns the number of points in the point set `p`. It is equivalent to `size(p, 1)`.

See Also

`qrandset` | `size`

Purpose

Length of categorical array

Syntax

```
n = length(A)
```

Description

`n = length(A)` returns the size of the longest dimension of the categorical array `A` when `A` is not empty. If `A` is a vector, this is the same as its length. `length` is equivalent to `max(size(x))` for nonempty arrays, and 0 for empty arrays.

See Also

`isempty` | `isscalar` | `size`

categorical.levelcounts

Purpose

Element counts by level

Syntax

```
C = levelcounts(A)
C = levelcounts(A,dim)
```

Description

`C = levelcounts(A)` for a categorical vector `A` counts the number of elements in `A` equal to each of the possible levels in `A`. The output is a vector `C` containing those counts, and has as many elements as `A` has levels. For matrix `A`, `C` is a matrix of column counts. For *N*-dimensional arrays, `levelcounts` operates along the first nonsingleton dimension.

`C = levelcounts(A,dim)` operates along the dimension `dim`.

Examples

Count the number of patients in each age group in the data in `hospital.mat`:

```
load hospital
edges = 0:10:100;
labels = strcat(num2str((0:10:90)','%d'),{'s'});
disp(labels')
 '0s' '10s' '20s' '30s' '40s' '50s' '60s' '70s' '80s' '90s'

AgeGroup = ordinal(hospital.Age,labels,[],edges);
I = islevel(labels,AgeGroup);
disp(I')
 0  1  1  1  1  1  1  1  1  1
c = levelcounts(AgeGroup);
disp(c')
 0  0 15 41 42  2  0  0  0  0

AgeGroup = droplevels(AgeGroup);
I = islevel(labels,AgeGroup);
disp(I')
 0  0  1  1  1  1  0  0  0  0
c = levelcounts(AgeGroup);
disp(c')
 15 41 42  2
```

See Also `islevel` | `ismember` | `summary`

leverage

Purpose

Leverage

Syntax

```
h = leverage(data)
h = leverage(data,model)
```

Description

`h = leverage(data)` finds the leverage of each row (point) in the matrix `data` for a linear additive regression model.

`h = leverage(data,model)` finds the leverage on a regression, using a specified model type, where *`model`* can be one of these strings:

- `'linear'` - includes constant and linear terms
- `'interaction'` - includes constant, linear, and cross product terms
- `'quadratic'` - includes interactions and squared terms
- `'purequadratic'` - includes constant, linear, and squared terms

Leverage is a measure of the influence of a given observation on a regression due to its location in the space of the inputs.

Algorithms

```
[Q,R] = qr(x2fx(data,'model'));
leverage = (sum(Q'.*Q'))'
```

Examples

One rule of thumb is to compare the leverage to $2p/n$ where n is the number of observations and p is the number of parameters in the model. For the Hald data set this value is 0.7692.

```
load hald
h = max(leverage(ingredients,'linear'))
h =
  0.7004
```

Since 0.7004 < 0.7692, there are no high leverage points using this rule.

References

[1] Goodall, C. R. “Computation Using the QR Decomposition.” *Handbook in Statistics*. Vol. 9, Amsterdam: Elsevier/North-Holland, 1993.

How To

- `regstats`

lhsdesign

Purpose

Latin hypercube sample

Syntax

```
X = lhsdesign(n,p)
X = lhsdesign(...,'smooth','off')
X = lhsdesign(...,'criterion',criterion)
X = lhsdesign(...,'iterations',k)
```

Description

`X = lhsdesign(n,p)` generates a latin hypercube sample `X` containing `n` values on each of `p` variables. For each column, the `n` values are randomly distributed with one from each interval `(0,1/n)`, `(1/n,2/n)`, ..., `(1-1/n,1)`, and they are randomly permuted.

`X = lhsdesign(...,'smooth','off')` produces points at the midpoints of the above intervals: `0.5/n`, `1.5/n`, ..., `1-0.5/n`. The default is `'on'`.

`X = lhsdesign(...,'criterion',criterion)` iteratively generates latin hypercube samples to find the best one according to the criterion *`criterion`*, which can be one of the following strings.

Criterion	Description
`'none'`	No iteration
`'maximin'`	Maximize minimum distance between points
`'correlation'`	Reduce correlation

`X = lhsdesign(...,'iterations',k)` iterates up to `k` times in an attempt to improve the design according to the specified criterion. The default is `k = 5`.

See Also

`haltonset` | `sobolset` | `lhsnorm` | `unifrnd`

Purpose

Latin hypercube sample from normal distribution

Syntax

```
X = lhsnorm(mu,sigma,n)
X = lhsnorm(mu,sigma,n,flag)
[X,Z] = lhsnorm(...)
```

Description

`X = lhsnorm(mu,sigma,n)` generates a latin hypercube sample `X` of size `n` from the multivariate normal distribution with mean vector `mu` and covariance matrix `sigma`. `X` is similar to a random sample from the multivariate normal distribution, but the marginal distribution of each column is adjusted so that its sample marginal distribution is close to its theoretical normal distribution.

`X = lhsnorm(mu,sigma,n,flag)` controls the amount of smoothing in the sample. If *`flag`* is `'off'`, each column has points equally spaced on the probability scale. In other words, each column is a permutation of the values G`(0.5/n), `G`(1.5/n), ..., `G`(1-0.5/n)` where G is the inverse normal cumulative distribution for that column's marginal distribution. If *`flag`* is `'on'` (the default), each column has points uniformly distributed on the probability scale. For example, in place of `0.5/n` you use a value having a uniform distribution on the interval `(0/n,1/n)`.

`[X,Z] = lhsnorm(...)` also returns `Z`, the original multivariate normal sample before the marginals are adjusted to obtain `X`.

References

[1] Stein, M. "Large sample properties of simulations using latin hypercube sampling." *Technometrics*. Vol. 29, No. 2, 1987, pp. 143–151. Correction, Vol. 32, p. 367.

See Also

`lhsdesign` | `mvnrnd`

lillietest

Purpose

Lilliefors test

Syntax

```
h = lillietest(x)
h = lillietest(x,alpha)
h = lillietest(x,alpha,distr)
[h,p] = lillietest(...)
[h,p,kstat] = lillietest(...)
[h,p,kstat,critval] = lillietest(...)
[h,p,...] = lillietest(x,alpha,distr,mctol)
```

Description

`h = lillietest(x)` performs a Lilliefors test of the default null hypothesis that the sample in vector `x` comes from a distribution in the normal family, against the alternative that it does not come from a normal distribution. The test returns the logical value `h = 1` if it rejects the null hypothesis at the 5% significance level, and `h = 0` if it cannot. The test treats `NaN` values in `x` as missing values, and ignores them.

The Lilliefors test is a 2-sided goodness-of-fit test suitable when a fully-specified null distribution is unknown and its parameters must be estimated. This is in contrast to the one-sample Kolmogorov-Smirnov test (see `kstest`), which requires that the null distribution be completely specified. The Lilliefors test statistic is the same as for the Kolmogorov-Smirnov test:

$$KS = \max_x \left| SCDF(x) - CDF(x) \right|$$

where *SCDF* is the empirical cdf estimated from the sample and *CDF* is the normal cdf with mean and standard deviation equal to the mean and standard deviation of the sample.

`lillietest` uses a table of critical values computed using Monte Carlo simulation for sample sizes less than 1000 and significance levels between 0.001 and 0.50. The table is larger and more accurate than the table introduced by Lilliefors. Critical values for a test are computed by interpolating into the table, using an analytic approximation when extrapolating for larger sample sizes.

`h = lillietest(x,alpha)` performs the test at significance level `alpha`. `alpha` is a scalar in the range [0.001, 0.50]. To perform the test at a significance level outside of this range, use the `mctol` input argument.

`h = lillietest(x,alpha,distr)` performs the test of the null hypothesis that `x` came from the location-scale family of distributions specified by `distr`. Acceptable values for `distr` are `'norm'` (normal, the default), `'exp'` (exponential), and `'ev'` (extreme value). The Lilliefors test can not be used when the null hypothesis is not a location-scale family of distributions.

`[h,p] = lillietest(...)` returns the *p* value `p`, computed using inverse interpolation into the table of critical values. Small values of `p` cast doubt on the validity of the null hypothesis. `lillietest` warns when `p` is not found within the tabulated range of [0.001, 0.50], and returns either the smallest or largest tabulated value. In this case, you can use the `mctol` input argument to compute a more accurate *p* value.

`[h,p,kstat] = lillietest(...)` returns the test statistic `kstat`.

`[h,p,kstat,critval] = lillietest(...)` returns the critical value `critval` for the test. When `kstat` > `critval`, the null hypothesis is rejected at significance level `alpha`

`[h,p,...] = lillietest(x,alpha,distr,mctol)` computes a Monte Carlo approximation for `p` directly, rather than interpolating into the table of pre-computed values. This is useful when `alpha` or `p` lie outside the range of the table. `lillietest` chooses the number of Monte Carlo replications, `mcreps`, large enough to make the Monte Carlo standard error for `p`, `sqrt(p*(1-p)/mcreps)`, less than `mctol`.

Examples

Use `lillietest` to determine if car mileage, in miles per gallon (MPG), follows a normal distribution across different makes of cars:

```
load carbig.mat
[h,p] = lillietest(MPG)
Warning: P is less than the smallest tabulated value, returning 0.001.
h =
     1
```

```
p =
  1.0000e-003
```

This is clear evidence for rejecting the null hypothesis of normality, but the p value returned is just the smallest value in the table of pre-computed values. To find a more accurate p value for the test, run a Monte Carlo approximation using the `mctol` input argument:

```
[h,p] = lillietest(MPG,0.05,'norm',1e-4)
h =
     1
p =
  8.3333e-006
```

References

[1] Conover, W. J. *Practical Nonparametric Statistics.* Hoboken, NJ: John Wiley & Sons, Inc., 1980.

[2] Lilliefors, H. W. "On the Kolmogorov-Smirnov test for the exponential distribution with mean unknown." *Journal of the American Statistical Association.* Vol. 64, 1969, pp. 387–389.

[3] Lilliefors, H. W. "On the Kolmogorov-Smirnov test for normality with mean and variance unknown." *Journal of the American Statistical Association.* Vol. 62, 1967, pp. 399–402.

See Also

`jbtest` | `kstest` | `kstest2` | `cdfplot`

Purpose

Linear hypothesis test

Syntax

```
p = linhyptest(beta,COVB,c,H,dfe)
[p,t,r] = linhyptest(...)
```

Description

`p = linhyptest(beta,COVB,c,H,dfe)` returns the p value `p` of a hypothesis test on a vector of parameters. `beta` is a vector of k parameter estimates. `COVB` is the k-by-k estimated covariance matrix of the parameter estimates. `c` and `H` specify the null hypothesis in the form `H*b = c`, where `b` is the vector of unknown parameters estimated by `beta`. `dfe` is the degrees of freedom for the `COVB` estimate, or `Inf` if `COVB` is known rather than estimated.

`beta` is required. The remaining arguments have default values:

- `COVB = eye(k)`
- `c = zeros(k,1)`
- `H = eye(K)`
- `dfe = Inf`

If `H` is omitted, `c` must have k elements and it specifies the null hypothesis values for the entire parameter vector.

Note The following functions return outputs suitable for use as the `COVB` input argument to `linhyptest`: `nlinfit`, `coxphfit`, `glmfit`, `mnrfit`, `regstats`, `robustfit`. `nlinfit` returns `COVB` directly; the other functions return `COVB` in `stats.covb`.

`[p,t,r] = linhyptest(...)` also returns the test statistic `t` and the rank `r` of the hypothesis matrix `H`. If `dfe` is `Inf` or is not given, `t*r` is a chi-square statistic with `r` degrees of freedom . If `dfe` is specified as a finite value, `t` is an F statistic with `r` and `dfe` degrees of freedom.

`linhyptest` performs a test based on an asymptotic normal distribution for the parameter estimates. It can be used after any estimation procedure for which the parameter covariances are available, such as `regstats` or `glmfit`. For linear regression, the *p*-values are exact. For other procedures, the *p*-values are approximate, and may be less accurate than other procedures such as those based on a likelihood ratio.

Examples

Fit a multiple linear model to the data in `hald.mat`:

```
load hald
stats = regstats(heat,ingredients,'linear');
beta = stats.beta
beta =
   62.4054
    1.5511
    0.5102
    0.1019
   -0.1441
```

Perform an *F*-test that the last two coefficients are both 0:

```
SIGMA = stats.covb;
dfe = stats.fstat.dfe;
H = [0 0 0 1 0;0 0 0 0 1];
c = [0;0];
[p,F] = linhyptest(beta,SIGMA,c,H,dfe)
p =
    0.4668
F =
    0.8391
```

See Also

`regstats` | `glmfit` | `robustfit` | `mnrfit` | `nlinfit` | `coxphfit`

Purpose

Agglomerative hierarchical cluster tree

Syntax

```
Z = linkage(X)
Z = linkage(X,method)
Z = linkage(X,method,metric)
Z = linkage(X,method,pdist_inputs)
Z = linkage(X,method,metric,'savememory',value)
Z = linkage(Y)
Z = linkage(Y,method)
```

Description

`Z = linkage(X)` returns a matrix `Z` that encodes a tree of hierarchical clusters of the rows of the real matrix `X`.

`Z = linkage(X,method)` creates the tree using the specified *`method`*, where *`method`* describes how to measure the distance between clusters.

`Z = linkage(X,method,metric)` performs clustering using the distance measure `metric` to compute distances between the rows of `X`.

`Z = linkage(X,method,pdist_inputs)` passes parameters to the `pdist` function, which is the function that computes the distance between rows of `X`.

`Z = linkage(X,method,metric,'savememory',value)` uses a memory-saving algorithm when *`value`* is `'true'`, and uses the standard algorithm when *`value`* is `'false'`.

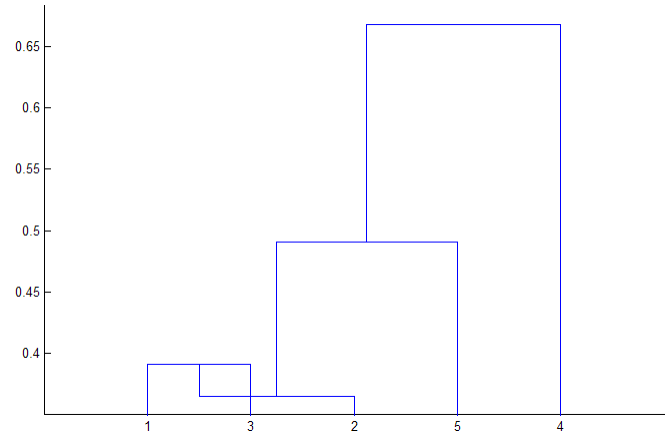
`Z = linkage(Y)` uses a vector representation `Y` of a distance matrix. `Y` can be a distance matrix as computed by `pdist`, or a more general dissimilarity matrix conforming to the output format of `pdist`.

`Z = linkage(Y,method)` creates the tree using the specified *`method`*, where *`method`* describes how to measure the distance between clusters.

Tips

- Computing `linkage(Y)` can be slow when `Y` is a vector representation of the distance matrix. For the `'centroid'`, `'median'`, and `'ward'` methods, `linkage` checks whether `Y` is a Euclidean distance. Avoid this time-consuming check by passing in `X` instead of `Y`.

- The `centroid` and `median` methods can produce a cluster tree that is not monotonic. This occurs when the distance from the union of two clusters, *r* and *s*, to a third cluster is less than the distance between *r* and *s*. In this case, in a dendrogram drawn with the default orientation, the path from a leaf to the root node takes some downward steps. To avoid this, use another method. The following image shows a nonmonotonic cluster tree.



In this case, cluster 1 and cluster 3 are joined into a new cluster, while the distance between this new cluster and cluster 2 is less than the distance between cluster 1 and cluster 3. This leads to a nonmonotonic tree.

- You can provide the output `Z` to other functions including `dendrogram` to display the tree, `cluster` to assign points to clusters, `inconsistent` to compute inconsistent measures, and `cophenet` to compute the cophenetic correlation coefficient.

Input Arguments

`X`

Matrix with two or more rows. The rows represent observations, the columns represent categories or dimensions.

`method`

Algorithm for computing distance between clusters.

Method	Description
`'average'`	Unweighted average distance (UPGMA)
`'centroid'`	Centroid distance (UPGMC), appropriate for Euclidean distances only
`'complete'`	Furthest distance
`'median'`	Weighted center of mass distance (WPGMC), appropriate for Euclidean distances only
`'single'`	Shortest distance
`'ward'`	Inner squared distance (minimum variance algorithm), appropriate for Euclidean distances only
`'weighted'`	Weighted average distance (WPGMA)

Default: `'single'`

`metric`

Any distance metric that the `pdist` function accepts.

Metric	Description
`'euclidean'`	Euclidean distance (default).
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between rows in X is scaled by dividing by the corresponding element of the standard deviation `S=nanstd(X)`. To specify another value for `S`, use `D=pdist(X,'seuclidean',S)`.
`'cityblock'`	City block metric.

Metric	Description
`'minkowski'`	Minkowski distance. The default exponent is 2. To specify a different exponent, use `D = pdist(X,'minkowski',P)`, where `P` is a
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'mahalanobis'`	Mahalanobis distance, using the sample covariance of `X` as computed by `nancov`. To compute the distance with a different covariance, use `D = pdist(X,'mahalanobis',C)`, where the matrix `C` is symmetric and positive definite.
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors).
`'correlation'`	One minus the sample correlation between points (treated as sequences of values).
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).
`'hamming'`	Hamming distance, which is the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.

custom distance function	A distance function specified using @:
	`D = pdist(X,@distfun)`
	A distance function must be of form
	`d2 = distfun(XI,XJ)`
	taking as arguments a 1-by-*n* vector `XI`, corresponding to a single row of `X`, and

Metric	Description
	an m2-by-n matrix `XJ`, corresponding to multiple rows of `X`. `distfun` must accept a matrix `XJ` with an arbitrary number of rows. `distfun` must return an m2-by-1 vector of distances `d2`, whose kth element is the distance between `XI` and `XJ(k,:)`.

Default: `'euclidean'`

`pdist_inputs`

A cell array of parameters accepted by the `pdist` function. For example, to set the *`metric`* to `minkowski` and use an exponent of `5`, set `pdist_inputs` to `{'minkowski',5}`.

`savememory`

A string, either `'on'` or `'off'`. When applicable, the `'on'` setting causes `linkage` to construct clusters without computing the distance matrix. `savememory` is applicable when:

- `linkage` is `'centroid'`, `'median'`, or `'ward'`
- `distance` is `'euclidean'` (default)

When `savememory` is `'on'`, `linkage` run time is proportional to the number of dimensions (number of columns of `X`). When `savememory` is `'off'`, `linkage` memory requirement is proportional to `N`^{2}, where `N` is the number of observations. So choosing the best (least-time) setting for `savememory` depends on the problem dimensions, number of observations, and available memory. The default `savememory` setting is a rough approximation of an optimal setting.

Default: `'on'` when `X` has 20 columns or fewer, or the computer does not have enough memory to store the distance matrix; otherwise `'off'`

`Y`

A vector of distances with the same format as the output of the `pdist` function:

- A row vector of length $m(m-1)/2$, corresponding to pairs of observations in a matrix `X` with m rows
- Distances arranged in the order (2,1), (3,1), ..., (m,1), (3,2), ..., (m,2), ..., (m,m–1))

`Y` can be a more general dissimilarity matrix conforming to the output format of `pdist`.

Output Arguments

`Z`

`Z` is a (`m` – 1)-by-3 matrix, where `m` is the number of observations in the original data. Columns 1 and 2 of `Z` contain cluster indices linked in pairs to form a binary tree. The leaf nodes are numbered from 1 to `m`. Leaf nodes are the singleton clusters from which all higher clusters are built. Each newly-formed cluster, corresponding to row `Z(I,:)`, is assigned the index `m+I`. `Z(I,1:2)` contains the indices of the two component clusters that form cluster `m+I`. There are `m`-1 higher clusters which correspond to the interior nodes of the clustering tree. `Z(I,3)` contains the linkage distances between the two clusters merged in row `Z(I,:)`.

For example, suppose there are 30 initial nodes and at step 12 cluster 5 and cluster 7 are combined. Suppose their distance at that time is 1.5. Then `Z(12,:)` will be `[5, 7, 1.5]`. The newly formed cluster will have index 12 + 30 = 42. If cluster 42 appears in a later row, it means the cluster created at step 12 is being combined into some larger cluster.

Definitions

Linkages

The following notation is used to describe the linkages used by the various methods:

- Cluster `r` is formed from clusters `p` and `q`.
- n_r is the number of objects in cluster r.
- x_{ri} is the `i`th object in cluster `r`.
- *Single linkage*, also called *nearest neighbor*, uses the smallest distance between objects in the two clusters:

$$d(r,s) = \min(dist(x_{ri}, x_{sj})), i \in (i,...,n_r), j \in (1,...,n_s)$$

- *Complete linkage*, also called *furthest neighbor*, uses the largest distance between objects in the two clusters:

$$d(r,s) = \max(dist(x_{ri}, x_{sj})), i \in (1,...,n_r), j \in (1,...,n_s)$$

- *Average linkage* uses the average distance between all pairs of objects in any two clusters:

$$d(r,s) = \frac{1}{n_r n_s} \sum_{i=1}^{n_r} \sum_{j=1}^{n_s} dist(x_{ri}, x_{sj})$$

- *Centroid linkage* uses the Euclidean distance between the centroids of the two clusters:

$$d(r,s) = \left\| \bar{x}_r - \bar{x}_s \right\|_2$$

  where

$$\bar{x}_r = \frac{1}{n_r} \sum_{i=1}^{n_r} x_{ri}$$

- *Median linkage* uses the Euclidean distance between weighted centroids of the two clusters,

$$d(r,s) = \left\| \tilde{x}_r - \tilde{x}_s \right\|_2$$

where $\tilde{x}_r$ and $\tilde{x}_s$ are weighted centroids for the clusters *r* and *s*. If cluster *r* was created by combining clusters *p* and *q*, $\tilde{x}_r$ is defined recursively as

$$\tilde{x}_r = \frac{1}{2}(\tilde{x}_p + \tilde{x}_q)$$

- *Ward's linkage* uses the incremental sum of squares; that is, the increase in the total within-cluster sum of squares as a result of joining two clusters. The within-cluster sum of squares is defined as the sum of the squares of the distances between all objects in the cluster and the centroid of the cluster. The sum of squares measure is equivalent to the following distance measure $d(r,s)$, which is the formula `linkage` uses:

  $$d(r,s) = \sqrt{\frac{2n_r n_s}{(n_r + n_s)}} \left\| \bar{x}_r - \bar{x}_s \right\|_2,$$

  where

  - $\| \ \|_2$ is Euclidean distance
  - $\bar{x}_r$ and $\bar{x}_s$ are the centroids of clusters *r* and *s*
  - n_r and n_s are the number of elements in clusters *r* and *s*

  In some references the Ward linkage does not use the factor of 2 multiplying $n_r n_s$. The `linkage` function uses this factor so the distance between two singleton clusters is the same as the Euclidean distance.

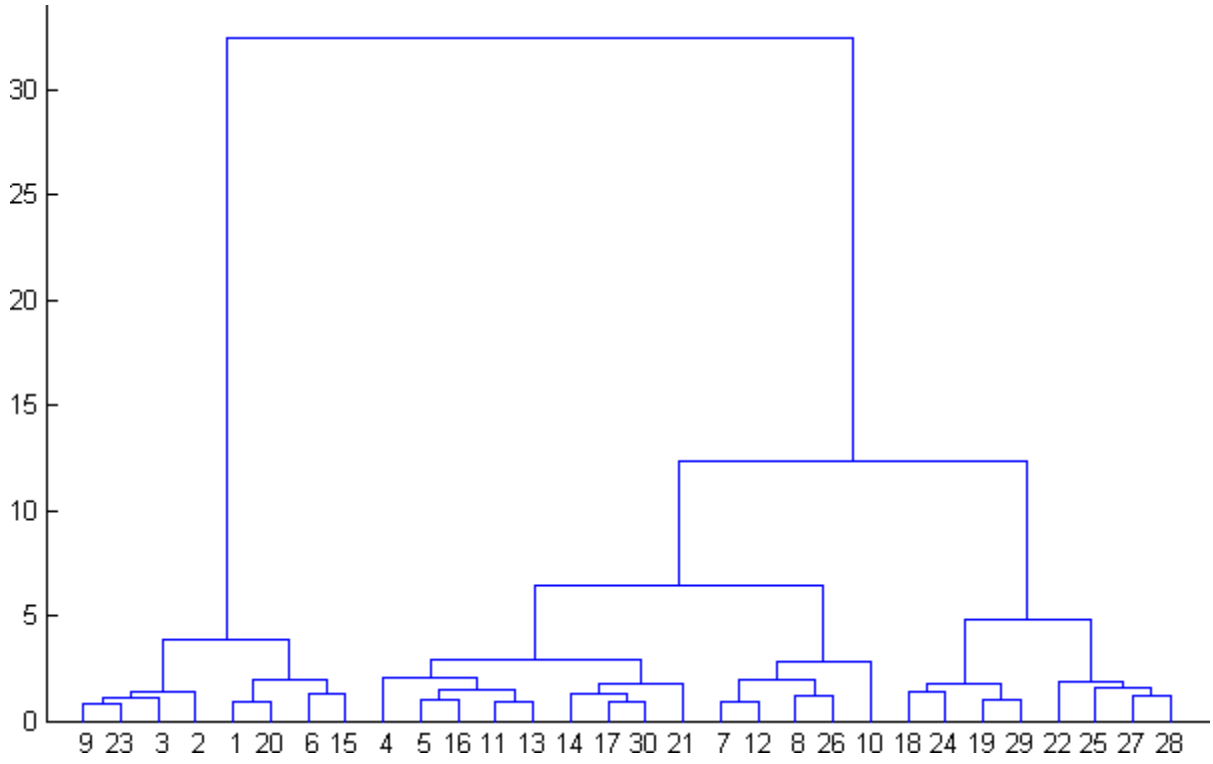
- *Weighted average linkage* uses a recursive definition for the distance between two clusters. If cluster *r* was created by combining clusters *p* and *q*, the distance between *r* and another cluster *s* is defined as the average of the distance between *p* and *s* and the distance between *q* and *s*:

$$d(r,s) = \frac{\left(d(p,s) + d(q,s)\right)}{2}$$

Examples

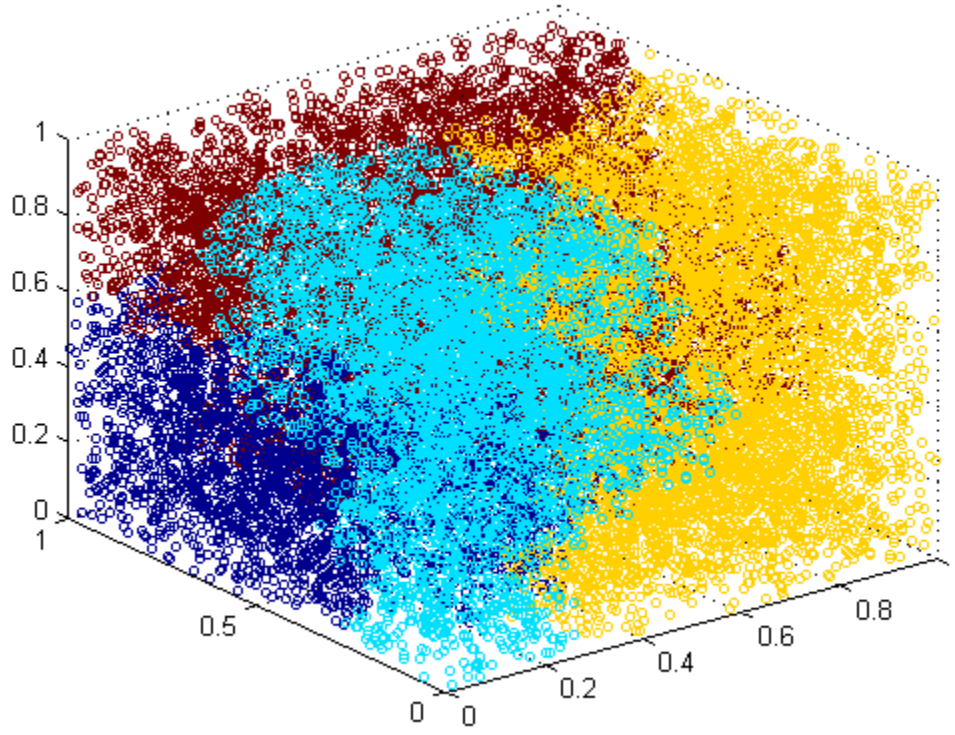
Compute four clusters of the Fisher iris data using Ward linkage and ignoring species information, and see how the cluster assignments correspond to the three species.

```
load fisheriris
Z = linkage(meas,'ward','euclidean');
c = cluster(Z,'maxclust',4);
crosstab(c,species)
firstfive = Z(1:5,:) % first 5 rows of Z
dendrogram(Z)

ans =
     0    25     1
     0    24    14
     0     1    35
    50     0     0

firstfive =
  102.0000  143.0000         0
    8.0000   40.0000    0.1000
    1.0000   18.0000    0.1000
   10.0000   35.0000    0.1000
  129.0000  133.0000    0.1000
```



Create a hierarchical cluster tree for a data with 20000 observations using Ward's linkage. If you set `savememory` to `'off'`, you can get an out-of-memory error if your machine doesn't have enough memory to hold the distance matrix. Cluster the data into four groups and plot the result.

```
X = rand(20000,3);
Z = linkage(X,'ward','euclidean','savememory','on');
c = cluster(Z,'maxclust',4);
scatter3(X(:,1),X(:,2),X(:,3),10,c)
```



See Also

`cluster` | `clusterdata` | `cophenet` | `dendrogram` | `inconsistent` | `kmeans` | `pdist` | `silhouette` | `squareform`

How To

- Chapter 11, “Cluster Analysis”

logncdf

Purpose

Lognormal cumulative distribution function

Syntax

```
P = logncdf(X,mu,sigma)
[P,PLO,PUP] = logncdf(X,mu,sigma,pcov,alpha)
```

Description

`P = logncdf(X,mu,sigma)` returns values at X of the lognormal cdf with distribution parameters `mu` and `sigma`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution. `X`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `X`, `mu`, or `sigma` is expanded to a constant array with the same dimensions as the other inputs.

`[P,PLO,PUP] = logncdf(X,mu,sigma,pcov,alpha)` returns confidence bounds for `P` when the input parameters `mu` and `sigma` are estimates. `pcov` is the covariance matrix of the estimated `parameters`. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is 0.05. `PLO` and `PUP` are arrays of the same size as `P` containing the lower and upper confidence bounds.

`logncdf` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\frac{X - \hat{\mu}}{\hat{\sigma}}$$

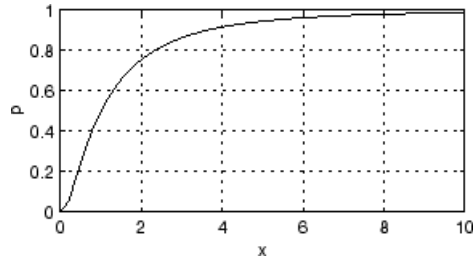
and then transforming those bounds to the scale of the output `P`. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The lognormal cdf is

$$p = F(x \mid \mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}} \int_0^x \frac{e^{\frac{-(\ln(t)-\mu)^2}{2\sigma^2}}}{t} dt$$

Examples

```
x = (0:0.2:10);
y = logncdf(x,0,1);
plot(x,y); grid;
xlabel('x'); ylabel('p');
```



References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 102–105.

See Also

`cdf` | `lognpdf` | `logninv` | `lognstat` | `lognfit` | `lognlike` | `lognrnd`

How To

- "Lognormal Distribution" on page B-51

lognfit

Purpose

Lognormal parameter estimates

Syntax

```
parmhat = lognfit(data)
[parmhat,parmci] = lognfit(data)
[parmhat,parmci] = lognfit(data,alpha)
[...] = lognfit(data,alpha,censoring)
[...] = lognfit(data,alpha,censoring,freq)
[...] = lognfit(data,alpha,censoring,freq,options)
```

Description

`parmhat = lognfit(data)` returns a vector of maximum likelihood estimates `parmhat(1) = mu` and `parmhat(2) = sigma` of parameters for a lognormal distribution fitting `data`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution.

`[parmhat,parmci] = lognfit(data)` returns 95% confidence intervals for the parameter estimates `mu` and `sigma` in the 2-by-2 matrix `parmci`. The first column of the matrix contains the lower and upper confidence bounds for parameter `mu`, and the second column contains the confidence bounds for parameter `sigma`.

`[parmhat,parmci] = lognfit(data,alpha)` returns 100(1 - `alpha`) % confidence intervals for the parameter estimates, where `alpha` is a value in the range `(0 1)` specifying the width of the confidence intervals. By default, `alpha` is `0.05`, which corresponds to 95% confidence intervals.

`[...] = lognfit(data,alpha,censoring)` accepts a Boolean vector `censoring`, of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = lognfit(data,alpha,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. Typically, `freq` contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `alpha`, `censoring`, or `freq` to use their default values.

`[...] = lognfit(data,alpha,censoring,freq,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates when there is censoring. The lognormal fit function accepts an `options`

structure which can be created using the function `statset`. Enter `statset('lognfit')` to see the names and default values of the parameters that `lognfit` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

Examples

This example generates 100 independent samples of lognormally distributed data with $\mu = 0$ and $\sigma = 3$. `parmhat` estimates μ and σ and `parmci` gives 99% confidence intervals around `parmhat`. Notice that `parmci` contains the true values of μ and σ.

```
data = lognrnd(0,3,100,1);
[parmhat,parmci] = lognfit(data,0.01)
parmhat =
  -0.2480  2.8902
parmci =
  -1.0071  2.4393
   0.5111  3.5262
```

See Also

`mle` | `lognlike` | `lognpdf` | `logncdf` | `logninv` | `lognstat` | `lognrnd`

How To

- “Lognormal Distribution” on page B-51

logninv

Purpose

Lognormal inverse cumulative distribution function

Syntax

```
X = logninv(P,mu,sigma)
[X,XLO,XUP] = logninv(P,mu,sigma,pcov,alpha)
```

Description

`X = logninv(P,mu,sigma)` returns values at `P` of the inverse lognormal cdf with distribution parameters `mu` and `sigma`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `X`. A scalar input for `P`, `mu`, or `sigma` is expanded to a constant array with the same dimensions as the other inputs.

`[X,XLO,XUP] = logninv(P,mu,sigma,pcov,alpha)` returns confidence bounds for `X` when the input parameters `mu` and `sigma` are estimates. `pcov` is the covariance matrix of the estimated parameters. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is 0.05. `XLO` and `XUP` are arrays of the same size as `X` containing the lower and upper confidence bounds.

`logninv` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\hat{\mu} + \hat{\sigma} q$$

where q is the `P`th quantile from a normal distribution with mean 0 and standard deviation 1. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The lognormal inverse function is defined in terms of the lognormal cdf as

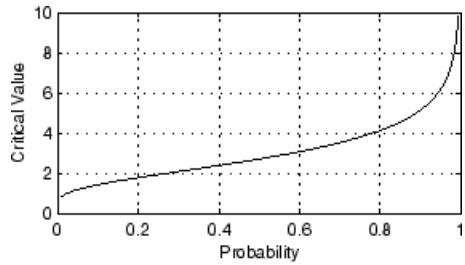
$$x = F^{-1}(p \mid \mu,\sigma) = \{x : F(x \mid \mu,\sigma) = p\}$$

where

$$p = F(x \mid \mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}} \int_0^x \frac{e^{\frac{-(\ln(t)-\mu)^2}{2\sigma^2}}}{t} dt$$

Examples

```
p = (0.005:0.01:0.995);
crit = logninv(p,1,0.5);
plot(p,crit)
xlabel('Probability'); ylabel('Critical Value'); grid
```



References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. Hoboken, NJ: Wiley-Interscience, 2000. pp. 102–105.

See Also

`icdf` | `logncdf` | `lognpdf` | `lognstat` | `lognfit` | `lognlike` | `lognrnd`

How To

- "Lognormal Distribution" on page B-51

lognlike

Purpose

Lognormal negative log-likelihood

Syntax

```
nlogL = lognlike(params,data)
[nlogL,avar] = lognlike(params,data)
[...] = lognlike(params,data,censoring)
[...] = lognlike(params,data,censoring,freq)
```

Description

`nlogL = lognlike(params,data)` returns the negative log-likelihood of `data` for the lognormal distribution with parameters `params`. `params(1)` is the mean of the associated normal distribution, `mu`, and `params(2)` is the standard deviation of the associated normal distribution, `sigma`. The values of `mu` and `sigma` are scalars, and the output `nlogL` is a scalar.

`[nlogL,avar] = lognlike(params,data)` returns the inverse of Fisher's information matrix. If the input parameter value in `params` is the maximum likelihood estimate, `avar` is its asymptotic variance. `avar` is based on the observed Fisher's information, not the expected information.

`[...] = lognlike(params,data,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = lognlike(params,data,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. The vector `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `censoring` to use its default value.

See Also

`lognfit` | `lognpdf` | `logncdf` | `logninv` | `lognstat` | `lognrnd`

How To

- "Lognormal Distribution" on page B-51

Purpose

Lognormal probability density function

Syntax

```
Y = lognpdf(X,mu,sigma)
```

Description

`Y = lognpdf(X,mu,sigma)` returns values at `X` of the lognormal pdf with distribution parameters `mu` and `sigma`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution. `X`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `Y`. A scalar input for `X`, `mu`, or `sigma` is expanded to a constant array with the same dimensions as the other inputs.

The lognormal pdf is

$$y = f(x \mid \mu,\sigma) = \frac{1}{x\sigma\sqrt{2\pi}} e^{\frac{-(\ln x-\mu)^2}{2\sigma^2}}$$

The normal and lognormal distributions are closely related. If X is distributed lognormally with parameters μ and σ, then $\log(X)$ is distributed normally with mean μ and standard deviation σ.

The mean m and variance v of a lognormal random variable are functions of μ and σ that can be calculated with the `lognstat` function. They are:

$$m = \exp\left(\mu + \sigma^2 / 2\right)$$
$$v = \exp\left(2\mu + \sigma^2\right)\left(\exp\left(\sigma^2\right) - 1\right)$$

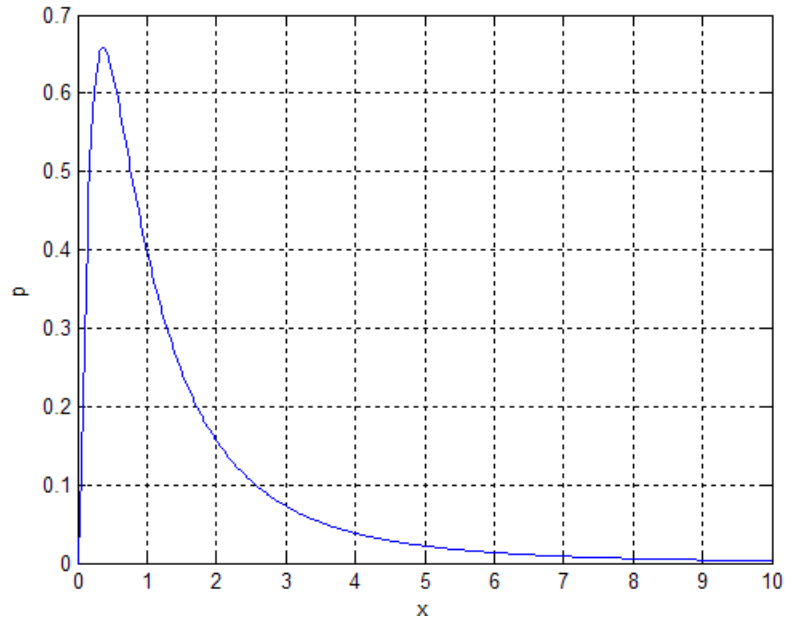
A lognormal distribution with mean m and variance v has parameters

$$\mu = \log\left(m^2 / \sqrt{v + m^2}\right)$$
$$\sigma = \sqrt{\log\left(v / m^2 + 1\right)}$$

The lognormal distribution is applicable when the quantity of interest must be positive, since log(*X*) exists only when *X* is positive.

Examples

```
x = (0:0.02:10);
y = lognpdf(x,0,1);
plot(x,y); grid;
xlabel('x'); ylabel('p')
```



References

[1] Mood, A. M., F. A. Graybill, and D. C. Boes. *Introduction to the Theory of Statistics.* 3rd ed., New York: McGraw-Hill, 1974. pp. 540–541.

See Also

`pdf` | `logncdf` | `logninv` | `lognstat` | `lognfit` | `lognlike` | `lognrnd`

How To

- “Lognormal Distribution” on page B-51

Purpose

Lognormal random numbers

Syntax

```
R = lognrnd(mu,sigma)
R = lognrnd(mu,sigma,m,n,...)
R = lognrnd(mu,sigma,[m,n,...])
```

Description

`R = lognrnd(mu,sigma)` returns an array of random numbers generated from the lognormal distribution with parameters `mu` and `sigma`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `mu` or `sigma` is expanded to a constant array with the same dimensions as the other input.

`R = lognrnd(mu,sigma,m,n,...)` or `R = lognrnd(mu,sigma,[m,n,...])` generates an `m`-by-`n`-by-... array. The `mu`, `sigma` parameters can each be scalars or arrays of the same size as `R`.

The normal and lognormal distributions are closely related. If X is distributed lognormally with parameters μ and σ, then $\log(X)$ is distributed normally with mean μ and standard deviation σ.

The mean m and variance v of a lognormal random variable are functions of μ and σ that can be calculated with the `lognstat` function. They are:

$$m = \exp\left(\mu + \sigma^2 / 2\right)$$

$$v = \exp\left(2\mu + \sigma^2\right)\left(\exp\left(\sigma^2\right) - 1\right)$$

A lognormal distribution with mean m and variance v has parameters

$$\mu = \log\left(m^2 / \sqrt{v + m^2}\right)$$

$$\sigma = \sqrt{\log\left(v / m^2 + 1\right)}$$

Examples

Generate one million lognormally distributed random numbers with mean 1 and variance 2:

```
m = 1;
v = 2;
mu = log((m^2)/sqrt(v+m^2));
sigma = sqrt(log(v/(m^2)+1));

[M,V]= lognstat(mu,sigma)
M =
     1
V =
    2.0000

X = lognrnd(mu,sigma,1,1e6);

MX = mean(X)
MX =
    0.9974
VX = var(X)
VX =
    1.9776
```

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. Hoboken, NJ: Wiley-Interscience, 2000. pp. 102–105.

See Also

`random` | `lognpdf` | `logncdf` | `logninv` | `lognstat` | `lognfit` | `lognlike` | `normrnd`

How To

- “Lognormal Distribution” on page B-51

Purpose

Lognormal mean and variance

Syntax

```
[M,V] = lognstat(mu,sigma)
```

Description

`[M,V] = lognstat(mu,sigma)` returns the mean of and variance of the lognormal distribution with parameters `mu` and `sigma`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `mu` or `sigma` is expanded to a constant array with the same dimensions as the other input.

The normal and lognormal distributions are closely related. If X is distributed lognormally with parameters μ and σ, then $\log(X)$ is distributed normally with mean μ and standard deviation σ.

The mean m and variance v of a lognormal random variable are functions of μ and σ that can be calculated with the `lognstat` function. They are:

$$m = \exp\left(\mu + \sigma^2 / 2\right)$$

$$v = \exp\left(2\mu + \sigma^2\right)\left(\exp\left(\sigma^2\right) - 1\right)$$

A lognormal distribution with mean m and variance v has parameters

$$\mu = \log\left(m^2 / \sqrt{v + m^2}\right)$$

$$\sigma = \sqrt{\log\left(v / m^2 + 1\right)}$$

Examples

Generate one million lognormally distributed random numbers with mean 1 and variance 2:

```
m = 1;
v = 2;
```

```
mu = log((m^2)/sqrt(v+m^2));
sigma = sqrt(log(v/(m^2)+1));

[M,V]= lognstat(mu,sigma)
M =
     1
V =
    2.0000

X = lognrnd(mu,sigma,1,1e6);

MX = mean(X)
MX =
    0.9974
VX = var(X)
VX =
    1.9776
```

References

[1] Mood, A. M., F. A. Graybill, and D. C. Boes. *Introduction to the Theory of Statistics*. 3rd ed., New York: McGraw-Hill, 1974. pp. 540–541.

See Also

`lognpdf` | `logncdf` | `logninv` | `lognfit` | `lognlike` | `lognrnd`

How To

- "Lognormal Distribution" on page B-51

Purpose

Classification error

Syntax

```
L = loss(obj,X,Y)
L = loss(obj,X,Y,Name,Value)
```

Description

`L = loss(obj,X,Y)` returns a scalar representing how well `obj` classifies the data in `X`, when `Y` contains the true classifications.

`L = loss(obj,X,Y,Name,Value)` returns the loss with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`obj`

Discriminant analysis classifier of class `ClassificationDiscriminant` or `CompactClassificationDiscriminant`, typically constructed with `ClassificationDiscriminant.fit`.

`X`

Matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `obj`.

`Y`

Class labels, with the same data type as exists in `obj`. The number of elements of `Y` must equal the number of rows of `X`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`lossfun`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 20-952.
- `'exponential'` — See "Loss Functions" on page 20-952.
- `'mincost'` — Smallest misclassification cost as given by the `obj.Cost` matrix.

You can write your own loss function using the syntax described in "Loss Functions" on page 20-952.

Default: `'mincost'`

`weights`

Numeric vector of length `N`, where `N` is the number of rows of `X`. `weights` are nonnegative. When you supply `weights`, `loss` computes weighted classification error.

Default: `ones(N,1)`

Output Arguments

`L`

Classification error, a scalar. The meaning of the error depends on the values in `weights` and `lossfun`. See "Classification Error" on page 20-952.

Definitions

Classification Error

The default classification error is the fraction of data `X` that `obj` misclassifies, where `Y` represents the true classifications.

Weighted classification error is the sum of weight *i* times the Boolean value that is `1` when `obj` misclassifies the *i*th row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'mincost'` — Smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `obj.Cost` matrix

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of `X`.
- `K` is the number of classes in `obj`, represented in `obj.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `obj.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights. If you pass `W`, the elements are normalized to sum to the prior probabilities in the respective classes.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. For example, you can use `COST=ones(K)-eye(K)`, which means a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Compute the resubstituted classification error for the Fisher iris data:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species);
L = loss(obj,meas,species)

L =
    0.0200
```

See Also

`ClassificationDiscriminant | edge | margin | predict`

How To

- "Discriminant Analysis" on page 12-3

Purpose

Classification error

Syntax

```
L = loss(ens,X,Y)
L = loss(ens,X,Y,Name,Value)
```

Description

`L = loss(ens,X,Y)` returns the classification error for ensemble `ens` computed using matrix of predictors `X` and true class labels `Y`.

`L = loss(ens,X,Y,Name,Value)` computes classification error with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

Classification ensemble created with `fitensemble`, or a compact classification ensemble created with `compact`.

`X`

Matrix of data to classify. Each row of `X` represents one observation, and each column represents one predictor. `X` must have the same number of columns as the data used to train `ens`. `X` should have the same number of rows as the number of elements in `Y`.

`Y`

Classification of `X`. `Y` should be of the same type as the classification used to train `ens`, and its number of elements should equal the number of rows of `X`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `ens.NTrained`. `loss` uses only these learners for calculating loss.

Default: `1:NTrained`

`lossfun`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 20-957
- `'classiferror'` — Fraction of misclassified data
- `'exponential'` — See "Loss Functions" on page 20-957

You can write your own loss function in the syntax described in "Loss Functions" on page 20-957.

Default: `'classiferror'`

`mode`

String representing the meaning of the output `L`:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

`UseObsForLearner`

A logical matrix of size `N`-by-`T`, where:

- `N` is the number of rows of `X`.
- `T` is the number of weak learners in `ens`.

When `UseObsForLearner(i,j)` is `true`, learner `j` is used in predicting the class of row `i` of `X`.

Default: `true(N,T)`

`weights`

Vector of observation weights, with nonnegative entries. The length of `weights` must equal the number of rows in `X`.

Default: `ones(size(X,1),1)`

Output Arguments

`L`

Loss, by default the fraction of misclassified data. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Definitions

Classification Error

The default classification error is the fraction of the data `X` that `ens` misclassifies, where `Y` are the true classifications.

Weighted classification error is the sum of weight i times the Boolean value that is `1` when `tree` misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of `ens.X`.
- `K` is the number of classes in `ens`, represented in `ens.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `tree.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `score` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` gives a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Create a compact classification ensemble for the ionosphere data, and find the fraction of training data that the ensemble misclassifies:

```
load ionosphere
ada = fitensemble(X,Y,'AdaBoostM1',100,'tree');
adb = compact(ada);
L = loss(adb,X,Y)

L =
```

```
    0.0085
```

See Also

`loss` | `edge` | `margin` | `predict`

How To

- Chapter 13, “Nonparametric Supervised Learning”

CompactClassificationTree.loss

Purpose

Classification error

Syntax

```
L = loss(tree,X,Y)
L = loss(tree,X,Y,Name,Value)
L = loss(tree,X,Y,'subtrees',subtreevector)
[L,se] = loss(tree,X,Y,'subtrees',subtreevector)
[L,se,NLeaf] = loss(tree,X,Y,'subtrees',subtreevector)
[L,se,NLeaf,bestlevel] = loss(tree,X,Y,'subtrees',
   subtreevector)
[L,...] =
loss(tree,X,Y,'subtrees',subtreevector,Name,Value)
```

Description

`L = loss(tree,X,Y)` returns a scalar representing how well `tree` classifies the data in `X`, when `Y` contains the true classifications.

`L = loss(tree,X,Y,Name,Value)` returns the loss with additional options specified by one or more `Name,Value` pair arguments.

`L = loss(tree,X,Y,'subtrees',subtreevector)` returns a vector of classification errors for the trees in the pruning sequence `subtreevector`.

`[L,se] = loss(tree,X,Y,'subtrees',subtreevector)` returns the vector of standard errors of the classification errors.

Note `loss` returns `se` and further outputs only when the `lossfun` name-value pair is the default `'classiferror'`.

`[L,se,NLeaf] = loss(tree,X,Y,'subtrees',subtreevector)` returns the vector of numbers of leaf nodes in the trees of the pruning sequence.

`[L,se,NLeaf,bestlevel] = loss(tree,X,Y,'subtrees',subtreevector)` returns the best pruning level as defined in the `treesize` name-value pair. By default, `bestlevel` is the pruning level that gives loss within one standard deviation of minimal loss.

`[L,...] = loss(tree,X,Y,'subtrees',subtreevector,Name,Value)` returns loss statistics with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`tree`

A classification tree or compact classification tree constructed by `ClassificationTree.fit` or `compact`.

`X`

Matrix of data to classify. Each row of `X` represents one observation, and each column represents one predictor. `X` must have the same number of columns as the data used to train `tree`. `X` should have the same number of rows as the number of elements in `Y`.

`Y`

Classification of `X`. `Y` should be of the same type as the classification used to train `tree`, and its number of elements should equal the number of rows of `X`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`lossfun`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 20-963
- `'classiferror'` — Fraction of misclassified data
- `'exponential'` — See "Loss Functions" on page 20-963

You can write your own loss function in the syntax described in "Loss Functions" on page 20-963.

Default: `'classiferror'`

`weights`

A numeric vector of length `N`, where `N` is the number of rows of `X`. `weights` are nonnegative. When you supply `weights`, `loss` computes weighted classification error.

Default: `ones(N,1)`

`Name,Value` arguments associated with pruning subtrees:

`subtrees`

A vector with integer values from `0` (full unpruned tree) to the maximal pruning level `max(tree.PruneList)`. You can set `subtrees` to `'all'`, meaning the entire pruning sequence.

Default: `0`

`treesize`

One of the following strings:

- `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L+se`, where `L` and `se` relate to the smallest value in `subtrees`).
- `'min'` — `loss` returns the element of `subtrees` with smallest loss, usually the smallest element of `subtrees`.

Output Arguments

`L`

Classification error, a vector the length of `subtrees`. The meaning of the error depends on the values in `weights` and `lossfun`; see "Classification Error" on page 20-963.

`se`

Standard error of loss, a vector the length of `subtrees`.

`NLeaf`

Number of leaves (terminal nodes) in the pruned subtrees, a vector the length of `subtrees`.

`bestlevel`

A scalar whose value depends on `treesize`:

- `treesize` = `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L+se`, where `L` and `se` relate to the smallest value in `subtrees`).
- `treesize` = `'min'` — `loss` returns the element of `subtrees` with smallest loss, usually the smallest element of `subtrees`.

Definitions

Classification Error

The default classification error is the fraction of data `X` that `tree` misclassifies, where `Y` represents the true classifications.

Weighted classification error is the sum of weight *i* times the Boolean value that is `1` when `tree` misclassifies the *i*th row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of `X`.
- `K` is the number of classes in `tree`, represented in `tree.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `tree.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights. If you pass `W`, the elements are normalized to sum to the prior probabilities in the respective classes.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. For example, you can use `COST=ones(K)-eye(K)`, which means a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Compute the resubstituted classification error for the `ionosphere` data:

```
load ionosphere
tree = ClassificationTree.fit(X,Y);
L = loss(tree,X,Y)

L =
```

```
    0.0114
```

See Also

`margin` | `edge` | `predict`

How To

- Chapter 13, “Nonparametric Supervised Learning”

CompactRegressionEnsemble.loss

Purpose

Regression error

Syntax

```
L = loss(ens,X,Y)
L = loss(ens,X,Y,Name,Value)
```

Description

`L = loss(ens,X,Y)` returns the mean squared error between the predictions of `ens` to the data in `X`, compared to the true responses `Y`.

`L = loss(ens,X,Y,Name,Value)` computes the error in prediction with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`, or the `compact` method.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`NaN` values in `X` are taken to be missing values. Observations with all missing values for `X` are not used in the calculation of loss.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

`NaN` values in `Y` are taken to be missing values. Observations with missing values for `Y` are not used in the calculation of loss.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `ens.NTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NTrained`

`lossfun`

Function handle for loss function, or the string `'mse'`, meaning mean squared error. If you pass a function handle `fun`, `loss` calls it as

```
fun(Y,Yfit,W)
```

where `Y`, `Yfit`, and `W` are numeric vectors of the same length.

- `Y` is the observed response.
- `Yfit` is the predicted response.
- `W` is the observation weights.

The returned value `fun(Y,Yfit,W)` should be a scalar.

Default: `'mse'`

`mode`

String representing the meaning of the output `L`:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

`UseObsForLearner`

A logical matrix of size `N`-by-`NTrained`, where `N` is the number of observations in `ens.X`, and `NTrained` is the number of weak learners. When `UseObsForLearner(I,J)` is `true`, `predict` uses learner `J` in predicting observation `I`.

Default: `true(N,NTrained)`

`weights`

Numeric vector of observation weights with the same number of elements as `Y`. The formula for `loss` with `weights` is in "Weighted Mean Squared Error" on page 20-968.

Default: `ones(size(Y))`

Output Arguments

`L`

Weighted mean squared error of predictions. The formula for `loss` is in "Weighted Mean Squared Error" on page 20-968.

Definitions

Weighted Mean Squared Error

Let n be the number of rows of data, x_j be the jth row of data, y_j be the true response to x_j, and let $f(x_j)$ be the response prediction of `ens` to x_j. Let w be the vector of weights (all one by default).

First the weights are divided by their sum so they add to one: $w \to w/\Sigma w$. The mean squared error L is

$$L = \sum_{j=1}^{n} w_j \left(f\left(x_j\right) - y_j \right)^2 .$$

Examples

Find the loss of an ensemble predictor of the `carsmall` data to find `MPG` as a function of engine displacement, horsepower, and vehicle weight:

```
load carsmall
```

```
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',100,'Tree');
L = loss(ens,X,MPG)

L =
    4.3904
```

See Also

`predict` | `fitensemble`

How To

- Chapter 13, “Nonparametric Supervised Learning”

CompactRegressionTree.loss

Purpose

Regression error

Syntax

```
L = loss(tree,X,Y)
[L,se] = loss(tree,X,Y)
[L,se,NLeaf] = loss(tree,X,Y)
[L,se,NLeaf,bestlevel] = loss(tree,X,Y)
L = loss(tree,X,Y,Name,Value)
```

Description

`L = loss(tree,X,Y)` returns the mean squared error between the predictions of `tree` to the data in `X`, compared to the true responses `Y`.

`[L,se] = loss(tree,X,Y)` returns the standard error of the loss.

`[L,se,NLeaf] = loss(tree,X,Y)` returns the number of leaves (terminal nodes) in the tree.

`[L,se,NLeaf,bestlevel] = loss(tree,X,Y)` returns the optimal pruning level for `tree`.

`L = loss(tree,X,Y,Name,Value)` computes the error in prediction with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`tree`

Regression tree created with `RegressionTree.fit`, or the `compact` method.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must

appear inside single quotes (''). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`lossfun`

Function handle for loss, or the string `'mse'` representing mean-squared error. If you pass a function handle `fun`, `loss` calls `fun` as:

```
fun(Y,Yfit,W)
```

- `Y` is the vector of true responses.
- `Yfit` is the vector of predicted responses.
- `W` is the observation weights. If you pass `W`, the elements are normalized to sum to `1`.

All the vectors have the same number of rows as `Y`.

Default: `'mse'`

`subtrees`

A vector with integer values from `0` (full unpruned tree) to the maximal pruning level `max(tree.PruneList)`. You can set `subtrees` to `'all'`, meaning the entire pruning sequence.

Default: 0

`treesize`

A string, either:

- `'se'` — `loss` returns `bestlevel` that corresponds to the smallest tree whose mean squared error (MSE) is within one standard error of the minimum MSE.
- `'min'` — `loss` returns `bestlevel` that corresponds to the minimal MSE tree.

`weights`

Numeric vector of observation weights with the same number of elements as `Y`.

Default: `ones(size(Y))`

Output Arguments

`L`

Classification error, a vector the length of `subtrees`. The error for each tree is the mean squared error, weighted with `weights`. If you include `lossfun`, `L` reflects the loss calculated with `lossfun`.

`se`

Standard error of loss, a vector the length of `subtrees`.

`NLeaf`

Number of leaves (terminal nodes) in the pruned subtrees, a vector the length of `subtrees`.

`bestlevel`

A scalar whose value depends on `treesize`:

- `treesize` = `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L+se`, where `L` and `se` relate to the smallest value in `subtrees`).
- `treesize` = `'min'` — `loss` returns the element of `subtrees` with smallest loss, usually the smallest element of `subtrees`.

Definitions

Mean Squared Error

The mean squared error m of the predictions $f(X_n)$ with weight vector w is

$$m = \frac{\sum w_n \left(f(X_n) - Y_n\right)^2}{\sum w_n}.$$

Examples

Find the loss of a regression tree predictor of the `carsmall` data to find `MPG` as a function of engine displacement, horsepower, and vehicle weight:

```
load carsmall
X = [Displacement Horsepower Weight];
tree = RegressionTree.fit(X,MPG);
L = loss(tree,X,MPG)

L =
    4.8952
```

Find the pruning level that gives the optimal level of loss for the `carsmall` data:

```
load carsmall
X = [Displacement Horsepower Weight];
tree = RegressionTree.fit(X,MPG);
[L,se,NLeaf,bestlevel] = loss(tree,X,MPG,'Subtrees','all');
bestlevel

bestlevel =
     4
```

See Also

`predict`

How To

- Chapter 13, “Nonparametric Supervised Learning”

paretotails.lowerparams

Purpose

Lower Pareto tails parameters

Syntax

```
params = lowerparams(obj)
```

Description

`params = lowerparams(obj)` returns the 2-element vector `params` of shape and scale parameters, respectively, of the lower tail of the Pareto tails object `obj`. `lowerparams` does not return a location parameter.

Examples

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);

lowerparams(obj)
ans =
   -0.1901    1.1898
upperparams(obj)
ans =
    0.3646    0.5103
```

See Also

`paretotails` | `upperparams`

Purpose

Less than relation for handles

Syntax

```
h1 < h2
```

Description

`h1 < h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise < result.

If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = lt(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `eq` | `ge` | `gt` | `le` | `ne`

lsline

Purpose

Add least-squares line to scatter plot

Syntax

```
lsline
h = lsline
```

Description

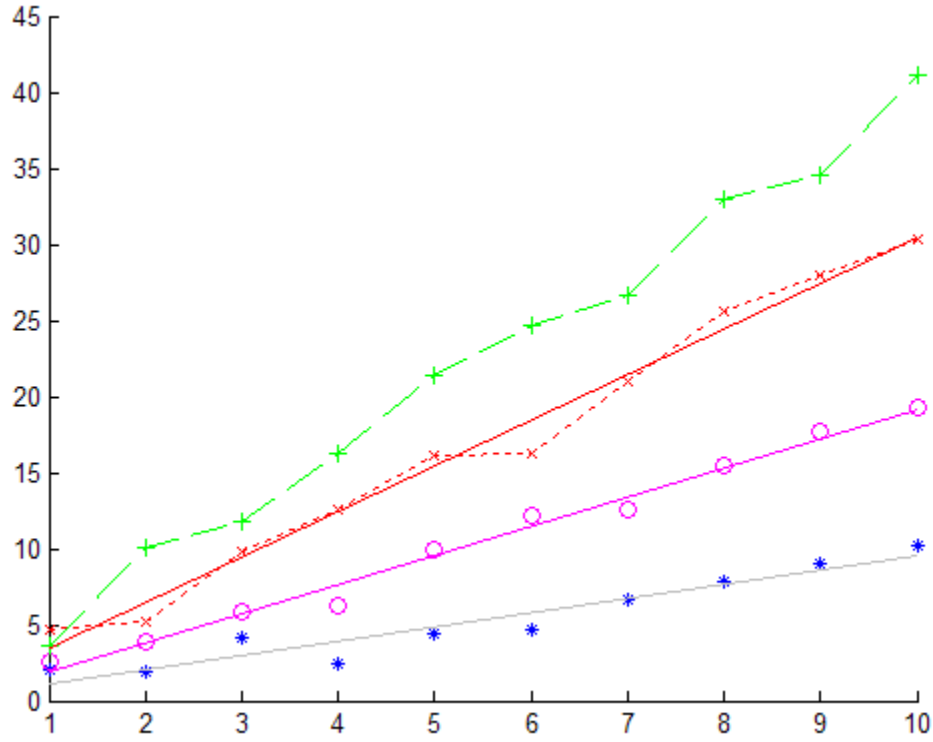
`lsline` superimposes a least-squares line on each scatter plot in the current axes. Scatter plots are produced by the MATLAB `scatter` and `plot` functions. Data points connected with solid, dashed, or dash-dot lines (`LineStyle` `'-'`, `'--'`, or `'.-'`) are not considered to be scatter plots by `lsline`, and are ignored.

`h = lsline` returns a column vector of handles `h` to the least-squares lines.

Examples

Use `lsline` together with scatter plots produced by `scatter` and various line styles of `plot`:

```
x = 1:10;

y1 = x + randn(1,10);
scatter(x,y1,25,'b','*')
hold on

y2 = 2*x + randn(1,10);
plot(x,y2,'mo')

y3 = 3*x + randn(1,10);
plot(x,y3,'rx:')

y4 = 4*x + randn(1,10);
plot(x,y4,'g+--')

lsline
```



See Also `scatter` | `plot` | `refline` | `refcurve` | `gline`

mad

Purpose

Mean or median absolute deviation

Syntax

```
y = mad(X)
Y = mad(X,1)
Y = mad(X,0)
```

Description

`y = mad(X)` returns the mean absolute deviation of the values in `X`. For vector input, `y` is `mean(abs(X-mean(X)))`. For a matrix input, `y` is a row vector containing the mean absolute deviation of each column of `X`. For *N*-dimensional arrays, `mad` operates along the first nonsingleton dimension of `X`.

`Y = mad(X,1)` returns the median absolute deviation of the values in `X`. For vector input, `y` is `median(abs(X-median(X)))`. For a matrix input, `y` is a row vector containing the median absolute deviation of each column of `X`. For *N*-dimensional arrays, `mad` operates along the first nonsingleton dimension of `X`.

`Y = mad(X,0)` is the same as `mad(X)`, and returns the mean absolute deviation of the values in `X`.

`mad(X,flag,dim)` computes absolute deviations along the dimension `dim` of `X`. `flag` is `0` or `1` to indicate mean or median absolute deviation, respectively.

`mad` treats `NaNs` as missing values and removes them.

For normally distributed data, multiply `mad` by one of the following factors to obtain an estimate of the normal scale parameter σ:

- `sigma = 1.253*mad(X,0)` — For mean absolute deviation
- `sigma = 1.4826*mad(X,1)` — For median absolute deviation

Examples

The following compares the robustness of different scale estimates for normally distributed data in the presence of outliers:

```
x = normrnd(0,1,1,50);
xo = [x 10]; % Add outlier
```

```
r1 = std(xo)/std(x)
r1 =
    1.7385

r2 = mad(xo,0)/mad(x,0)
r2 =
    1.2306

r3 = mad(xo,1)/mad(x,1)
r3 =
    1.0602
```

References

[1] Mosteller, F., and J. Tukey. *Data Analysis and Regression.* Upper Saddle River, NJ: Addison-Wesley, 1977.

[2] Sachs, L. *Applied Statistics: A Handbook of Techniques.* New York: Springer-Verlag, 1984, p. 253.

See Also

`std` | `range` | `iqr`

mahal

Purpose

Mahalanobis distance

Syntax

```
d = mahal(Y,X)
```

Description

`d = mahal(Y,X)` computes the Mahalanobis distance (in squared units) of each observation in `Y` from the reference sample in matrix `X`. If `Y` is n-by-m, where n is the number of observations and m is the dimension of the data, `d` is n-by-1. `X` and `Y` must have the same number of columns, but can have different numbers of rows. `X` must have more rows than columns.

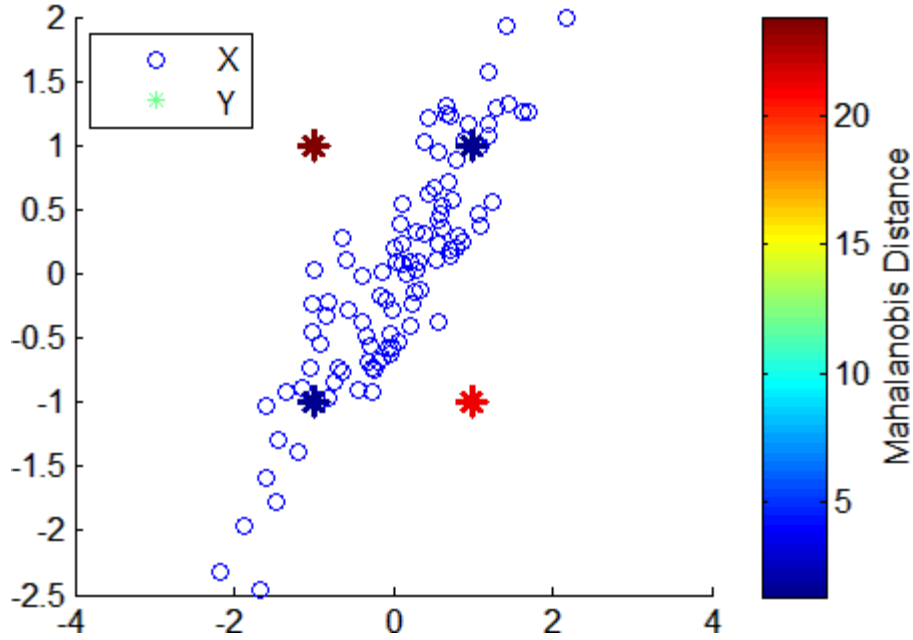
For observation `I`, the Mahalanobis distance is defined by `d(I) = (Y(I,:)-mu)*inv(SIGMA)*(Y(I,:)-mu)'`, where `mu` and `SIGMA` are the sample mean and covariance of the data in `X`. `mahal` performs an equivalent, but more efficient, computation.

Examples

Generate some correlated bivariate data in `X` and compare the Mahalanobis and squared Euclidean distances of observations in `Y`:

```
X = mvnrnd([0;0],[1 .9;.9 1],100);
Y = [1 1;1 -1;-1 1;-1 -1];

d1 = mahal(Y,X) % Mahalanobis
d1 =
    1.3592
   21.1013
   23.8086
    1.4727

d2 = sum((Y-repmat(mean(X),4,1)).^2, 2) % Squared Euclidean
d2 =
    1.9310
    1.8821
    2.1228
    2.0739

scatter(X(:,1),X(:,2))
```

```
hold on
scatter(Y(:,1),Y(:,2),100,d1,'*','LineWidth',2)
hb = colorbar;
ylabel(hb,'Mahalanobis Distance')
legend('X','Y','Location','NW')
```



The observations in `Y` with equal coordinate values are much closer to `X` in Mahalanobis distance than observations with opposite coordinate values, even though all observations are approximately equidistant from the mean of `X` in Euclidean distance. The Mahalanobis distance, by considering the covariance of the data and the scales of the different variables, is useful for detecting outliers in such cases.

See Also

`pdist` | `mahal`

CompactClassificationDiscriminant.mahal

Purpose

Mahalanobis distance to class means

Syntax

```
M = mahal(obj,X)
M = mahal(obj,X,Name,Value)
```

Description

`M = mahal(obj,X)` returns the squared Mahalanobis distances from observations in `X` to the class means in `obj`.

`M = mahal(obj,X,Name,Value)` computes the squared Mahalanobis distance with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`obj`

Discriminant analysis classifier of class `ClassificationDiscriminant` or `CompactClassificationDiscriminant`, typically constructed with `ClassificationDiscriminant.fit`.

`X`

Numeric matrix of size `n`-by-`p`, where `p` is the number of predictors in `obj`, and `n` is any positive integer. `mahal` computes the Mahalanobis distances from the rows of `X` to each of the `K` means of the classes in `obj`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`ClassLabels`

Class labels consisting of `n` elements of `obj.Y`, where `n` is the number of rows of `X`.

Output Arguments

`M`

Size and meaning of output `M` depends on whether the `ClassLabels` name-value pair is present:

- No `ClassLabels` — `M` is a numeric matrix of size `n`-by-`K`, where `K` is the number of classes in `obj`, and `n` is the number of rows in `X`. `M(i,j)` is the squared Mahalanobis distance from the `i`th row of `X` to the mean of class `j`.
- `ClassLabels` exists — `M` is a column vector with `n` elements. `M(i)` is the squared Mahalanobis distance from the `i`th row of `X` to the mean for the class of the `i`th element of `ClassLabels`.

Definitions

Mahalanobis Distance

The Mahalanobis distance $d(x,y)$ between n-dimensional points x and y, with respect to a given n-by-n covariance matrix S, is

$$d(x,y) = \sqrt{(x-y)^T S^{-1} (x-y)}.$$

Examples

Find the Mahalanobis distances from the mean of the Fisher iris data to the class means, using distinct covariance matrices for each class:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species,...
    'DiscrimType','quadratic');
mahadist = mahal(obj,mean(meas))

mahadist =
  220.0667    5.0254   30.5804
```

See Also

`CompactClassificationDiscriminant` | `mahal` | `gmdistribution`

How To

- "Discriminant Analysis" on page 12-3

gmdistribution.mahal

Purpose

Mahalanobis distance to component means

Syntax

```
D = mahal(obj,X)
```

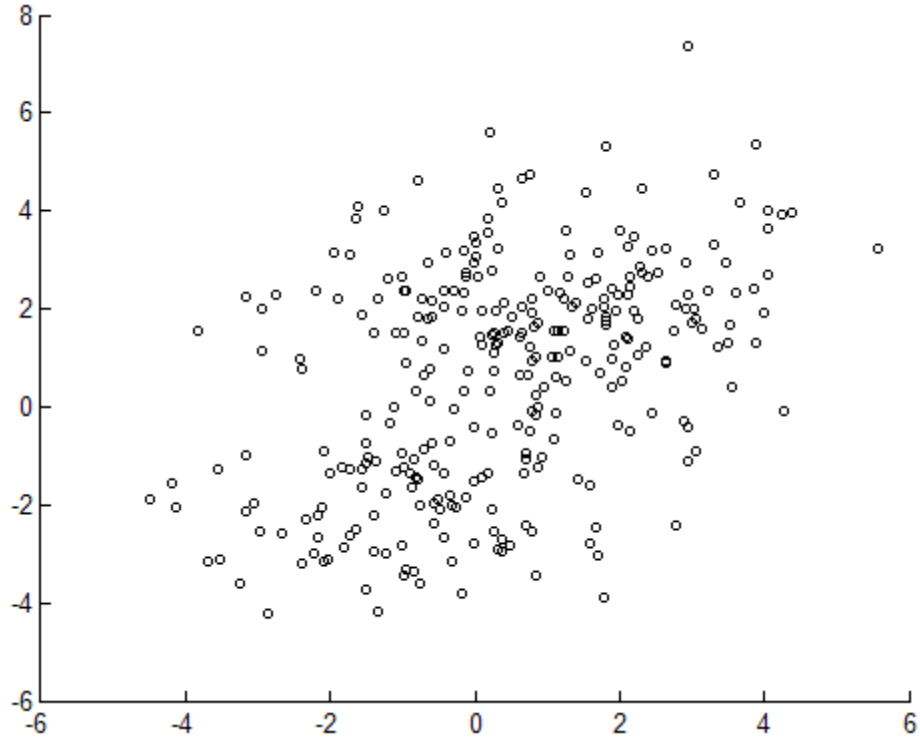
Description

`D = mahal(obj,X)` computes the Mahalanobis distance (in squared units) of each observation in `X` to the mean of each of the k components of the Gaussian mixture distribution defined by `obj`. `obj` is an object created by `gmdistribution` or `fit`. `X` is an n-by-d matrix, where n is the number of observations and d is the dimension of the data. `D` is n-by-k, with `D(I,J)` the distance of observation `I` from the mean of component `J`.

Examples

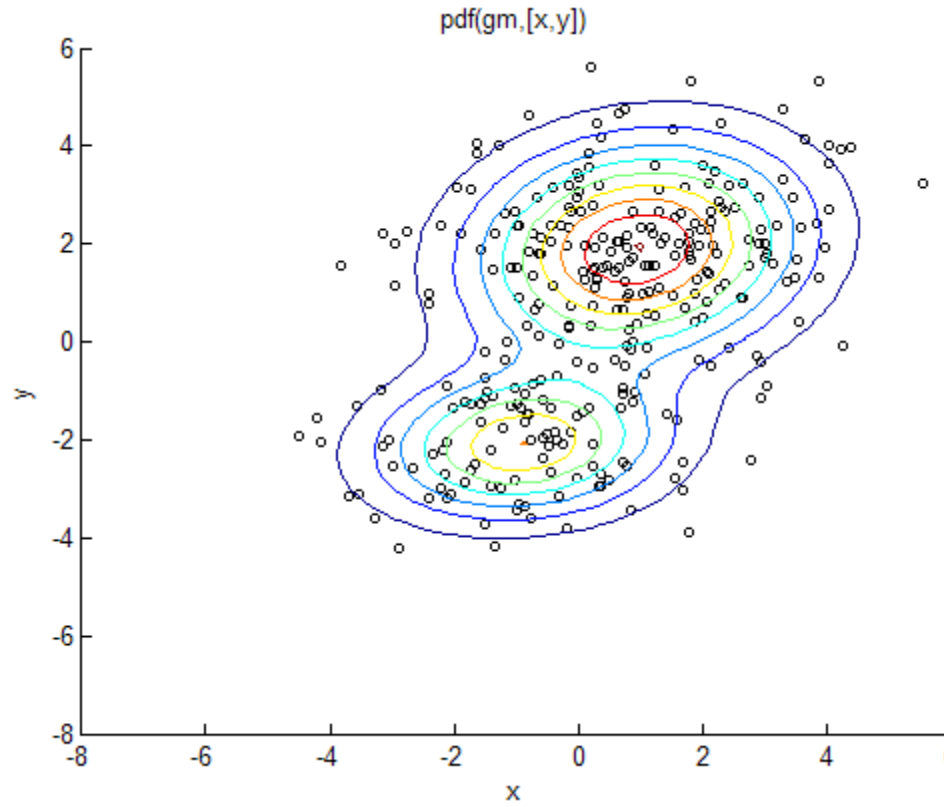
Generate data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function:

```
MU1 = [1 2];
SIGMA1 = [2 0; 0 .5];
MU2 = [-3 -5];
SIGMA2 = [1 0; 0 1];
X = [mvnrnd(MU1,SIGMA1,1000);mvnrnd(MU2,SIGMA2,1000)];

scatter(X(:,1),X(:,2),10,'.')
hold on
```



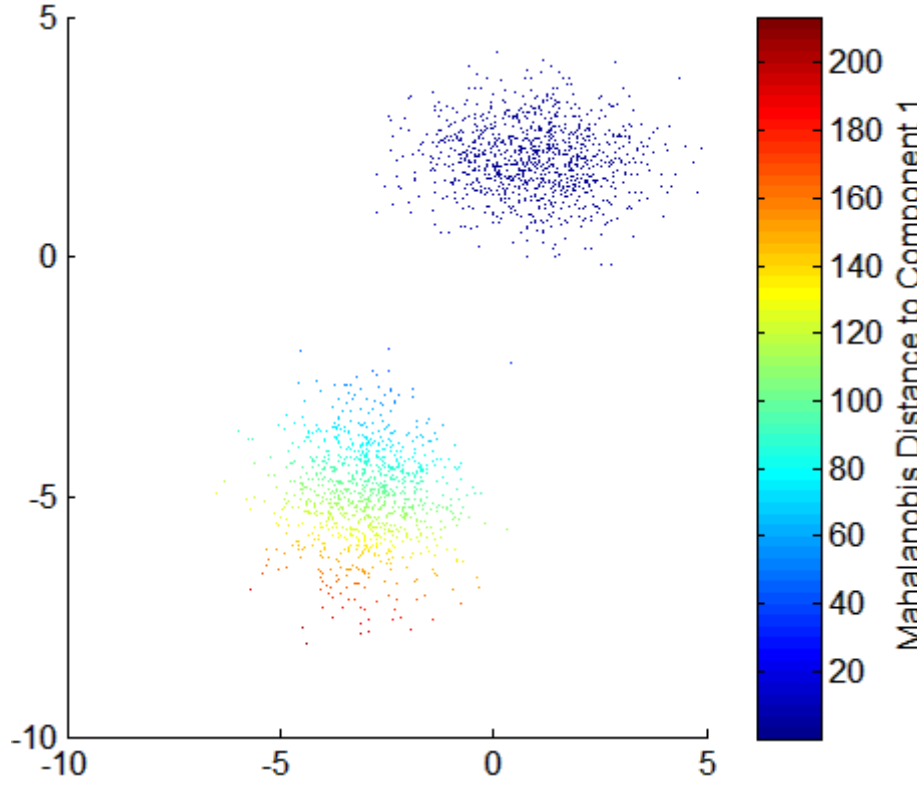
Fit a two-component Gaussian mixture model:

```
obj = gmdistribution.fit(X,2);
h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
```



Compute the Mahalanobis distance of each point in `X` to the mean of each component of `obj`:

```
D = mahal(obj,X);

delete(h)
scatter(X(:,1),X(:,2),10,D(:,1),'.')
hb = colorbar;
ylabel(hb,'Mahalanobis Distance to Component 1')
```



See Also

`gmdistribution` | `cluster` | `posterior` | `mahal`

maineffectsplot

Purpose

Main effects plot for grouped data

Syntax

```
maineffectsplot(Y,GROUP)
maineffectsplot(Y,GROUP,param1,val1,param2,val2,...)
[figh,AXESH] = maineffectsplot(...)
```

Description

`maineffectsplot(Y,GROUP)` displays main effects plots for the group means of matrix `Y` with groups defined by entries in the cell array `GROUP`. `Y` is a numeric matrix or vector. If `Y` is a matrix, the rows represent different observations and the columns represent replications of each observation. Each cell of `GROUP` must contain a grouping variable that can be a categorical variable, numeric vector, character matrix, or single-column cell array of strings. (See "Grouped Data" on page 2-34.) `GROUP` can also be a matrix whose columns represent different grouping variables. Each grouping variable must have the same number of rows as `Y`. The number of grouping variables must be greater than 1.

The display has one subplot per grouping variable, with each subplot showing the group means of `Y` as a function of one grouping variable.

`maineffectsplot(Y,GROUP,param1,val1,param2,val2,...)` specifies one or more of the following name/value pairs:

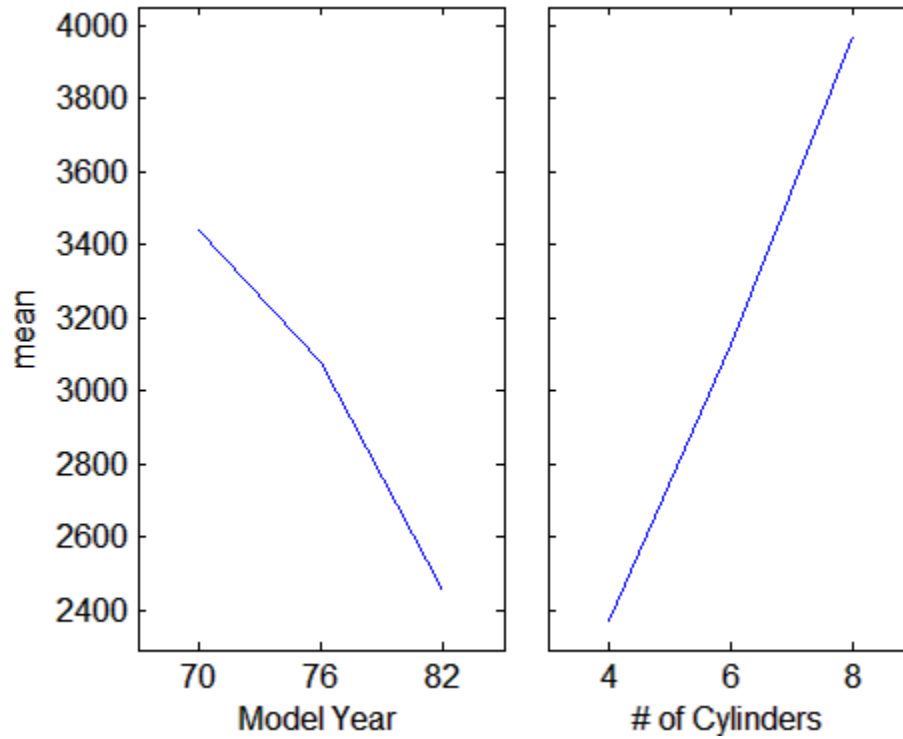
- `'varnames'` — Grouping variable names in a character matrix or a cell array of strings, one per grouping variable. Default names are `'X1'`, `'X2'`, ...
- `'statistic'` — String values that indicate whether the group mean or the group standard deviation should be plotted. Use `'mean'` or `'std'`. The default is `'mean'`. If the value is `'std'`, `Y` is required to have multiple columns.
- `'parent'` — A handle to the figure window for the plots. The default is the current figure window.

`[figh,AXESH] = maineffectsplot(...)` returns the handle `figh` to the figure window and an array of handles `AXESH` to the subplot axes.

Examples

Display main effects plots for car weight with two grouping variables, model year and number of cylinders:

```
load carsmall;
maineffectsplot(Weight,{Model_Year,Cylinders}, ...
                'varnames',{'Model Year','# of Cylinders'})
```



See Also

`interactionplot` | `multivarichart`

How To

- “Grouped Data” on page 2-34

ClassificationDiscriminant.make

Purpose

Construct discriminant analysis classifier from parameters

Syntax

```
cobj = ClassificationDiscriminant.make(Mu,Sigma)
cobj = ClassificationDiscriminant.make(Mu,Sigma,Name,Value)
```

Description

`cobj = ClassificationDiscriminant.make(Mu,Sigma)` constructs a compact discriminant analysis classifier from the class means `Mu` and covariance matrix `Sigma`.

`cobj = ClassificationDiscriminant.make(Mu,Sigma,Name,Value)` constructs a compact classifier with additional options specified by one or more `Name,Value` pair arguments.

Tips

- You can change the discriminant type using dot addressing after constructing `cobj`:

  ```
  cobj.DiscrimType = 'discrimType'
  ```

  where *`discrimType`* is one of `'linear'`, `'quadratic'`, `'diagLinear'`, `'diagQuadratic'`, `'pseudoLinear'`, or `'pseudoQuadratic'`. You can change between linear types or between quadratic types, but cannot change between a linear and a quadratic type.

- `cobj` is a linear classifier when `Sigma` is a matrix. `cobj` is a quadratic classifier when `Sigma` is a three-dimensional array.

Input Arguments

`Mu`

Matrix of class means of size `K`-by-`p`, where `K` is the number of classes, and `p` is the number of predictors. Each row of `Mu` represents the mean of the multivariate normal distribution of the corresponding class. The class indices are in the `ClassNames` attribute.

`Sigma`

Within-class covariance matrix or matrices.

- For a linear discriminant, `Sigma` is a symmetric, positive semidefinite matrix of size `p`-by-`p`, where `p` is the number of predictors.
- For a quadratic discriminant, `Sigma` is an array of size `p`-by-`p`-by-`K`, where `K` is the number of classes. For each `i`, `Sigma(:,:,i)` is a symmetric, positive semidefinite matrix.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`ClassNames`

Array of class names. Use any data type for a grouping variable: a numeric vector, vector of categorical variables (nominal or ordinal), logical vector, character array, or cell array of strings.

`ClassNames` names the classes, as ordered in `Mu`.

Default: `1:K`, where `K` is the number of classes (the number of rows of `Mu`)

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. Alternatively, `Cost` can be a structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same type as `Y`, and `S.ClassificationCosts` containing the cost matrix.

Default: `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`

`PredictorNames`

Cell array of names for the predictor variables, in the order in which they appear in `X`.

Default: `{'x1','x2',...}`

`prior`

Prior probabilities for each class. Specify as one of:

- `'uniform'`, a string meaning all class prior probabilities are equal
- A vector (one scalar value for each class)
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as `ClassNames`
  - `S.ClassProbs` containing a vector of corresponding probabilities

Default: `'uniform'`

`ResponseName`

Name of the response variable `Y`, a string.

Default: `'Y'`

Output Arguments

`cobj`

Discriminant analysis classifier, of class `CompactClassificationDiscriminant`.

Examples

Construct a compact linear discriminant analysis classifier from the means and covariances of the Fisher iris data:

```
load fisheriris
mu(1,:) = mean(meas(1:50,:));
mu(2,:) = mean(meas(51:100,:));
mu(3,:) = mean(meas(101:150,:));
```

```
mm1 = repmat(mu(1,:),50,1);
mm2 = repmat(mu(2,:),50,1);
mm3 = repmat(mu(3,:),50,1);
cc = meas;
cc(1:50,:) = cc(1:50,:) - mm1;
cc(51:100,:) = cc(51:100,:) - mm2;
cc(101:150,:) = cc(101:150,:) - mm3;
sigstar = cc' * cc / 147; % unbiased estimator of sigma
cpct = ClassificationDiscriminant.make(mu,sigstar,...
   'ClassNames',{'setosa','versicolor','virginica'})

cpct =
classreg.learning.classif.CompactClassificationDiscriminant:
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
       DiscrimType: 'linear'
                Mu: [3x4 double]
            Coeffs: [3x3 struct]
```

See Also

`ClassificationDiscriminant.fit` | `compact` | `CompactClassificationDiscriminant`

How To

- “Discriminant Analysis” on page 12-3

Purpose

One-way multivariate analysis of variance

Syntax

```
d = manova1(X,group)
d = manova1(X,group,alpha)
[d,p] = manova1(...)
[d,p,stats] = manova1(...)
```

Description

`d = manova1(X,group)` performs a one-way Multivariate Analysis of Variance (MANOVA) for comparing the multivariate means of the columns of `X`, grouped by `group`. `X` is an m-by-n matrix of data values, and each row is a vector of measurements on n variables for a single observation. `group` is a grouping variable defined as a categorical variable, vector, string array, or cell array of strings. Two observations are in the same group if they have the same value in the `group` array. (See "Grouped Data" on page 2-34.) The observations in each group represent a sample from a population.

The function returns `d`, an estimate of the dimension of the space containing the group means. `manova1` tests the null hypothesis that the means of each group are the same n-dimensional multivariate vector, and that any difference observed in the sample `X` is due to random chance. If `d = 0`, there is no evidence to reject that hypothesis. If `d = 1`, then you can reject the null hypothesis at the 5% level, but you cannot reject the hypothesis that the multivariate means lie on the same line. Similarly, if `d = 2` the multivariate means may lie on the same plane in n-dimensional space, but not on the same line.

`d = manova1(X,group,alpha)` gives control of the significance level, `alpha`. The return value `d` will be the smallest dimension having `p > alpha`, where `p` is a p value for testing whether the means lie in a space of that dimension.

`[d,p] = manova1(...)` also returns a `p`, a vector of p-values for testing whether the means lie in a space of dimension 0, 1, and so on. The largest possible dimension is either the dimension of the space, or one less than the number of groups. There is one element of `p` for each dimension up to, but not including, the largest.

If the ith p value is near zero, this casts doubt on the hypothesis that the group means lie on a space of i-1 dimensions. The choice of a critical p value to determine whether the result is judged statistically significant is left to the researcher and is specified by the value of the input argument `alpha`. It is common to declare a result significant if the p value is less than 0.05 or 0.01.

`[d,p,stats] = manova1(...)` also returns `stats`, a structure containing additional MANOVA results. The structure contains the following fields.

Field	Contents
`W`	Within-groups sum of squares and cross-products matrix
`B`	Between-groups sum of squares and cross-products matrix
`T`	Total sum of squares and cross-products matrix
`dfW`	Degrees of freedom for `W`
`dfB`	Degrees of freedom for `B`
`dfT`	Degrees of freedom for `T`
`lambda`	Vector of values of Wilk's lambda test statistic for testing whether the means have dimension 0, 1, etc.
`chisq`	Transformation of `lambda` to an approximate chi-square distribution
`chisqdf`	Degrees of freedom for `chisq`
`eigenval`	Eigenvalues of $W^{-1}B$
`eigenvec`	Eigenvectors of $W^{-1}B$; these are the coefficients for the canonical variables `C`, and they are scaled so the within-group variance of the canonical variables is 1

Field	Contents
`canon`	Canonical variables `C`, equal to `XC*eigenvec`, where `XC` is `X` with columns centered by subtracting their means
`mdist`	A vector of Mahalanobis distances from each point to the mean of its group
`gmdist`	A matrix of Mahalanobis distances between each pair of group means

The canonical variables `C` are linear combinations of the original variables, chosen to maximize the separation between groups. Specifically, `C(:,1)` is the linear combination of the `X` columns that has the maximum separation between groups. This means that among all possible linear combinations, it is the one with the most significant F statistic in a one-way analysis of variance. `C(:,2)` has the maximum separation subject to it being orthogonal to `C(:,1)`, and so on.

You may find it useful to use the outputs from `manova1` along with other functions to supplement your analysis. For example, you may want to start with a grouped scatter plot matrix of the original variables using `gplotmatrix`. You can use `gscatter` to visualize the group separation using the first two canonical variables. You can use `manovacluster` to graph a dendrogram showing the clusters among the group means.

Assumptions

The MANOVA test makes the following assumptions about the data in `X`:

- The populations for each group are normally distributed.
- The variance-covariance matrix is the same for each population.
- All observations are mutually independent.

Examples

you can use `manova1` to determine whether there are differences in the averages of four car characteristics, among groups defined by the country where the cars were made.

```
load carbig
[d,p] = manova1([MPG Acceleration Weight Displacement],...
                Origin)
d =
   3
p =
      0
  0.0000
  0.0075
  0.1934
```

There are four dimensions in the input matrix, so the group means must lie in a four-dimensional space. `manova1` shows that you cannot reject the hypothesis that the means lie in a 3-D subspace.

References

[1] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

See Also

`anova1` | `canoncorr` | `gscatter` | `gplotmatrix`

How To

- "Grouped Data" on page 2-34
- `manovacluster`

manovacluster

Purpose

Dendrogram of group mean clusters following MANOVA

Syntax

```
manovacluster(stats)
manovacluster(stats,method)
H = manovacluster(stats,method)
```

Description

`manovacluster(stats)` generates a dendrogram plot of the group means after a multivariate analysis of variance (MANOVA). `stats` is the output `stats` structure from `manova1`. The clusters are computed by applying the single linkage method to the matrix of Mahalanobis distances between group means.

See `dendrogram` for more information on the graphical output from this function. The dendrogram is most useful when the number of groups is large.

`manovacluster(stats,method)` uses the specified method in place of single linkage. *`method`* can be any of the following character strings that identify ways to create the cluster hierarchy. (See `linkage` for additional information.)

Method	Description
`'single'`	Shortest distance (default)
`'complete'`	Largest distance
`'average'`	Average distance
`'centroid'`	Centroid distance
`'ward'`	Incremental sum of squares

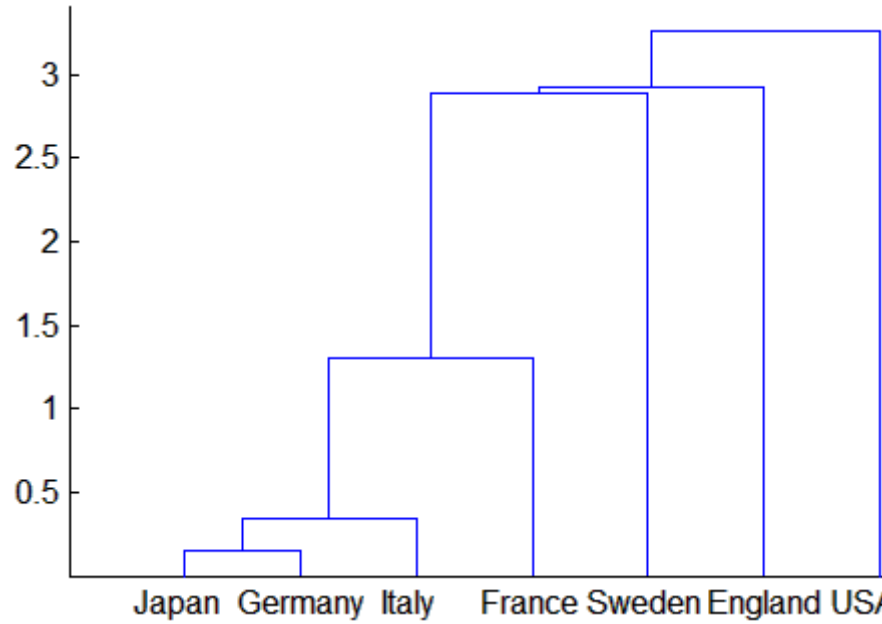
`H = manovacluster(stats,method)` returns a vector of handles to the lines in the figure.

Examples

Let's analyze the larger car data set to determine which countries produce cars with the most similar characteristics.

```
load carbig
```

```
X = [MPG Acceleration Weight Displacement];
[d,p,stats] = manova1(X,Origin);
manovacluster(stats)
```



See Also

`cluster` | `dendrogram` | `linkage` | `manova1`

CompactClassificationDiscriminant.margin

Purpose

Classification margins

Syntax

```
m = margin(obj,X,Y)
```

Description

`m = margin(obj,X,Y)` returns the classification margins for the matrix of predictors `X` and class labels `Y`. For the definition, see "Definitions" on page 20-1000.

Input Arguments

`obj`

Discriminant analysis classifier of class `ClassificationDiscriminant` or `CompactClassificationDiscriminant`, typically constructed with `ClassificationDiscriminant.fit`.

`X`

Matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `obj`.

`Y`

Class labels, with the same data type as exists in `obj`. The number of elements of `Y` must equal the number of rows of `X`.

Output Arguments

`m`

Numeric column vector of length `size(X,1)`. Each entry in `m` represents the margin for the corresponding rows of `X` and (true class) `Y`, computed using `obj`.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `X`. A high value of margin indicates a more reliable prediction than a low value.

Score (discriminant analysis)

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see "Posterior Probability" on page 12-7.

Examples

Compute the classification margin for the Fisher iris data, trained on its first two columns of data, and view the last 10 entries:

```
load fisheriris
X = meas(:,1:2);
obj = ClassificationDiscriminant.fit(X,species);
M = margin(obj,X,species);
M(end-10:end)

ans =
    0.6551
    0.4838
    0.6551
   -0.5127
    0.5659
    0.4611
    0.4949
    0.1024
    0.2787
   -0.1439
   -0.4444
```

The classifier trained on all the data is better:

```
obj = ClassificationDiscriminant.fit(meas,species);
M = margin(obj,meas,species);
M(end-10:end)

ans =
    0.9983
    1.0000
```

```
    0.9991
    0.9978
    1.0000
    1.0000
    0.9999
    0.9882
    0.9937
    1.0000
    0.9649
```

See Also

`ClassificationDiscriminant` | `edge` | `loss` | `predict`

How To

- "Discriminant Analysis" on page 12-3

Purpose

Classification margins

Syntax

```
M = margin(ens,X,Y)
M = margin(ens,X,Y,Name,Value)
```

Description

`M = margin(ens,X,Y)` returns the classification margin for the predictions of `ens` on data `X`, when the true classifications are `Y`.

`M = margin(ens,X,Y,Name,Value)` calculates margin with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

Classification ensemble created with `fitensemble`, or a compact classification ensemble created with `compact`.

`X`

Matrix of data to classify. Each row of `X` represents one observation, and each column represents one predictor. `X` must have the same number of columns as the data used to train `ens`. `X` should have the same number of rows as the number of elements in `Y`.

`Y`

Classification of `X`. `Y` should be of the same type as the classification used to train `ens`, and its number of elements should equal the number of rows of `X`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `ens.NTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NTrained`

`UseObsForLearner`

A logical matrix of size `N`-by-`T`, where:

- `N` is the number of rows of `X`.
- `T` is the number of weak learners in `ens`.

When `UseObsForLearner(i,j)` is `true`, learner `j` is used in predicting the class of row `i` of `X`.

Default: `true(N,T)`

Output Arguments

`M`

A numeric column vector with the same number of rows as `X`. Each row of `M` gives the classification margin for that row of `X`.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `X`.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Find the margin for classifying an average flower from the `Fisheriris` data as `'versicolor'`:

```
load fisheriris % X = meas, Y = species
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
flower = mean(meas);
predict(ens,flower)

ans =
    'versicolor'

margin(ens,mean(meas),'versicolor')

ans =
    3.2140
```

See Also

`predict` | `edge` | `loss`

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CompactClassificationTree.margin

Purpose

Classification margins

Syntax

```
m = margin(tree,X,Y)
```

Description

`m = margin(tree,X,Y)` returns the classification margins for the matrix of predictors `X` and class labels `Y`. For the definition, see "Margin" on page 20-1006.

Input Arguments

`tree`

A classification tree created by `ClassificationTree.fit`, or a compact classification tree created by `compact`.

`X`

A matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `tree`.

`Y`

Class labels, with the same data type as exists in `tree`.

Output Arguments

`m`

A numeric column vector of length `size(X,1)`. Each entry in `m` represents the margin for the corresponding rows of `X` and (true class) `Y`, computed using `tree`.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `X`.

Score (tree)

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that

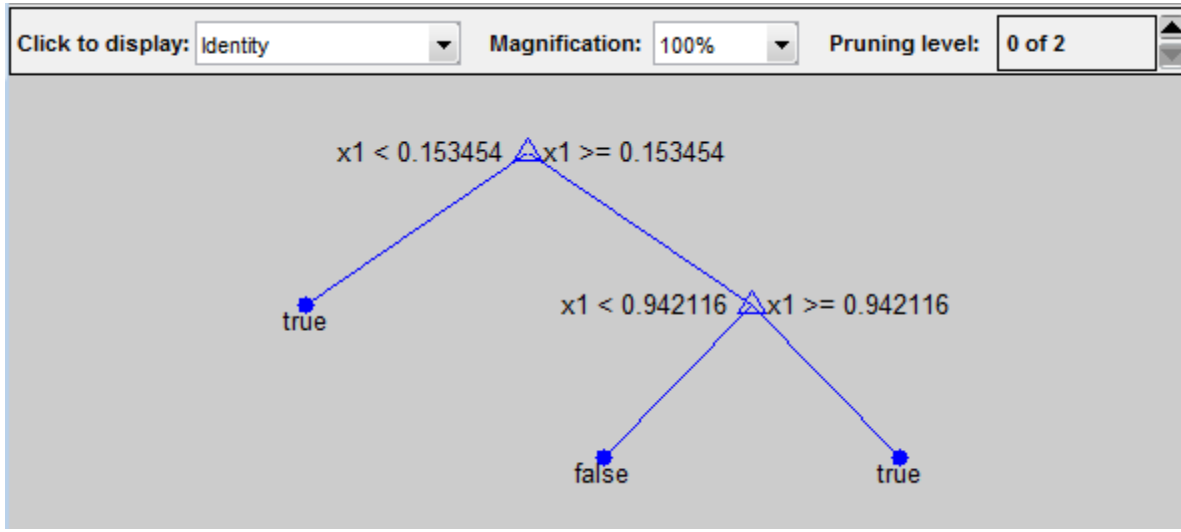
lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

1

Generate 100 random points and classify them:

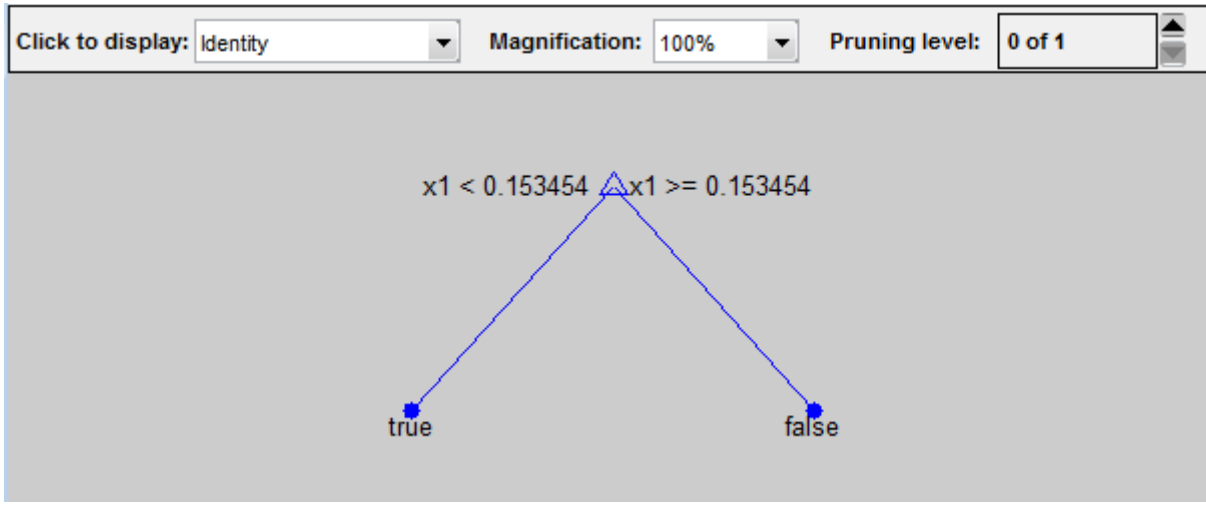
```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = ClassificationTree.fit(X,Y);
view(tree,'mode','graph')
```



2

Prune the tree:

```
tree1 = prune(tree,'level',1);
view(tree1,'mode','graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

3

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]

ans =
    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
```

```
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the rightmost column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Compute the classification margin for the Fisher iris data, trained on its first two columns of data, and view the last 10 entries:

```
load fisheriris
X = meas(:,1:2);
tree = ClassificationTree.fit(X,species);
M = margin(tree,X,species);
M(end-10:end)

ans =
    0.1111
    0.1111
    0.1111
   -0.2857
    0.6364
    0.6364
    0.1111
    0.7500
    1.0000
    0.6364
    0.2000
```

The classification tree trained on all the data is better:

```
tree = ClassificationTree.fit(meas,species);
M = margin(tree,meas,species);
M(end-10:end)
```

```
ans =
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
```

See Also

`predict` | `loss` | `edge`

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Purpose

Classification margin

Syntax

```
mar = margin(B,X,Y)
mar = margin(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`mar = margin(B,X,Y)` computes the classification margins for predictors `X` given true response `Y`. The `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. `mar` is a numeric array of size `Nobs`-by-`NTrees`, where `Nobs` is the number of rows of `X` and `Y`, and `NTrees` is the number of trees in the ensemble `B`. For observation `I` and tree `J`, `mar(I,J)` is the difference between the score for the true class and the largest score for other classes. This method is available for classification ensembles only.

`mar = margin(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how the method computes errors. If set to `'cumulative'` (default), `margin` computes cumulative errors and `mar` is an `Nobs`-by-`NTrees` matrix, where the first column gives error from `trees(1)`, second column gives error from`trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is a `Nobs`-by-`NTrees` matrix, where each element is an error from each tree in the ensemble. If set to `'ensemble'`, `mar` a single column of length `Nobs` showing the cumulative margins for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element

gives error from `trees(1)`, the second element gives error from `trees(1:2)` etc.

`'treeweights'` Vector of tree weights. This vector must have the same length as the `'trees'` vector. The method uses these weights to combine output from the specified trees by taking a weighted average instead of the simple non-weighted majority vote. You cannot use this argument in the `'individual'` mode.

`'useifort'` Logical matrix of size `Nobs`-by-`NTrees` indicating which trees should be used to make predictions for each observation. By default the method uses all trees for all observations.

See Also

`TreeBagger.margin`

Purpose

Classification margin

Syntax

```
mar = margin(B,X,Y)
mar = margin(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`mar = margin(B,X,Y)` computes the classification margins for predictors `X` given true response `Y`. The `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. `mar` is a numeric array of size `Nobs`-by-`NTrees`, where `Nobs` is the number of rows of `X` and `Y`, and `NTrees` is the number of trees in the ensemble `B`. For observation `I` and tree `J`, `mar(I,J)` is the difference between the score for the true class and the largest score for other classes. This method is available for classification ensembles only.

`mar = margin(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how the method computes errors. If set to `'cumulative'` (default), `margin` computes cumulative errors and `mar` is an `Nobs`-by-`NTrees` matrix, where the first column gives error from `trees(1)`, second column gives error from`trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is a `Nobs`-by-`NTrees` matrix, where each element is an error from each tree in the ensemble. If set to `'ensemble'`, `mar` a single column of length `Nobs` showing the cumulative margins for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element

gives error from `trees(1)`, the second element gives error from `trees(1:2)` etc.

`'treeweights'` Vector of tree weights. This vector must have the same length as the `'trees'` vector. The method uses these weights to combine output from the specified trees by taking a weighted average instead of the simple non-weighted majority vote. You cannot use this argument in the `'individual'` mode.

`'useifort'` Logical matrix of size `Nobs`-by-`NTrees` indicating which trees should be used to make predictions for each observation. By default the method uses all trees for all observations.

See Also

`CompactTreeBagger.margin`

Purpose

Nonclassical multidimensional scaling

Syntax

```
Y = mdscale(D,p)
[Y,stress] = mdscale(D,p)
[Y,stress,disparities] = mdscale(D,p)
[...] = mdscale(D,p,'Name',value)
```

Description

`Y = mdscale(D,p)` performs nonmetric multidimensional scaling on the n-by-n dissimilarity matrix `D`, and returns `Y`, a configuration of n points (rows) in `p` dimensions (columns). The Euclidean distances between points in `Y` approximate a monotonic transformation of the corresponding dissimilarities in `D`. By default, `mdscale` uses Kruskal's normalized stress1 criterion.

You can specify `D` as either a full n-by-n matrix, or in upper triangle form such as is output by `pdist`. A full dissimilarity matrix must be real and symmetric, and have zeros along the diagonal and non-negative elements everywhere else. A dissimilarity matrix in upper triangle form must have real, non-negative entries. `mdscale` treats `NaN`s in `D` as missing values, and ignores those elements. `Inf` is not accepted.

You can also specify `D` as a full similarity matrix, with ones along the diagonal and all other elements less than one. `mdscale` transforms a similarity matrix to a dissimilarity matrix in such a way that distances between the points returned in `Y` approximate `sqrt(1-D)`. To use a different transformation, transform the similarities prior to calling `mdscale`.

`[Y,stress] = mdscale(D,p)` returns the minimized stress, i.e., the stress evaluated at `Y`.

`[Y,stress,disparities] = mdscale(D,p)` returns the disparities, that is, the monotonic transformation of the dissimilarities `D`.

`[...] = mdscale(D,p,'Name',value)` specifies one or more optional parameter name/value pairs that control further details of `mdscale`. Specify *`Name`* in single quotes. Available parameters are

- `Criterion`— The goodness-of-fit criterion to minimize. This also determines the type of scaling, either non-metric or metric, that `mdscale` performs. Choices for non-metric scaling are:
  - `'stress'` — Stress normalized by the sum of squares of the inter-point distances, also known as stress1. This is the default.
  - `'sstress'` — Squared stress, normalized with the sum of 4th powers of the inter-point distances.

  Choices for metric scaling are:
  - `'metricstress'` — Stress, normalized with the sum of squares of the dissimilarities.
  - `'metricsstress'` — Squared stress, normalized with the sum of 4th powers of the dissimilarities.
  - `'sammon'` — Sammon's nonlinear mapping criterion. Off-diagonal dissimilarities must be strictly positive with this criterion.
  - `'strain'` — A criterion equivalent to that used in classical multidimensional scaling.
- `Weights` — A matrix or vector the same size as `D`, containing nonnegative dissimilarity weights. You can use these to weight the contribution of the corresponding elements of `D` in computing and minimizing stress. Elements of `D` corresponding to zero weights are effectively ignored.

  Note When you specify weights as a full matrix, its diagonal elements are ignored and have no effect, since the corresponding diagonal elements of `D` do not enter into the stress calculation.

- `Start` — Method used to choose the initial configuration of points for Y. The choices are

  - `'cmdscale'` — Use the classical multidimensional scaling solution. This is the default. `'cmdscale'` is not valid when there are zero weights.
  - `'random'` — Choose locations randomly from an appropriately scaled p-dimensional normal distribution with uncorrelated coordinates.
  - An *n*-by-`p` matrix of initial locations, where n is the size of the matrix `D` and `p` is the number of columns of the output matrix `Y`. In this case, you can pass in `[]` for `p` and `mdscale` infers `p` from the second dimension of the matrix. You can also supply a 3-D array, implying a value for `'Replicates'` from the array's third dimension.

- `Replicates` — Number of times to repeat the scaling, each with a new initial configuration. The default is `1`.
- `Options` — Options for the iterative algorithm used to minimize the fitting criterion. Pass in an options structure created by `statset`. For example,

  ```
  opts = statset(param1,val1,param2,val2, ...);
  [...] = mdscale(...,'Options',opts)
  ```

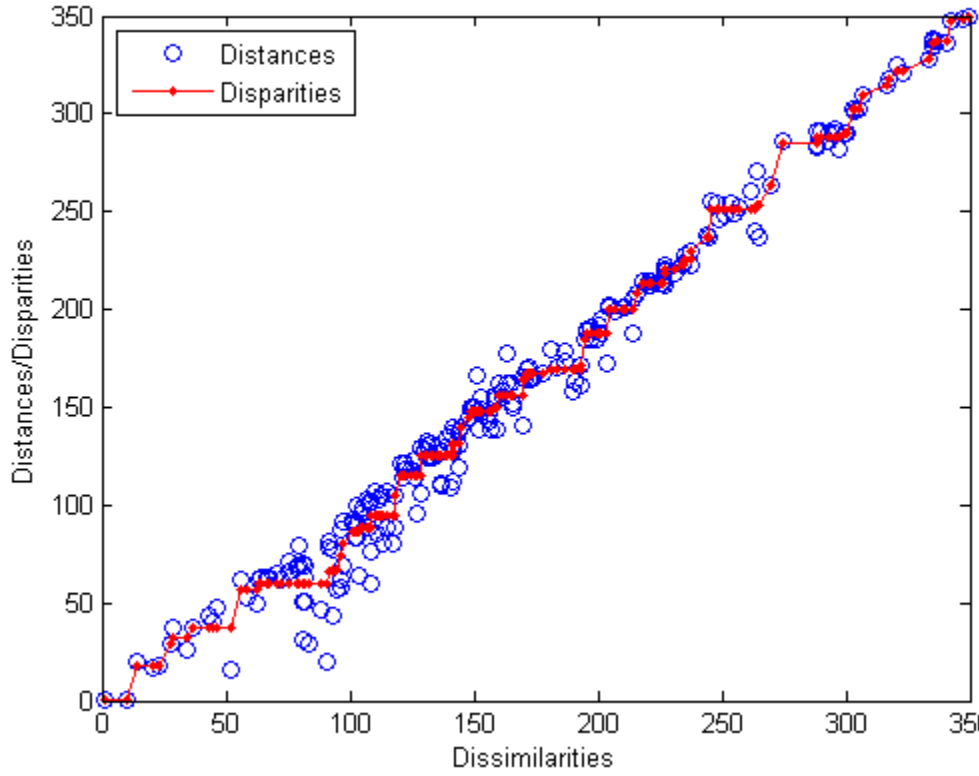
  The choices of `statset` parameters are

  - `'Display'` — Level of display output. The choices are `'off'` (the default), `'iter'`, and `'final'`.
  - `'MaxIter'` — Maximum number of iterations allowed. The default is `200`.
  - `'TolFun'` — Termination tolerance for the stress criterion and its gradient. The default is `1e-4`.
  - `'TolX'`— Termination tolerance for the configuration location step size. The default is `1e-4`.

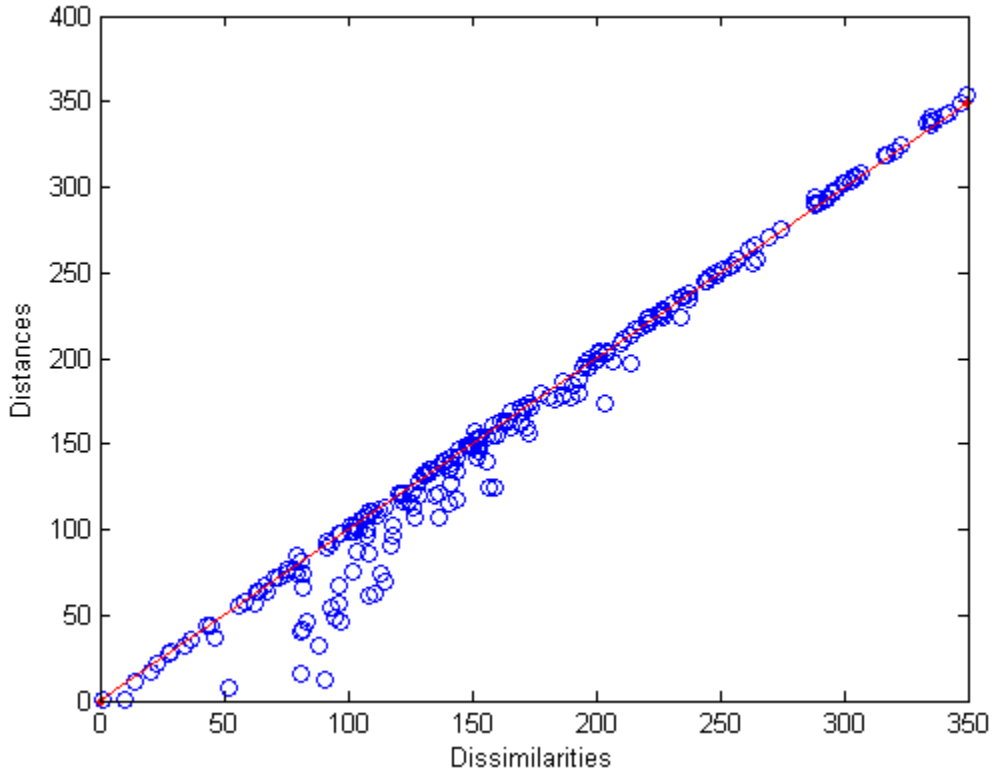
Examples

```
load cereal.mat
X = [Calories Protein Fat Sodium Fiber ...
```

```
     Carbo Sugars Shelf Potass Vitamins];

% Take a subset from a single manufacturer.
X = X(strcmp('K',cellstr(Mfg)),:);

% Create a dissimilarity matrix.
dissimilarities = pdist(X);

% Use non-metric scaling to recreate the data in 2D,
% and make a Shepard plot of the results.
[Y,stress,disparities] = mdscale(dissimilarities,2);
distances = pdist(Y);
[dum,ord] = sortrows([disparities(:) dissimilarities(:)]);
plot(dissimilarities,distances,'bo', ...
dissimilarities(ord),disparities(ord),'r.-');
xlabel('Dissimilarities'); ylabel('Distances/Disparities')
legend({'Distances' 'Disparities'},'Location','NW');
```




```
% Do metric scaling on the same dissimilarities.
figure
[Y,stress] = ...
mdscale(dissimilarities,2,'criterion','metricsstress');
distances = pdist(Y);
plot(dissimilarities,distances,'bo', ...
[0 max(dissimilarities)],[0 max(dissimilarities)],'r.-');
xlabel('Dissimilarities'); ylabel('Distances')
```



See Also `cmdscale` | `pdist` | `statset`

Purpose

Multidimensional scaling of proximity matrix

Syntax

```
[SC,EIGEN] = mdsProx(B,X)
[SC,EIGEN] = mdsProx(B,X,'param1',val1,'param2',val2,...)
```

Description

`[SC,EIGEN] = mdsProx(B,X)` applies classical multidimensional scaling to the proximity matrix computed for the data in the matrix `X`, and returns scaled coordinates `SC` and eigenvalues `EIGEN` of the scaling transformation. The method applies multidimensional scaling to the matrix of distances defined as 1-`prox`, where `prox` is the proximity matrix returned by the `proximity` method.

You can supply the proximity matrix directly by using the `'data'` parameter.

`[SC,EIGEN] = mdsProx(B,X,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'data'`	Flag indicating how the method treats the `X` input argument. If set to `'predictors'` (default), `mdsProx` assumes `X` to be a matrix of predictors and used for computation of the proximity matrix. If set to `'proximity'`, the method treats `X` as a proximity matrix returned by the `proximity` method.
`'colors'`	If you supply this argument, `mdsProx` makes overlaid scatter plots of two scaled coordinates using specified colors for different classes. You must supply the colors as a string with one character for each color. If there are more classes in the data than characters in the supplied string, `mdsProx` only plots the first `C` classes, where `C` is the length of the string. For regression or if you do not provide the vector of true class labels, the method uses the first color for all observations in `X`.

`'labels'`	Vector of true class labels for a classification ensemble. True class labels can be either a numeric vector, character matrix, or cell array of strings. If supplied, this vector must have as many elements as there are observations (rows) in `X`. This argument has no effect unless you also supply the `'colors'` argument.
`'mdscoords'`	Indices of the two scaled coordinates to plot. By default, `mdsProx` makes a scatter plot of the first and second scaled coordinates which correspond to the two largest eigenvalues. You can specify any other two or three indices not exceeding the dimensionality of the scaled data. This argument has no effect unless you also supply the `'colors'` argument.

See Also

`cmdscale` | `TreeBagger.mdsProx` | `proximity`

Purpose

Multidimensional scaling of proximity matrix

Syntax

```
[S,E] = mdsProx(B)
[S,E] = mdsProx(B,'param1',val1,'param2',val2,...)
```

Description

`[S,E] = mdsProx(B)` returns scaled coordinates, `S`, and eigenvalues, `E`, for the proximity matrix in the ensemble `B`. An earlier call to `fillProximities(B)` must create the proximity matrix.

`[S,E] = mdsProx(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'keep'`	Array of indices of observations in the training data to use for multidimensional scaling. By default, this argument is set to `'all'`. If you provide numeric or logical indices, the method uses only the subset of the training data specified by these indices to compute the scaled coordinates and eigenvalues.
`'colors'`	If you supply this argument, `mdsProx` makes overlaid scatter plots of two scaled coordinates using specified colors for different classes. You must supply the colors as a string with one character for each color. If there are more classes in the data than characters in the supplied string, `mdsProx` only plots the first `C` classes, where `C` is the length of the string. For regression or if you do not provide the vector of true class labels, the method uses the first color for all observations in `X`.
`'mdscoords'`	Indices of the two scaled coordinates to plot. By default, `mdsProx` makes a scatter plot of the first and second scaled coordinates which correspond to the two largest eigenvalues. You can specify any other two or three indices not exceeding the dimensionality of the scaled data. This argument has no effect unless you also supply the `'colors'` argument.

See Also

`cmdscale` | `CompactTreeBagger.mdsProx` | `fillProximities`

ProbDistUnivParam.mean

Purpose

Return mean of ProbDistUnivParam object

Syntax

```
M = mean(PD)
```

Description

`M = mean(PD)` returns *M*, the mean of the ProbDistUnivParam object *PD*.

Input Arguments

PD	An object of the class `ProbDistUnivParam`.

Output Arguments

M	The mean of the ProbDistUnivParam object *PD*.

See Also

`mean`

Purpose

Mean classification margin

Syntax

```
mar = meanMargin(B,X,Y)
mar = meanMargin(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`mar = meanMargin(B,X,Y)` computes average classification margins for predictors `X` given true response `Y`. The `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. `meanMargin` averages the margins over all observations (rows) in `X` for each tree. `mar` is a matrix of size 1-by-`NTrees`, where `NTrees` is the number of trees in the ensemble `B`. This method is available for classification ensembles only.

`mar = meanMargin(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how `meanMargin` computes errors. If set to `'cumulative'` (default), is a vector of length NTrees where the first element gives mean margin from `trees(1)`, second column gives mean margins from `trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is a vector of length `NTrees`, where each element is a mean margin from each tree in the ensemble . If set to `'ensemble'`, `mar` is a scalar showing the cumulative mean margin for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element

gives mean margin from `trees(1)`, the second element gives mean margin from `trees(1:2)` etc.

`'treeweights'` Vector of tree weights. This vector must have the same length as the `'trees'` vector. `meanMargin` uses these weights to combine output from the specified trees by taking a weighted average instead of the simple nonweighted majority vote. You cannot use this argument in the `'individual'` mode.

See Also

`TreeBagger.meanMargin`

Purpose

Mean classification margin

Syntax

```
mar = meanMargin(B,X,Y)
mar = meanMargin(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`mar = meanMargin(B,X,Y)` computes average classification margins for predictors `X` given true response `Y`. The `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. `meanMargin` averages the margins over all observations (rows) in `X` for each tree. `mar` is a matrix of size 1-by-`NTrees`, where `NTrees` is the number of trees in the ensemble `B`. This method is available for classification ensembles only.

`mar = meanMargin(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how `meanMargin` computes errors. If set to `'cumulative'` (default), is a vector of length NTrees where the first element gives mean margin from `trees(1)`, second column gives mean margins from `trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is a vector of length `NTrees`, where each element is a mean margin from each tree in the ensemble . If set to `'ensemble'`, `mar` is a scalar showing the cumulative mean margin for the entire ensemble .
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element

gives mean margin from `trees(1)`, the second element gives mean margin from `trees(1:2)` etc.

`'treeweights'` Vector of tree weights. This vector must have the same length as the `'trees'` vector. `meanMargin` uses these weights to combine output from the specified trees by taking a weighted average instead of the simple nonweighted majority vote. You cannot use this argument in the `'individual'` mode.

See Also

`CompactTreeBagger.meanMargin`

Purpose

Mean predictive measure of association for surrogate splits in decision tree

Syntax

```
MA = meansurrvarassoc(T)
MA = meansurrvarassoc(T,N)
```

Description

`MA = meansurrvarassoc(T)` returns a p-by-p matrix, `MA`, with predictive measures of association for p predictors. Element `MA(`i`,`j`)` is the predictive measure of association averaged over surrogate splits on predictor j for which predictor i is the optimal split predictor. This average is computed by summing positive values of the predictive measure of association over optimal splits on predictor i and surrogate splits on predictor j and dividing by the total number of optimal splits on predictor i, including splits for which the predictive measure of association between predictors i and j is negative.

`MA = meansurrvarassoc(T,N)` takes an array `N` of node numbers and returns the predictive measure of association averaged over the specified nodes.

See Also

`classregtree` | `surrcutvar` | `surrvarassoc` | `surrcutcategories` | `surrcuttype` | `surrcutpoint` | `surrcutflip`

CompactClassificationTree.meanSurrVarAssoc

Purpose

Mean predictive measure of association for surrogate splits in decision tree

Syntax

```
ma = meanSurrVarAssoc(tree)
ma = meanSurrVarAssoc(tree,N)
```

Description

`ma = meanSurrVarAssoc(tree)` returns a matrix of predictive measures of association for the predictors in `tree`.

`ma = meanSurrVarAssoc(tree,N)` returns a matrix of predictive measures of association averaged over the nodes in vector `N`.

Input Arguments

`tree`

A classification tree constructed with `ClassificationTree.fit`, or a compact regression tree constructed with `compact`.

`N`

Vector of node numbers in `tree`.

Output Arguments

`ma`

- `ma = meanSurrVarAssoc(tree)` returns a `P`-by-`P` matrix, where `P` is the number of predictors in `tree`. `ma(i,j)` is the predictive measure of association between the optimal split on variable `i` and a surrogate split on variable `j`. See "Predictive Measure of Association" on page 20-1030.
- `ma = meanSurrVarAssoc(tree,N)` returns a `P`-by-`P` representing the predictive measure of association between variables averaged over nodes in the vector `N`. `N` contains node numbers from `1` to `max(tree.NumNodes)`.

Definitions

Predictive Measure of Association

The predictive measure of association between the optimal split on variable i and a surrogate split on variable j is:

$$\lambda_{i,j} = \frac{\min(P_L, P_R) - \left(1 - P_{L_i L_j} - P_{R_i R_j}\right)}{\min(P_L, P_R)}.$$

Here

- P_L and P_R are the node probabilities for the optimal split of node i into Left and Right nodes respectively.
- $P_{L_i L_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Left.
- $P_{R_i R_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Right.

Clearly, $\lambda_{i,j}$ lies from $-\infty$ to 1. Variable j is a worthwhile surrogate split for variable i if $\lambda_{i,j}>0$.

Element `ma(i,j)` is the predictive measure of association averaged over surrogate splits on predictor `j` for which predictor `i` is the optimal split predictor. This average is computed by summing positive values of the predictive measure of association over optimal splits on predictor `i` and surrogate splits on predictor `j` and dividing by the total number of optimal splits on predictor `i`, including splits for which the predictive measure of association between predictors `i` and `j` is negative.

Examples

Find the mean predictive measure of association between the variables in the Fisher iris data:

```
load fisheriris
obj = ClassificationTree.fit(meas,species,'surrogate','on');
msva = meanSurrVarAssoc(obj)

msva =
    1.0000         0         0         0
         0    1.0000         0         0
    0.4633    0.2500    1.0000    0.5000
```

```
    0.2065    0.1413    0.4022    1.0000
```

Find the mean predictive measure of association averaged over the odd-numbered nodes in `obj`:

```
N = 1:2:obj.NumNodes;
msva = meanSurrVarAssoc(obj,N)

msva =
    1.0000         0         0         0
         0    1.0000         0         0
    0.7600    0.5000    1.0000    1.0000
    0.4130    0.2826    0.8043    1.0000
```

See Also

`ClassificationTree`

How To

- Chapter 13, "Nonparametric Supervised Learning"

Purpose

Mean predictive measure of association for surrogate splits in decision tree

Syntax

```
ma = meanSurrVarAssoc(tree)
ma = meanSurrVarAssoc(tree,N)
```

Description

`ma = meanSurrVarAssoc(tree)` returns a matrix of predictive measures of association for the predictors in `tree`.

`ma = meanSurrVarAssoc(tree,N)` returns a matrix of predictive measures of association averaged over the nodes in vector `N`.

Input Arguments

`tree`

A regression tree constructed with `RegressionTree.fit`, or a compact regression tree constructed with `compact`.

`N`

Vector of node numbers in `tree`.

Output Arguments

`ma`

- `ma = meanSurrVarAssoc(tree)` returns a `P`-by-`P` matrix, where `P` is the number of predictors in `tree`. `ma(i,j)` is the predictive measure of association between the optimal split on variable `i` and a surrogate split on variable `j`. See "Predictive Measure of Association" on page 20-1033.
- `ma = meanSurrVarAssoc(tree,N)` returns a `P`-by-`P` representing the predictive measure of association between variables averaged over nodes in the vector `N`. `N` contains node numbers from `1` to `max(tree.NumNodes)`.

Definitions

Predictive Measure of Association

The predictive measure of association between the optimal split on variable i and a surrogate split on variable j is:

$$\lambda_{i,j} = \frac{\min(P_L, P_R) - \left(1 - P_{L_i L_j} - P_{R_i R_j}\right)}{\min(P_L, P_R)}.$$

Here

- P_L and P_R are the node probabilities for the optimal split of node i into Left and Right nodes respectively.
- $P_{L_i L_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Left.
- $P_{R_i R_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Right.

Clearly, $\lambda_{i,j}$ lies from $-\infty$ to 1. Variable j is a worthwhile surrogate split for variable i if $\lambda_{i,j} > 0$.

Element `ma(i,j)` is the predictive measure of association averaged over surrogate splits on predictor `j` for which predictor `i` is the optimal split predictor. This average is computed by summing positive values of the predictive measure of association over optimal splits on predictor `i` and surrogate splits on predictor `j` and dividing by the total number of optimal splits on predictor `i`, including splits for which the predictive measure of association between predictors `i` and `j` is negative.

Examples

Find the mean predictive measure of association between the `Displacement`, `Horsepower`, and `Weight` variables in the `carsmall` data:

```
load carsmall
X = [Displacement Horsepower Weight];
tree = RegressionTree.fit(X,MPG,'surrogate','on');
ma = meanSurrVarAssoc(tree)

ma =
    1.0000    0.2708    0.3854
    0.4764    1.0000    0.4568
```

```
    0.3472    0.2326    1.0000
```

Find the mean predictive measure of association averaged over the odd-numbered nodes in `tree`:

```
N = 1:2:tree.NumNodes;
ma = meanSurrVarAssoc(tree,N)

ma =
    1.0000    0.2500    0.3750
    0.5910    1.0000    0.5861
    0.5000    0.2361    1.0000
```

See Also

`prune` | `RegressionTree`

How To

- Chapter 13, "Nonparametric Supervised Learning"

ProbDistUnivKernel.median

Purpose

Return median of ProbDistUnivKernel object

Syntax

```
M = median(PD)
```

Description

`M = median(PD)` returns *M*, the median of the ProbDistUnivKernel object *PD*.

Input Arguments

PD	An object of the class `ProbDistUnivKernel`.

Output Arguments

M	The median of the ProbDistUnivKernel object *PD*.

See Also

`median`

Purpose

Return median of ProbDistUnivParam object

Syntax

```
M = median(PD)
```

Description

`M = median(PD)` returns *M*, the median of the ProbDistUnivParam object *PD*.

Input Arguments

PD	An object of the class `ProbDistUnivParam`.

Output Arguments

M	The median of the ProbDistUnivParam object *PD*.

See Also

`median`

TreeBagger.MergeLeaves property

Purpose

Flag to merge leaves that do not improve risk

Description

The `MergeLeaves` property is true if decision trees have their leaves with the same parent merged for splits that do not decrease the total risk, and false otherwise. The default value is false.

See Also

`classregtree`

Purpose

Merge levels

Syntax

```
B = mergelevels(A,oldlevels,newlevel)
B = mergelevels(A,oldlevels)
```

Description

`B = mergelevels(A,oldlevels,newlevel)` merges two or more levels of the categorical array `A` into a single new level. `oldlevels` is a cell array of strings or a 2-D character matrix that specifies the levels to be merged. Any elements of `A` that have levels in `oldlevels` are assigned the new level in the corresponding elements of `B`. `newlevel` is a character string that specifies the label for the new level. For ordinal arrays, the levels of `A` specified by `oldlevels` must be consecutive, and `mergelevels` inserts the new level to preserve the order of the levels.

`B = mergelevels(A,oldlevels)` merges two or more levels of `A`. For nominal arrays, `mergelevels` uses the first label in `oldlevels` as the label for the new level. For ordinal arrays, `mergelevels` uses the label corresponding to the lowest level in `oldlevels` as the label for the new level.

Examples

Example 1

For nominal data:

```
load fisheriris
species = nominal(species);
species = mergelevels(species,...
                      {'setosa','virginica'},'parent');
species = setlabels(species,'hybrid','versicolor');
getlabels(species)
ans =
    'hybrid'   'parent'
```

Example 2

For ordinal data:

```
A = ordinal([1 2 3 2 1],{'lo','med','hi'})
A =
     lo      med      hi      med      lo

A = mergelevels(A,{'lo','med'},'bad')
A =
     bad      bad      hi      bad      bad
```

See Also

addlevels | droplevels | islevel | reorderlevels | getlabels

Purpose

Method used by trees (classification or regression)

Description

The `Method` property is `'classification'` for classification ensembles and `'regression'` for regression ensembles.

mhsample

Purpose

Metropolis-Hastings sample

Syntax

```
smpl = mhsample(start,nsamples,'pdf',pdf,'proppdf',proppdf,
   'proprnd',proprnd)
smpl = mhsample(...,'symmetric',sym)
smpl = mhsample(...,'burnin',K)
smpl = mhsample(...,'thin',m)
smpl = mhsample(...,'nchain',n)
[smpl,accept] = mhsample(...)
```

Description

`smpl = mhsample(start,nsamples,'pdf',pdf,'proppdf',proppdf, 'proprnd',proprnd)` draws `nsamples` random samples from a target stationary distribution `pdf` using the Metropolis-Hastings algorithm.

`start` is a row vector containing the start value of the Markov Chain, `nsamples` is an integer specifying the number of samples to be generated, and `pdf`, `proppdf`, and `proprnd` are function handles created using `@`. `proppdf` defines the proposal distribution density, and `proprnd` defines the random number generator for the proposal distribution. `pdf` and `proprnd` take one argument as an input with the same type and size as `start`. `proppdf` takes two arguments as inputs with the same type and size as `start`.

`smpl` is a column vector or matrix containing the samples. If the log density function is preferred, `'pdf'` and `'proppdf'` can be replaced with `'logpdf'` and `'logproppdf'`. The density functions used in Metropolis-Hastings algorithm are not necessarily normalized.

The proposal distribution $q(x,y)$ gives the probability density for choosing x as the next point when y is the current point. It is sometimes written as $q(x|y)$.

If the `proppdf` or `logproppdf` satisfies $q(x,y) = q(y,x)$, that is, the proposal distribution is symmetric, `mhsample` implements Random Walk Metropolis-Hastings sampling. If the `proppdf` or `logproppdf` satisfies $q(x,y) = q(x)$, that is, the proposal distribution is independent of current values, `mhsample` implements Independent Metropolis-Hastings sampling.

`smpl = mhsample(...,'symmetric',sym)` draws `nsamples` random samples from a target stationary distribution `pdf` using the Metropolis-Hastings algorithm. `sym` is a logical value that indicates whether the proposal distribution is symmetric. The default value is false, which corresponds to the asymmetric proposal distribution. If `sym` is true, for example, the proposal distribution is symmetric, `proppdf` and `logproppdf` are optional.

`smpl = mhsample(...,'burnin',K)` generates a Markov chain with values between the starting point and the k^{th} point omitted in the generated sequence. Values beyond the k^{th} point are kept. `k` is a nonnegative integer with default value of `0`.

`smpl = mhsample(...,'thin',m)` generates a Markov chain with `m-1` out of `m` values omitted in the generated sequence. `m` is a positive integer with default value of `1`.

`smpl = mhsample(...,'nchain',n)` generates `n` Markov chains using the Metropolis-Hastings algorithm. `n` is a positive integer with a default value of 1. `smpl` is a matrix containing the samples. The last dimension contains the indices for individual chains.

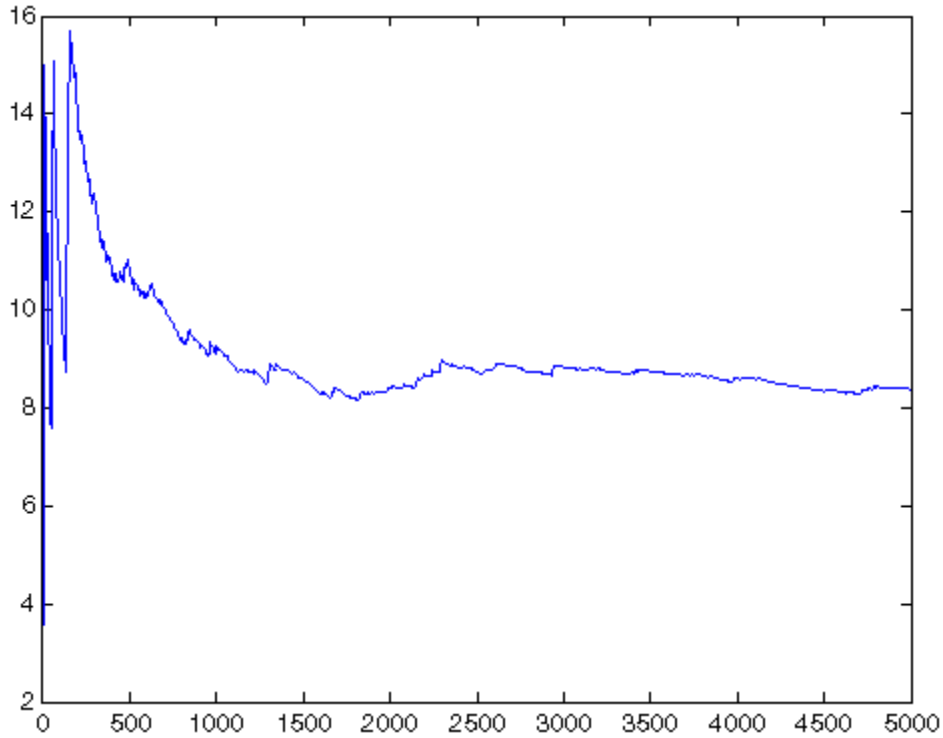
`[smpl,accept] = mhsample(...)` also returns `accept`, the acceptance rate of the proposed distribution. `accept` is a scalar if a single chain is generated and is a vector if multiple chains are generated.

Examples

Estimate the second order moment of a Gamma distribution using the Independent Metropolis-Hastings sampling.

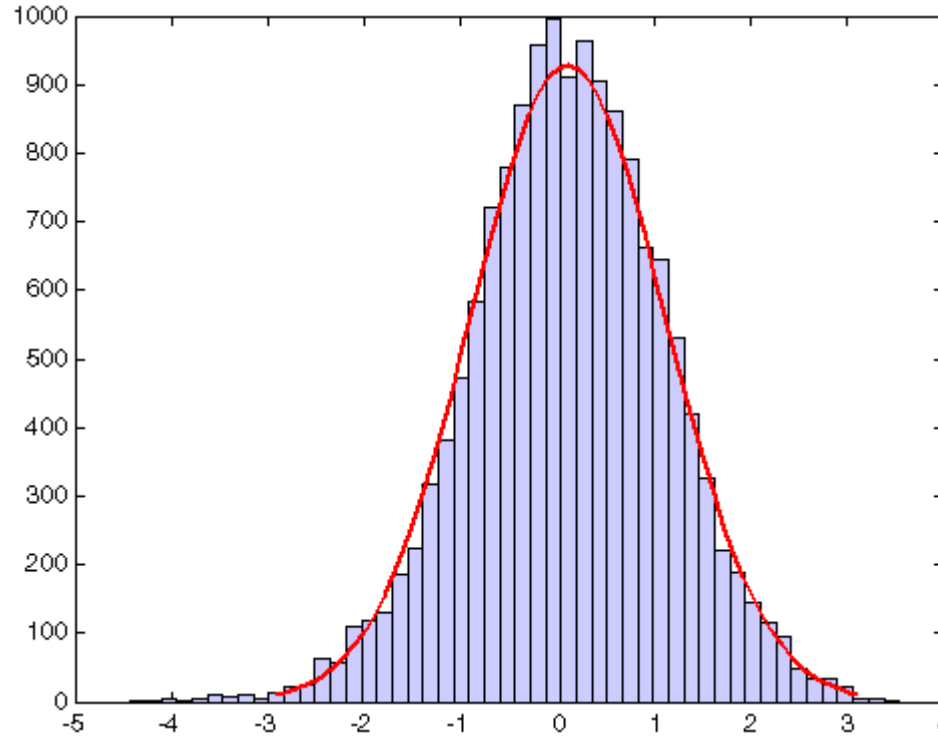
```
alpha = 2.43;
beta = 1;
pdf = @(x)gampdf(x,alpha,beta); %target distribution
proppdf = @(x,y)gampdf(x,floor(alpha),floor(alpha)/alpha);
proprnd = @(x)sum(...
              exprnd(floor(alpha)/alpha,floor(alpha),1));
nsamples = 5000;
smpl = mhsample(1,nsamples,'pdf',pdf,'proprnd',proprnd,...
                'proppdf',proppdf);
xxhat = cumsum(smpl.^2)./(1:nsamples)';
```

```
plot(1:nsamples,xxhat)
```



Generate random samples from `N(0,1)` using the Random Walk Metropolis-Hastings sampling.

```
delta = .5;
pdf = @(x) normpdf(x);
proppdf = @(x,y) unifpdf(y-x,-delta,delta);
proprnd = @(x) x + rand*2*delta - delta;
nsamples = 15000;
x = mhsample(1,nsamples,'pdf',pdf,'proprnd',proprnd,'symmetric',1);
histfit(x,50)
h = get(gca,'Children');
set(h(2),'FaceColor',[.8 .8 1])
```



See Also

`slicesample` | `rand`

TreeBagger.MinLeaf property

Purpose

Minimum number of observations per tree leaf

Description

The `MinLeaf` property specifies the minimum number of observations per tree leaf. The default values are 1 for classification and 5 for regression. For `classregtree` training, the `'minparent'` value is set to `2*MinLeaf`.

See Also

`classregtree`

Purpose

Maximum likelihood estimates

Syntax

```
phat = mle(data)
[phat,pci] = mle(data)
[...] = mle(data,'distribution',dist)
[...] = mle(data,...,name1,val1,name2,val2,...)
[...] = mle(data,'pdf',pdf,'cdf',cdf,'start',start,...)
[...] = mle(data,'logpdf',logpdf,'logsf',logsf,'start',start,
   ...)
[...] = mle(data,'nloglf',nloglf,'start',start,...)
```

Description

`phat = mle(data)` returns maximum likelihood estimates (MLEs) for the parameters of a normal distribution, computed using the sample data in the vector `data`.

`[phat,pci] = mle(data)` returns MLEs and 95% confidence intervals for the parameters.

`[...] = mle(data,'distribution',dist)` computes parameter estimates for the distribution specified by *`dist`*. Acceptable strings for *`dist`*, and the returned parameters, are:

name	Distribution	Parameter 1	Parameter 2	Parameter 3
`'bernoulli'`	"Bernoulli Distribution" on page B-3	`p`: probability of success for each trial	—	—
`'beta'` or `'Beta'`	"Beta Distribution" on page B-4	`a`	`b`	—
`'bino'` or `'Binomial'`	"Binomial Distribution" on page B-7	`n`: number of trials	`p`: probability of success for each trial	—

name	Distribution	Parameter 1	Parameter 2	Parameter 3
'birnbaumsaunders'	"Birnbaum-Saunders Distribution" on page B-10	β	γ	—
'Discrete Uniform' or 'unid'	"Uniform Distribution (Discrete)" on page B-101	N: maximum observable value	—	—
'exp' or 'Exponential'	"Exponential Distribution" on page B-16	μ: mean	—	—
'ev' or 'Extreme Value'	"Extreme Value Distribution" on page B-19	μ: location parameter	σ: scale parameter	—
'gam' or 'Gamma'	"Gamma Distribution" on page B-27	a: shape parameter	b: scale parameter	—
'gev' or 'Generalized Extreme Value'	"Generalized Extreme Value Distribution" on page B-32	k: shape parameter	σ: scale parameter	μ: location parameter
'gp' or 'Generalized Pareto'	"Generalized Pareto Distribution" on page B-37	k: tail index (shape) parameter	σ: scale parameter	—
'geo' or 'Geometric'	"Geometric Distribution" on page B-41	p: probability parameter	—	—

name	Distribution	Parameter 1	Parameter 2	Parameter 3
'inversegaussian'	"Inverse Gaussian Distribution" on page B-45	μ	λ	—
'logistic'	"Logistic Distribution" on page B-49	μ	σ	—
'loglogistic'	"Loglogistic Distribution" on page B-50	μ	σ	—
'logn' or 'Lognormal'	"Lognormal Distribution" on page B-51	μ	σ	—
'nakagami'	"Nakagami Distribution" on page B-70	μ	ω	—
'nbin' or 'Negative Binomial'	"Negative Binomial Distribution" on page B-72	r: number of successes	p: probability of success in a single trial	—
'norm' or 'Normal'	"Normal Distribution" on page B-83	μ: mean	σ: standard deviation	—
'poiss' or 'Poisson'	"Poisson Distribution" on page B-89	λ: mean	—	—
'rayl' or 'Rayleigh'	"Rayleigh Distribution" on page B-91	b: scale parameter	—	—

name	Distribution	Parameter 1	Parameter 2	Parameter 3
'rician'	"Rician Distribution" on page B-93	s: noncentrality parameter	σ: scale parameter	—
'tlocationscale'	"t Location-Scale Distribution" on page B-97	μ: location parameter	σ: scale parameter	ν: shape parameter
'unif' or 'Uniform'	"Uniform Distribution (Continuous)" on page B-99	a: lower endpoint (minimum)	b: upper endpoint (maximum)	—
'wbl' or 'Weibull'	"Weibull Distribution" on page B-103	a: scale parameter	b: shape parameter	—

`[...] = mle(data,...,name1,val1,name2,val2,...)` specifies optional argument name/value pairs chosen from the following list.

Name	Value
'censoring'	A Boolean vector of the same size as data, containing ones when the corresponding elements of data are right-censored observations and zeros when the corresponding elements are exact observations. The default is that all observations are observed exactly. Censoring is not supported for all distributions.
'frequency'	A vector of the same size as data, containing nonnegative integer frequencies for the corresponding elements in data. The default is one observation per element of data.

Name	Value
'alpha'	A value between 0 and 1 specifying a confidence level of 100(1-alpha)% for pci. The default is 0.05 for 95% confidence.
'ntrials'	A scalar, or a vector of the same size as data, containing the total number of trials for the corresponding element of data. Applies only to the binomial distribution.
'options'	A structure created by a call to statset, containing numerical options for the fitting algorithm. Not applicable to all distributions.

mle can also fit custom distributions that you define using distribution functions, in one of three ways.

[...] = mle(data,'pdf',pdf,'cdf',cdf,'start',start,...) returns MLEs for the parameters of the distribution defined by the probability density and cumulative distribution functions pdf and cdf. pdf and cdf are function handles created using the @ sign. They accept as inputs a vector data and one or more individual distribution parameters, and return vectors of probability density values and cumulative probability values, respectively. If the 'censoring' name/value pair is not present, you can omit the 'cdf' name/value pair. mle computes the estimates by numerically maximizing the distribution's log-likelihood, and start is a vector containing initial values for the parameters.

[...] = mle(data,'logpdf',logpdf,'logsf',logsf,'start',start,...) returns MLEs for the parameters of the distribution defined by the log probability density and log survival functions logpdf and logsf. logpdf and logsf are function handles created using the @ sign. They accept as inputs a vector data and one or more individual distribution parameters, and return vectors of logged probability density values and logged survival function values, respectively. This form is sometimes more robust to the choice of starting point than using pdf and cdf

functions. If the 'censoring' name/value pair is not present, you can omit the 'logsf' name/value pair. start is a vector containing initial values for the distribution's parameters.

[...] = mle(data,'nloglf',nloglf,'start',start,...) returns MLEs for the parameters of the distribution whose negative log-likelihood is given by nloglf. nloglf is a function handle, specified using the @ sign, that accepts the four input arguments:

- params - a vector of distribution parameter values
- data - a vector of data
- cens - a Boolean vector of censoring values
- freq - a vector of integer data frequencies

nloglf must accept all four arguments even if you do not supply the 'censoring' or 'frequency' name/value pairs (see above). However, nloglf can safely ignore its cens and freq arguments in that case. nloglf returns a scalar negative log-likelihood value and, optionally, a negative log-likelihood gradient vector (see the 'GradObj' statset parameter below). start is a vector containing initial values for the distribution's parameters.

pdf, cdf, logpdf, logsf, or nloglf can also be cell arrays whose first element is a function handle as defined above, and whose remaining elements are additional arguments to the function. mle places these arguments at the end of the argument list in the function call.

The following optional argument name/value pairs are valid only when 'pdf' and 'cdf', 'logpdf' and 'logcdf', or 'nloglf' are given:

- 'lowerbound' — A vector the same size as start containing lower bounds for the distribution parameters. The default is -Inf.
- 'upperbound' — A vector the same size as start containing upper bounds for the distribution parameters. The default is Inf.
- 'optimfun' — A string, either 'fminsearch' or 'fmincon', naming the optimization function to be used in maximizing the likelihood.

The default is 'fminsearch'. You can only specify 'fmincon' if Optimization Toolbox software is available.

When fitting a custom distribution, use the 'options' parameter to control details of the maximum likelihood optimization. See statset('mlecustom') for parameter names and default values. mle interprets the following statset parameters for custom distribution fitting as follows:

Parameter	Value
'GradObj'	'on' or 'off', indicating whether or not fmincon can expect the function provided with the 'nloglf' name/value pair to return the gradient vector of the negative log-likelihood as a second output. The default is 'off'. Ignored when using fminsearch.
'DerivStep'	The relative difference used in finite difference derivative approximations when using fmincon, and 'GradObj' is 'off'. 'DerivStep' can be a scalar, or the same size as 'start'. The default is eps^(1/3). Ignored when using fminsearch.
'FunValCheck'	'on' or 'off', indicating whether or not mle should check the values returned by the custom distribution functions for validity. The default is 'on'. A poor choice of starting point can sometimes cause these functions to return NaNs, infinite values, or out of range values if they are written without suitable error-checking.
'TolBnd'	An offset for upper and lower bounds when using fmincon. mle treats upper and lower bounds as strict inequalities (i.e., open bounds). With fmincon, this is approximated by creating closed bounds inset from the specified upper and lower bounds by TolBnd. The default is 1e-6.

Examples

The following returns an MLE and a 95% confidence interval for the success probability of a binomial distribution with 20 trials:

```
data = binornd(20,0.75,100,1); % Simulated data, p = 0.75

[phat,pci] = mle(data,'distribution','binomial',...
                 'alpha',.05,'ntrials',20)
phat =
    0.7370
pci =
    0.7171
    0.7562
```

See Also

betafit | binofit | evfit | expfit | gamfit | gevfit | gpfit | lognfit | nbinfit | normfit | mlecov | poissfit | raylfit | statset | unifit | wblfit

Purpose

Asymptotic covariance of maximum likelihood estimators

Syntax

```
ACOV = mlecov(params,data,...)
ACOV = mlecov(params,data,'pdf',pdf,'cdf',cdf)
ACOV = mlecov(params,data,'logpdf',logpdf,'logsf',logsf)
ACOV = mlecov(params,data,'nloglf',nloglf)
[...] = mlecov(params,data,...,param1,val1,param2,val2,...)
```

Description

`ACOV = mlecov(params,data,...)` returns an approximation to the asymptotic covariance matrix of the maximum likelihood estimators of the parameters for a specified distribution. The following paragraphs describe how to specify the distribution. `mlecov` computes a finite difference approximation to the Hessian of the log-likelihood at the maximum likelihood estimates `params`, given the observed data, and returns the negative inverse of that Hessian. `ACOV` is a p-by-p matrix, where p is the number of elements in `params`.

You must specify a distribution after the input argument `data`, as follows.

`ACOV = mlecov(params,data,'pdf',pdf,'cdf',cdf)` enables you to define a distribution by its probability density and cumulative distribution functions, `pdf` and `cdf`, respectively. `pdf` and `cdf` are function handles that you create using the `@` sign. They accept a vector of data and one or more individual distribution parameters as inputs and return vectors of probability density function values and cumulative distribution values, respectively. If the `'censoring'` name/value pair (see below) is not present, you can omit the `'cdf'` name/value pair.

`ACOV = mlecov(params,data,'logpdf',logpdf,'logsf',logsf)` enables you to define a distribution by its log probability density and log survival functions, `logpdf` and `logsf`, respectively. `logpdf` and `logsf` are function handles that you create using the `@` sign. They accept as inputs a vector of data and one or more individual distribution parameters, and return vectors of logged probability density values and logged survival function values, respectively. If the `'censoring'` name/value pair (see below) is not present, you can omit the `'logsf'` name/value pair.

`ACOV = mlecov(params,data,'nloglf',nloglf)` enables you to define a distribution by its log-likelihood function. `nloglf` is a function handle, specified using the `@` sign, that accepts the following four input arguments:

- `params` — Vector of distribution parameter values
- `data` — Vector of data
- `cens` — Boolean vector of censoring values
- `freq` — Vector of integer data frequencies

`nloglf` must accept all four arguments even if you do not supply the `'censoring'` or `'frequency'` name/value pairs (see below). However, `nloglf` can safely ignore its `cens` and `freq` arguments in that case. `nloglf` returns a scalar negative log-likelihood value and, optionally, the negative log-likelihood gradient vector (see the `'gradient'` name/value pair below).

`pdf`, `cdf`, `logpdf`, `logsf`, and `nloglf` can also be cell arrays whose first element is a function handle, as defined above, and whose remaining elements are additional arguments to the function. The `mle` function places these arguments at the end of the argument list in the function call.

`[...] = mlecov(params,data,...,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` specifies optional parameter name/value pairs chosen from the following table.

Parameter	Value
'censoring'	Boolean vector of the same size as data, containing 1's when the corresponding elements of data are right-censored observations and 0's when the corresponding elements are exact observations. The default is that all observations are observed exactly. Censoring is not supported for all distributions.
'frequency'	A vector of the same size as data containing nonnegative frequencies for the corresponding elements in data. The default is one observation per element of data.
'options'	A structure opts containing numerical options for the finite difference Hessian calculation. You create opts by calling statset. The applicable statset parameters are: • 'GradObj' — 'on' or 'off', indicating whether or not the function provided with the 'nloglf' name/value pair can return the gradient vector of the negative log-likelihood as its second output. The default is 'off'. • 'DerivStep' — Relative step size used in finite difference for Hessian calculations. Can be a scalar, or the same size as params. The default is eps^(1/4). A smaller value might be appropriate if 'GradObj' is 'on'.

Examples

Create the following function:

```
function logpdf = betalogpdf(x,a,b)
logpdf = (a-1)*log(x)+(b-1)*log(1-x)-betaln(a,b);
```

Fit a beta distribution to some simulated data, and compute the approximate covariance matrix of the parameter estimates:

```
x = betarnd(1.23,3.45,25,1);
phat = mle(x,'dist','beta')
acov = mlecov(phat,x,'logpdf',@betalogpdf)
```

See Also

mle

Purpose

Multinomial probability density function

Syntax

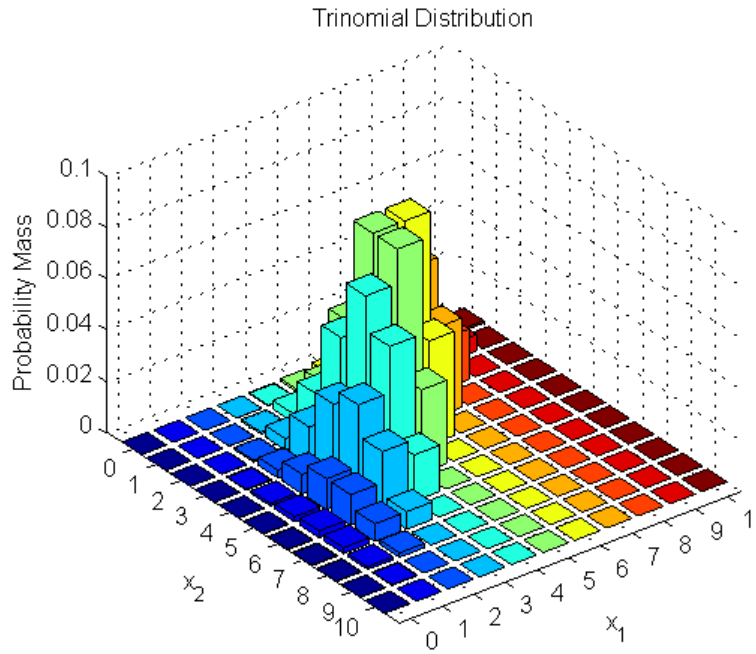
```
Y = mnpdf(X,PROB)
```

Description

`Y = mnpdf(X,PROB)` returns the pdf for the multinomial distribution with probabilities `PROB`, evaluated at each row of `X`. `X` and `PROB` are m-by-k matrices or 1-by-k vectors, where k is the number of multinomial bins or categories. Each row of `PROB` must sum to one, and the sample sizes for each observation (rows of `X`) are given by the row sums `sum(X,2)`. `Y` is an m-by-k matrix, and `mnpdf` computes each row of `Y` using the corresponding rows of the inputs, or replicates them if needed.

Examples

```
% Compute the distribution
p = [1/2 1/3 1/6]; % Outcome probabilities
n = 10; % Sample size
x1 = 0:n;
x2 = 0:n;
[X1,X2] = meshgrid(x1,x2);
X3 = n-(X1+X2);
Y = mnpdf([X1(:),X2(:),X3(:)],repmat(p,(n+1)^2,1));

% Plot the distribution
Y = reshape(Y,n+1,n+1);
bar3(Y)
set(gca,'XTickLabel',0:n)
set(gca,'YTickLabel',0:n)
xlabel('x_1')
ylabel('x_2')
zlabel('Probability Mass')
title('Trinomial Distribution')
```



Note that the visualization does not show x_3, which is determined by the constraint $x_1 + x_2 + x_3 = n$.

See Also

`mnrnd`

How To

- “Multinomial Distribution” on page B-54

Purpose

Multinomial logistic regression

Syntax

```
B = mnrfit(X,Y)
B = mnrfit(X,Y,param1,val1,param2,val2,...)
[B,dev] = mnrfit(...)
[B,dev,stats] = mnrfit(...)
```

Description

`B = mnrfit(X,Y)` returns a matrix `B` of coefficient estimates for a multinomial logistic regression of the responses in `Y` on the predictors in `X`. `X` is an n-by-p matrix of p predictors at each of n observations. `Y` is an n-by-k matrix, where `Y(i,j)` is the number of outcomes of the multinomial category `j` for the predictor combinations given by `X(i,:)`. The sample sizes for each observation are given by the row sums `sum(Y,2)`.

Alternatively, `Y` can be an n-by-1 column vector of scalar integers from 1 to k indicating the value of the response for each observation, and all sample sizes are taken to be 1.

The result `B` is a (p+1)-by-(k–1) matrix of estimates, where each column corresponds to the estimated intercept term and predictor coefficients, one for each of the first k–1 multinomial categories. The estimates for the k^{th} category are taken to be zero.

Note `mnrfit` automatically includes a constant term in all models. Do not enter a column of 1s directly into `X`.

`mnrfit` treats `NaN`s in either `X` or `Y` as missing values, and ignores them.

`B = mnrfit(X,Y,param1,val1,param2,val2,...)` allows you to specify optional parameter name/value pairs to control the model fit. Parameters are:

- `'model'` — The type of model to fit; one of the text strings `'nominal'` (the default), `'ordinal'`, or `'hierarchical'`

- `'interactions'` — Determines whether the model includes an interaction between the multinomial categories and the coefficients. Specify as `'off'` to fit a model with a common set of coefficients for the predictor variables, across all multinomial categories. This is often described as *parallel regression*. Specify as `'on'` to fit a model with different coefficients across categories. In all cases, the model has different intercepts across categories. Thus, `B` is a vector containing $k-1+p$ coefficient estimates when `'interaction'` is `'off'`, and a $(p+1)$-by-$(k-1)$ matrix when it is `'on'`. The default is `'off'` for ordinal models, and `'on'` for nominal and hierarchical models.
- `'link'` — The link function to use for ordinal and hierarchical models. The link function defines the relationship $g(\mu_{ij}) = x_i b_j$ between the mean response for the i^{th} observation in the j^{th} category, μ_{ij} , and the linear combination of predictors $x_i b_j$. Specify the link parameter value as one of the text strings `'logit'`(the default), `'probit'`, `'comploglog'`, or `'loglog'`. You may not specify the `'link'` parameter for nominal models; these always use a multivariate logistic link.
- `'estdisp'` — Specify as `'on'` to estimate a dispersion parameter for the multinomial distribution in computing standard errors, or `'off'` (the default) to use the theoretical dispersion value of 1.

`[B,dev] = mnrfit(...)` returns the deviance of the fit `dev`.

`[B,dev,stats] = mnrfit(...)` returns a structure `stats` that contains the following fields:

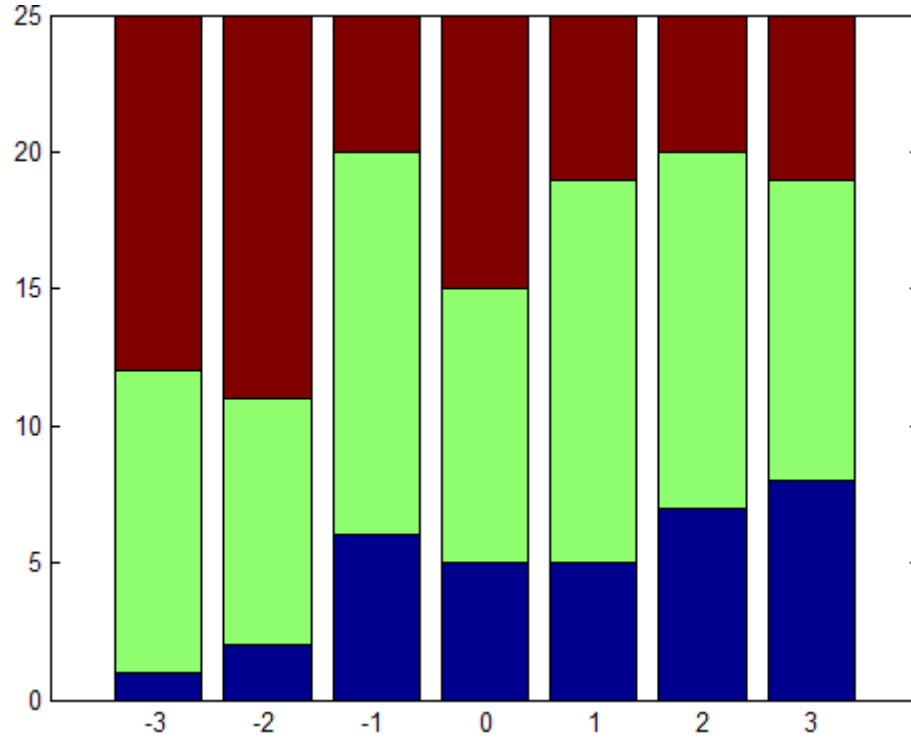
- `dfe` — Degrees of freedom for error
- `s` — Theoretical or estimated dispersion parameter
- `sfit` — Estimated dispersion parameter
- `se` — Standard errors of coefficient estimates `B`
- `coeffcorr` — Estimated correlation matrix for `B`
- `covb` — Estimated covariance matrix for `B`

- `t` — *t* statistics for `B`
- `p` — *p*-values for `B`
- `resid` — Residuals
- `residp` — Pearson residuals
- `residd` — Deviance residuals

Examples

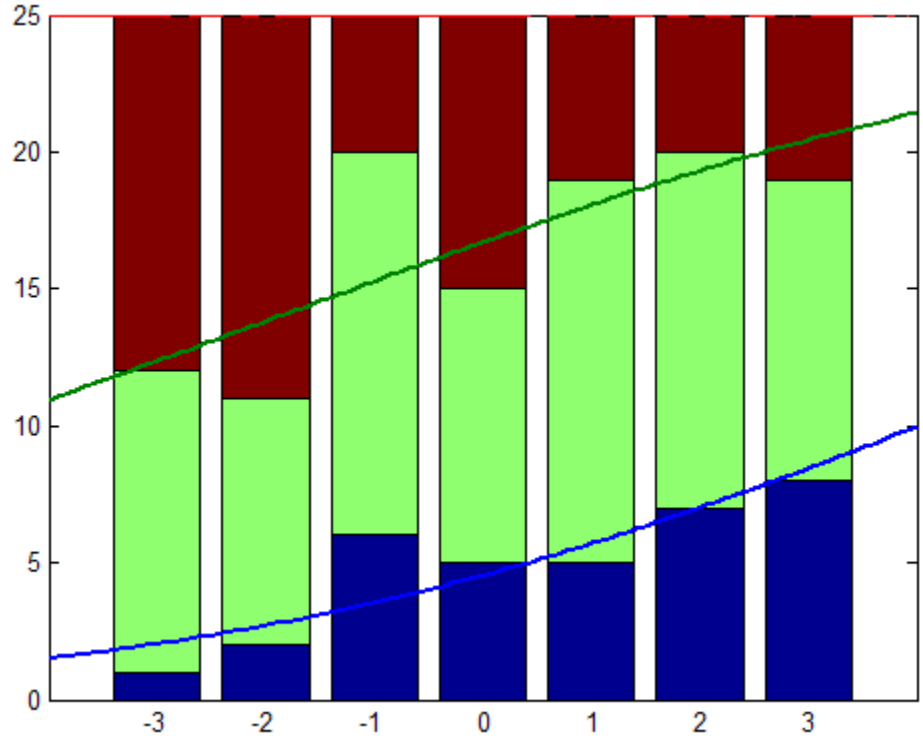
Fit multinomial logistic regression models to data with one predictor variable and three categories in the response variable:

```
x = [-3 -2 -1 0 1 2 3]';
Y = [1 11 13; 2 9 14; 6 14 5; 5 10 10; 5 14 6; 7 13 5;...
    8 11 6];
bar(x,Y,'stacked'); ylim([0 25]);
```



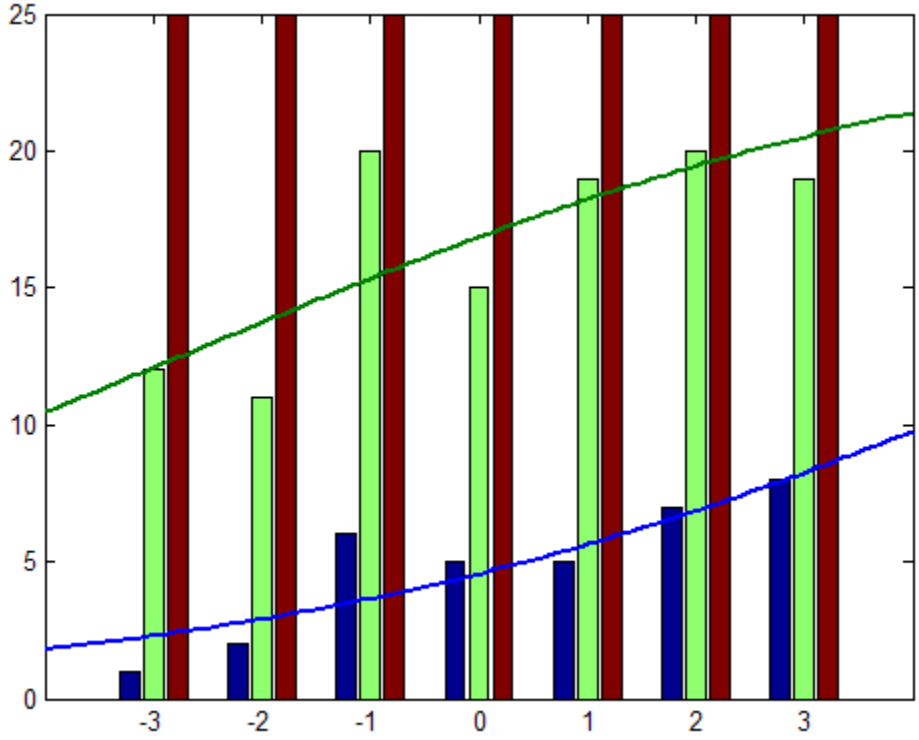

```
% Now fit a nominal model for the individual response
% category probabilities, with separate slopes on the
% single predictor variable, x, for each
% category:

% The first row of betaHatNom contains the intercept terms
% for the first two response categories.  The second row
% contains the slopes.
betaHatNom = mnrfit(x,Y,'model','nominal',...
'interactions','on')

% Compute the predicted probabilities for the three
```

```
% response categories:
xx = linspace(-4,4)';
pHatNom = mnrval(betaHatNom,xx,'model','nominal',...
'interactions','on');
line(xx,cumsum(25*pHatNom,2),'LineWidth',2);
```



Fit a "parallel" ordinal model for the cumulative response category probabilities, with a common slope on the single predictor variable, `x`, across all categories:

```
% The first two elements of betaHatOrd are the
% intercept terms for the first two response categories.
% The last element of betaHatOrd is the common slope.
betaHatOrd = mnrfit(x,Y,'model','ordinal',...
 'interactions','off')

% Compute the predicted cumulative probabilities for the
% first two response categories.  The cumulative
% probability for the third category is always 1.
pHatOrd = mnrval(betaHatOrd,xx,'type','cumulative',...
'model','ordinal','interactions','off');
bar(x,cumsum(Y,2),'grouped'); ylim([0 25]);
line(xx,25*pHatOrd,'LineWidth',2);
```



References

[1] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

See Also

`mnrval` | `glmfit` | `glmval` | `regress` | `regstats`

How To

- "Multinomial Distribution" on page B-54

mnrnd

Purpose

Multinomial random numbers

Syntax

```
r = mnrnd(n,p)
R = mnrnd(n,p,m)
R = mnrnd(N,P)
```

Description

`r = mnrnd(n,p)` returns random values `r` from the multinomial distribution with parameters `n` and `p`. `n` is a positive integer specifying the number of trials (sample size) for each multinomial outcome. `p` is a 1-by-k vector of multinomial probabilities, where k is the number of multinomial bins or categories. `p` must sum to one. (If `p` does not sum to one, `r` consists entirely of `NaN` values.) `r` is a 1-by-k vector, containing counts for each of the k multinomial bins.

`R = mnrnd(n,p,m)` returns `m` random vectors from the multinomial distribution with parameters `n` and `p`. `R` is a `m`-by-k matrix, where k is the number of multinomial bins or categories. Each row of `R` corresponds to one multinomial outcome.

`R = mnrnd(N,P)` generates outcomes from different multinomial distributions. `P` is a m-by-k matrix, where k is the number of multinomial bins or categories and each of the m rows contains a different set of multinomial probabilities. Each row of `P` must sum to one. (If any row of `P` does not sum to one, the corresponding row of `R` consists entirely of `NaN` values.) `N` is a m-by-1 vector of positive integers or a single positive integer (replicated by `mnrnd` to a m-by-1 vector). `R` is a `m`-by-k matrix. Each row of `R` is generated using the corresponding rows of `N` and `P`.

Examples

Generate 2 random vectors with the same probabilities:

```
n = 1e3;
p = [0.2,0.3,0.5];
R = mnrnd(n,p,2)
R =
   215   282   503
   194   303   503
```

Generate 2 random vectors with different probabilities:

```
n = 1e3;
P = [0.2, 0.3, 0.5; ...
     0.3, 0.4, 0.3;];
R = mnrnd(n,P)
R =
   186   290   524
   290   389   321
```

See Also

mnpdf

How To

- "Multinomial Distribution" on page B-54

mnrval

Purpose

Multinomial logistic regression values

Syntax

```
PHAT = mnrval(B,X)
YHAT = mnrval(B,X,ssize)
[...,DLO,DHI] = mnrval(B,X,...,stats)
[...] = mnrval(...,param1,val1,param2,val2,...)
```

Description

`PHAT = mnrval(B,X)` computes predicted probabilities for the multinomial logistic regression model with predictors `X`. `B` contains intercept and coefficient estimates as returned by the `mnrfit` function. `X` is an n-by-p matrix of p predictors at each of n observations. `PHAT` is an n-by-k matrix of predicted probabilities for each multinomial category.

Note `mnrval` automatically includes a constant term in all models. Do not enter a column of 1s directly into `X`.

`YHAT = mnrval(B,X,ssize)` computes predicted category counts for sample sizes `ssize`. `ssize` is an n-by-1 column vector of positive integers.

`[...,DLO,DHI] = mnrval(B,X,...,stats)` also computes 95% confidence bounds on the predicted probabilities `PHAT` or counts `YHAT`. `stats` is the structure returned by the `mnrfit` function. `DLO` and `DHI` define a lower confidence bound of `PHAT` or `YHAT` minus `DLO` and an upper confidence bound of `PHAT` or `YHAT` plus `DHI`. Confidence bounds are nonsimultaneous and they apply to the fitted curve, not to new observations.

`[...] = mnrval(...,param1,val1,param2,val2,...)` allows you to specify optional parameter name/value pairs to control the predicted values. These parameters must be set to the corresponding values used with the `mnrfit` function to compute `B`. Parameters are:

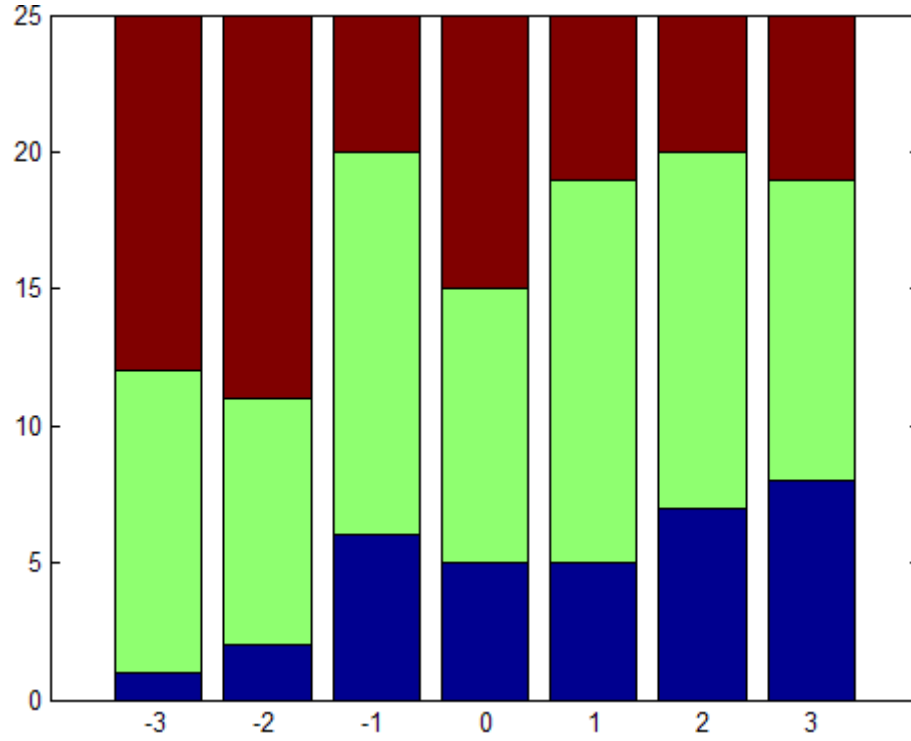
- `'model'` — The type of model that was fit by `mnrfit`; one of the text strings `'nominal'` (the default), `'ordinal'`, or `'hierarchical'`.

- `'interactions'` — Determines whether the model fit by `mnrfit` included an interaction between the multinomial categories and the coefficients. The default is `'off'` for ordinal models, and `'on'` for nominal and hierarchical models.
- `'link'` — The link function that was used by `mnrfit` for ordinal and hierarchical models. Specify the link parameter value as one of the text strings `'logit'`(the default), `'probit'`, `'comploglog'`, or `'loglog'`. You may not specify the `'link'` parameter for nominal models; these always use a multivariate logistic link.
- `'type'` — Set to `'category'` (the default) to return predictions and confidence bounds for the probabilities (or counts) of the k multinomial categories. Set to `'cumulative'` to return predictions and confidence bounds for the cumulative probabilities (or counts) of the first k–1 multinomial categories, as an n-by-(k–1) matrix. The predicted cumulative probability for the kth category is 1. Set to `'conditional'` to return predictions and confidence bounds in terms of the first k–1 conditional category probabilities, i.e., the probability for category j, given an outcome in category j or higher. When `'type'` is `'conditional'`, and you supply the sample size argument `ssize`, the predicted counts at each row of `X` are conditioned on the corresponding element of `ssize`, across all categories.
- `'confidence'` — The confidence level for the confidence bounds; a value between 0 and 1. The default is 0.95.

Examples

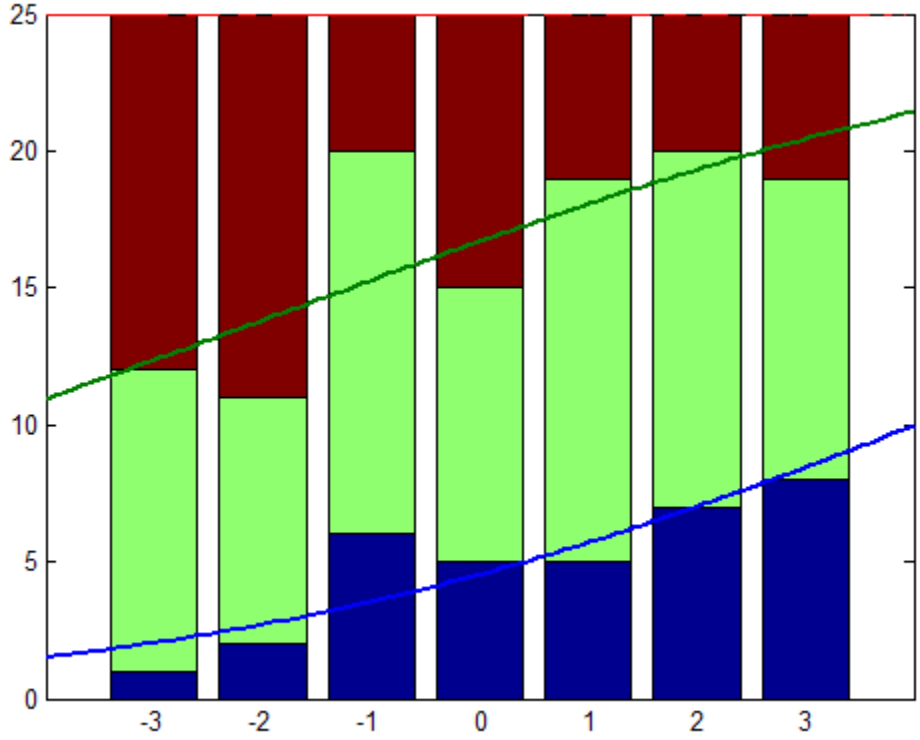
Fit multinomial logistic regression models to data with one predictor variable and three categories in the response variable:

```
x = [-3 -2 -1 0 1 2 3]';
Y = [1 11 13; 2 9 14; 6 14 5; 5 10 10; 5 14 6; 7 13 5;...
    8 11 6];
bar(x,Y,'stacked');
ylim([0 25]);
```



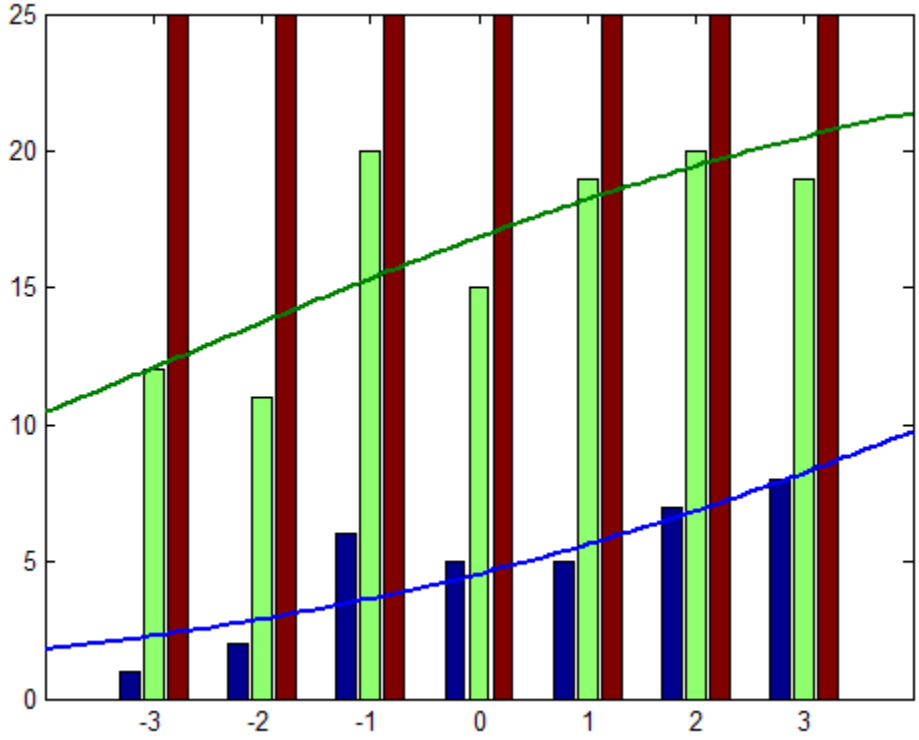

```
% Now fit a nominal model for the individual response
% category probabilities, with separate slopes on the
% single predictor variable, x, for each
% category:

% The first row of betaHatNom contains the intercept terms
% for the first two response categories.  The second row
% contains the slopes.
betaHatNom = mnrfit(x,Y,'model','nominal',...
    'interactions','on')

% Compute the predicted probabilities for the three
% response categories:
```

```
xx = linspace(-4,4)';
pHatNom = mnrval(betaHatNom,xx,'model','nominal',...
    'interactions','on');
line(xx,cumsum(25*pHatNom,2),'LineWidth',2);
```



Fit a "parallel" ordinal model for the cumulative response category probabilities, with a common slope on the single predictor variable, `x`, across all categories:

```
% The first two elements of betaHatOrd are the
% intercept terms for the first two response categories.
% The last element of betaHatOrd is the common slope.
betaHatOrd = mnrfit(x,Y,'model','ordinal',...
    'interactions','off')

% Compute the predicted cumulative probabilities for the
% first two response categories.  The cumulative
% probability for the third category is always 1.
pHatOrd = mnrval(betaHatOrd,xx,'type','cumulative',...
    'model','ordinal','interactions','off');
bar(x,cumsum(Y,2),'grouped');
ylim([0 25]);
line(xx,25*pHatOrd,'LineWidth',2);
```



References

[1] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

See Also

`mnrfit` | `glmfit` | `glmval`

How To

- "Multinomial Distribution" on page B-54

Purpose

Central moments

Syntax

```
m = moment(X,order)
moment(X,order,dim)
```

Description

`m = moment(X,order)` returns the central sample moment of `X` specified by the positive integer `order`. For vectors, `moment(x,order)` returns the central moment of the specified order for the elements of `x`. For matrices, `moment(X,order)` returns central moment of the specified order for each column. For N-dimensional arrays, `moment` operates along the first nonsingleton dimension of `X`.

`moment(X,order,dim)` takes the moment along dimension `dim` of `X`.

Tips

Note that the central first moment is zero, and the second central moment is the variance computed using a divisor of n rather than $n – 1$, where n is the length of the vector `x` or the number of rows in the matrix `X`.

The central moment of order k of a distribution is defined as

$$m_k = E(x - \mu)^k$$

where $E(x)$ is the expected value of x.

Examples

```
X = randn([6 5])
X =
  1.1650  0.0591  1.2460 -1.2704 -0.0562
  0.6268  1.7971 -0.6390  0.9846  0.5135
  0.0751  0.2641  0.5774 -0.0449  0.3967
  0.3516  0.8717 -0.3600 -0.7989  0.7562
 -0.6965 -1.4462 -0.1356 -0.7652  0.4005
  1.6961 -0.7012 -1.3493  0.8617 -1.3414

m = moment(X,3)
m =
  -0.0282  0.0571  0.1253  0.1460  -0.4486
```

See Also

kurtosis | mean | skewness | std | var

gmdistribution.Mu property

Purpose Input matrix of means `MU`

Description Input matrix of means `mu`.

Purpose

Multiple comparison test

Syntax

```
c = multcompare(stats)
c = multcompare(stats,param1,val1,param2,val2,...)
[c,m] = multcompare(...)
[c,m,h] = multcompare(...)
[c,m,h,gnames] = multcompare(...)
```

Description

`c = multcompare(stats)` performs a multiple comparison test using the information in the `stats` structure, and returns a matrix `c` of pairwise comparison results. It also displays an interactive graph of the estimates with comparison intervals around them. See "Examples" on page 20-1084.

In a one-way analysis of variance, you compare the means of several groups to test the hypothesis that they are all the same, against the general alternative that they are not all the same. Sometimes this alternative may be too general. You may need information about which pairs of means are significantly different, and which are not. A test that can provide such information is called a *multiple comparison procedure*.

When you perform a simple t-test of one group mean against another, you specify a significance level that determines the cutoff value of the t statistic. For example, you can specify the value `alpha = 0.05` to insure that when there is no real difference, you will incorrectly find a significant difference no more than 5% of the time. When there are many group means, there are also many pairs to compare. If you applied an ordinary t-test in this situation, the `alpha` value would apply to each comparison, so the chance of incorrectly finding a significant difference would increase with the number of comparisons. Multiple comparison procedures are designed to provide an upper bound on the probability that *any* comparison will be incorrectly found significant.

The output `c` contains the results of the test in the form of a five-column matrix. Each row of the matrix represents one test, and there is one row for each pair of groups. The entries in the row indicate the means being compared, the estimated difference in means, and a confidence interval for the difference.

For example, suppose one row contains the following entries.

```
   2.0000   5.0000   1.9442   8.2206   14.4971
```

These numbers indicate that the mean of group 2 minus the mean of group 5 is estimated to be 8.2206, and a 95% confidence interval for the true difference of the means is [1.9442, 14.4971].

In this example the confidence interval does not contain 0.0, so the difference is significant at the 0.05 level. If the confidence interval did contain 0.0, the difference would not be significant at the 0.05 level.

The `multcompare` function also displays a graph with each group mean represented by a symbol and an interval around the symbol. Two means are significantly different if their intervals are disjoint, and are not significantly different if their intervals overlap. You can use the mouse to select any group, and the graph will highlight any other groups that are significantly different from it.

`c = multcompare(stats,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` specifies one or more of the parameter name/value pairs described in the following table.

Parameter	Values
`'alpha'`	Scalar between `0` and `1` that determines the confidence levels of the intervals in the matrix `c` and in the figure (default is `0.05`). The confidence level is `100(1-alpha)`%.
`'display'`	Either `'on'` (the default) to display a graph of the estimates with comparison intervals around them, or `'off'` to omit the graph. See “Examples” on page 20-1084.
`'ctype'`	Specifies the type of critical value to use for the multiple comparison. “Values of `ctype`” on page 20-1082 describes the allowed values for `ctype`.

Parameter	Values
'dimension'	A vector specifying the dimension or dimensions over which the population marginal means are to be calculated. Use only if you create stats with the function anovan. The default is 1 to compute over the first dimension. See "Dimension Parameter" on page 20-1084 for more information.
'estimate'	Specifies the estimate to be compared. The allowable values of estimate depend on the function that was the source of the stats structure, as described in "Values of estimate" on page 20-1083

`[c,m] = multcompare(...)` returns an additional matrix `m`. The first column of `m` contains the estimated values of the means (or whatever statistics are being compared) for each group, and the second column contains their standard errors.

`[c,m,h] = multcompare(...)` returns a handle `h` to the comparison graph. Note that the title of this graph contains instructions for interacting with the graph, and the *x*-axis label contains information about which means are significantly different from the selected mean. If you plan to use this graph for presentation, you may want to omit the title and the *x*-axis label. You can remove them using interactive features of the graph window, or you can use the following commands.

```
title('')
xlabel('')
```

`[c,m,h,gnames] = multcompare(...)` returns `gnames`, a cell array with one row for each group, containing the names of the groups.

The intervals shown in the graph are computed so that to a very close approximation, two estimates being compared are significantly different if their intervals are disjoint, and are not significantly different if their intervals overlap. (This is exact for multiple comparison of means from

anova1, if all means are based on the same sample size.) You can click on any estimate to see which means are significantly different from it.

Values of `ctype`

The following table describes the allowed values for the parameter `ctype`.

Value	Description
`'hsd'` or `'tukey-kramer'`	Use Tukey's honestly significant difference criterion. This is the default, and it is based on the Studentized range distribution. It is optimal for balanced one-way ANOVA and similar procedures with equal sample sizes. It has been proven to be conservative for one-way ANOVA with different sample sizes. According to the unproven Tukey-Kramer conjecture, it is also accurate for problems where the quantities being compared are correlated, as in analysis of covariance with unbalanced covariate values.
`'lsd'`	Use Tukey's least significant difference procedure. This procedure is a simple t-test. It is reasonable if the preliminary test (say, the one-way ANOVA *F* statistic) shows a significant difference. If it is used unconditionally, it provides no protection against multiple comparisons.
`'bonferroni'`	Use critical values from the t distribution, after a Bonferroni adjustment to compensate for multiple comparisons. This procedure is conservative, but usually less so than the Scheffé procedure.

Value	Description
`'dunn-sidak'`	Use critical values from the t distribution, after an adjustment for multiple comparisons that was proposed by Dunn and proved accurate by Sidák. This procedure is similar to, but less conservative than, the Bonferroni procedure.
`'scheffe'`	Use critical values from Scheffé's S procedure, derived from the F distribution. This procedure provides a simultaneous confidence level for comparisons of all linear combinations of the means, and it is conservative for comparisons of simple differences of pairs.

Values of estimate

The allowable values of the parameter `'estimate'` depend on the function that was the source of the `stats` structure, according to the following table.

Source	Values
`'anova1'`	Ignored. Always compare the group means.
`'anova2'`	Either `'column'` (the default) or `'row'` to compare column or row means.
`'anovan'`	Ignored. Always compare the population marginal means as specified by the `dim` argument.
`'aoctool'`	Either `'slope'`, `'intercept'`, or `'pmm'` to compare slopes, intercepts, or population marginal means. If the analysis of covariance model did not include separate slopes, then `'slope'` is not allowed. If it did not include separate intercepts, then no comparisons are possible.

Source	Values
'friedman'	Ignored. Always compare average column ranks.
'kruskalwallis'	Ignored. Always compare average group ranks.

Dimension Parameter

The dimension parameter is a vector specifying the dimension or dimensions over which the population marginal means are to be calculated. For example, if `dim = 1`, the estimates that are compared are the means for each value of the first grouping variable, adjusted by removing effects of the other grouping variables as if the design were balanced. If `dim = [1 3]`, population marginal means are computed for each combination of the first and third grouping variables, removing effects of the second grouping variable. If you fit a singular model, some cell means may not be estimable and any population marginal means that depend on those cell means will have the value `NaN`.

Population marginal means are described by Milliken and Johnson (1992) and by Searle, Speed, and Milliken (1980). The idea behind population marginal means is to remove any effect of an unbalanced design by fixing the values of the factors specified by `dim`, and averaging out the effects of other factors as if each factor combination occurred the same number of times. The definition of population marginal means does not depend on the number of observations at each factor combination. For designed experiments where the number of observations at each factor combination has no meaning, population marginal means can be easier to interpret than simple means ignoring other factors. For surveys and other studies where the number of observations at each combination does have meaning, population marginal means may be harder to interpret.

Examples

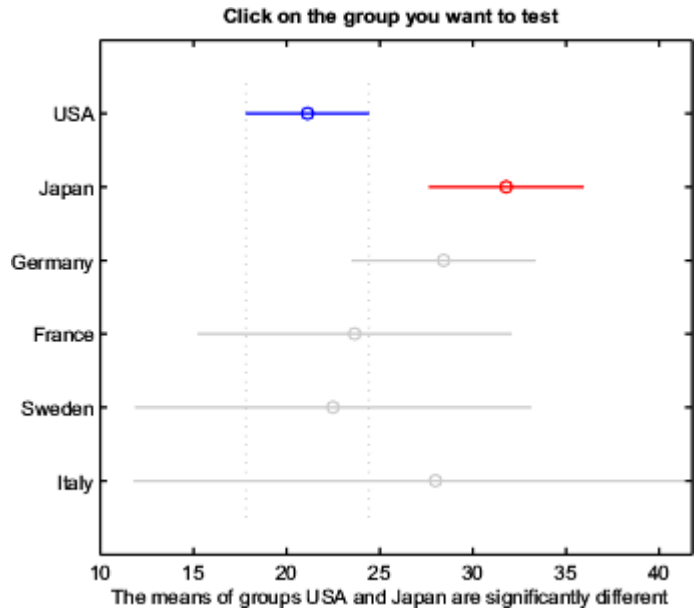
Example 1

The following example performs a 1-way analysis of variance (ANOVA) and displays group means with their names.

```
load carsmall
```

```
[p,t,st] = anova1(MPG,Origin,'off');
[c,m,h,nms] = multcompare(st,'display','off');
[nms num2cell(m)]
ans =
  'USA'     [21.1328]  [0.8814]
  'Japan'   [31.8000]  [1.8206]
  'Germany' [28.4444]  [2.3504]
  'France'  [23.6667]  [4.0711]
  'Sweden'  [22.5000]  [4.9860]
  'Italy'   [28.0000]  [7.0513]
```

`multcompare` also displays the following graph of the estimates with comparison intervals around them.



You can click the graphs of each country to compare its mean to those of other countries.

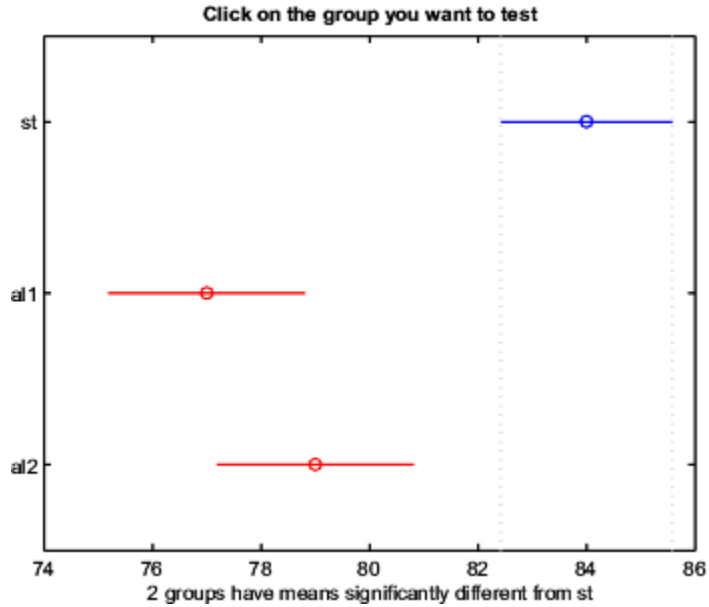
Example 2

The following continues the example described in the anova1 reference page, which is related to testing the material strength in structural beams. From the anova1 output you found significant evidence that the three types of beams are not equivalent in strength. Now you can determine where those differences lie. First you create the data arrays and you perform one-way ANOVA.

```
strength = [82 86 79 83 84 85 86 87 74 82 ...
            78 75 76 77 79 79 77 78 82 79];
alloy = {'st','st','st','st','st','st','st','st',...
         'al1','al1','al1','al1','al1','al1',...
         'al2','al2','al2','al2','al2','al2'};
[p,a,s] = anova1(strength,alloy);
```

Among the outputs is a structure that you can use as input to multcompare.

```
[c,m,h,nms] = multcompare(s);
[nms num2cell(c)]
ans =
  'st'   [1]  [2]  [ 3.6064]  [ 7]  [10.3936]
  'al1'  [1]  [3]  [ 1.6064]  [ 5]  [ 8.3936]
  'al2'  [2]  [3]  [-5.6280]  [-2]  [ 1.6280]
```



The third row of the output matrix shows that the differences in strength between the two alloys is not significant. A 95% confidence interval for the difference is [-5.6, 1.6], so you cannot reject the hypothesis that the true difference is zero.

The first two rows show that both comparisons involving the first group (steel) have confidence intervals that do not include zero. In other words, those differences are significant. The graph shows the same information.

References

[1] Hochberg, Y., and A. C. Tamhane. *Multiple Comparison Procedures*. Hoboken, NJ: John Wiley & Sons, 1987.

[2] Milliken, G. A., and D. E. Johnson. *Analysis of Messy Data, Volume 1: Designed Experiments*. Boca Raton, FL: Chapman & Hall/CRC Press, 1992.

[3] Searle, S. R., F. M. Speed, and G. A. Milliken. “Population marginal means in the linear model: an alternative to least-squares means.” *American Statistician*. 1980, pp. 216–221.

See Also

`anova1` | `anova2` | `anovan` | `aoctool` | `friedman` | `kruskalwallis`

Purpose

Multivari chart for grouped data

Syntax

```
multivarichart(y,GROUP)
multivarichart(Y)
multivarichart(...,param1,val1,param2,val2,...)
[charthandle,AXESH] = multivarichart(...)
```

Description

`multivarichart(y,GROUP)` displays the multivari chart for the vector `y` grouped by entries in the cell array `GROUP`. Each cell of `GROUP` must contain a grouping variable that can be a categorical variable, numeric vector, character matrix, or single-column cell array of strings. (See "Grouped Data" on page 2-34.) `GROUP` can also be a matrix whose columns represent different grouping variables. Each grouping variable must have the same number of elements as `y`. The number of grouping variables must be 2, 3, or 4.

Each subplot of the plot matrix contains a multivari chart for the first and second grouping variables. The *x*-axis in each subplot indicates values of the first grouping variable. The legend at the bottom of the figure window indicates values of the second grouping variable. The subplot at position (*i*,*j*) is the multivari chart for the subset of `y` at the *i*th level of the third grouping variable and the *j*th level of the fourth grouping variable. If the third or fourth grouping variable is absent, it is considered to have only one level.

`multivarichart(Y)` displays the multivari chart for a matrix `Y`. The data in different columns represent changes in one factor. The data in different rows represent changes in another factor.

`multivarichart(...,param1,val1,param2,val2,...)` specifies one or more of the following name/value pairs:

- `'varnames'` — Grouping variable names in a character matrix or a cell array of strings, one per grouping variable. Default names are `'X1'`, `'X2'`, ...
- `'plotorder'` — A string with the value `'sorted'` or a vector containing a permutation of the integers from 1 to the number of grouping variables.

If `'plotorder'` is a string with value `'sorted'`, the grouping variables are rearranged in descending order according to the number of levels in each variable.

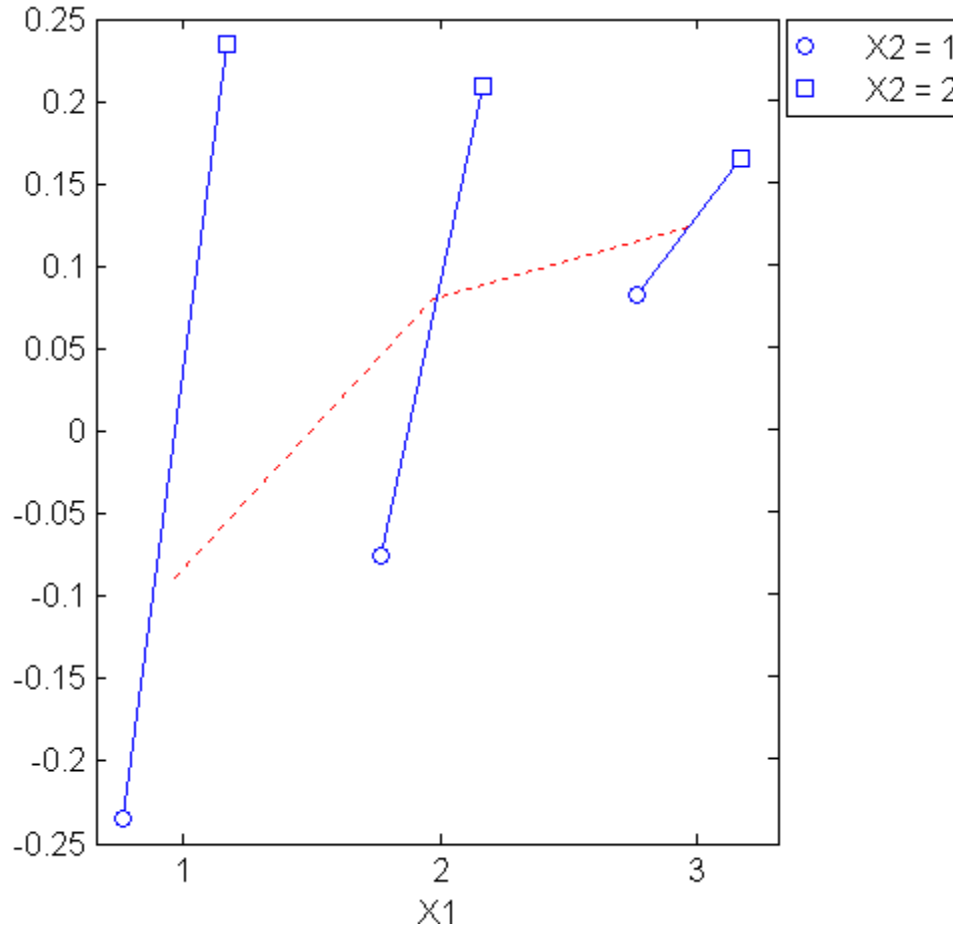
If `'plotorder'` is a vector, it indicates the order in which each grouping variable should be plotted. For example, `[2,3,1,4]` indicates that the second grouping variable should be used as the *x*-axis of each subplot, the third grouping variable should be used as the legend, the first grouping variable should be used as the columns of the plot, and the fourth grouping variable should be used as the rows of the plot.

`[charthandle,AXESH] = multivarichart(...)` returns a handle `charthandle` to the figure window and a matrix `AXESH` of handles to the subplot axes.

Examples

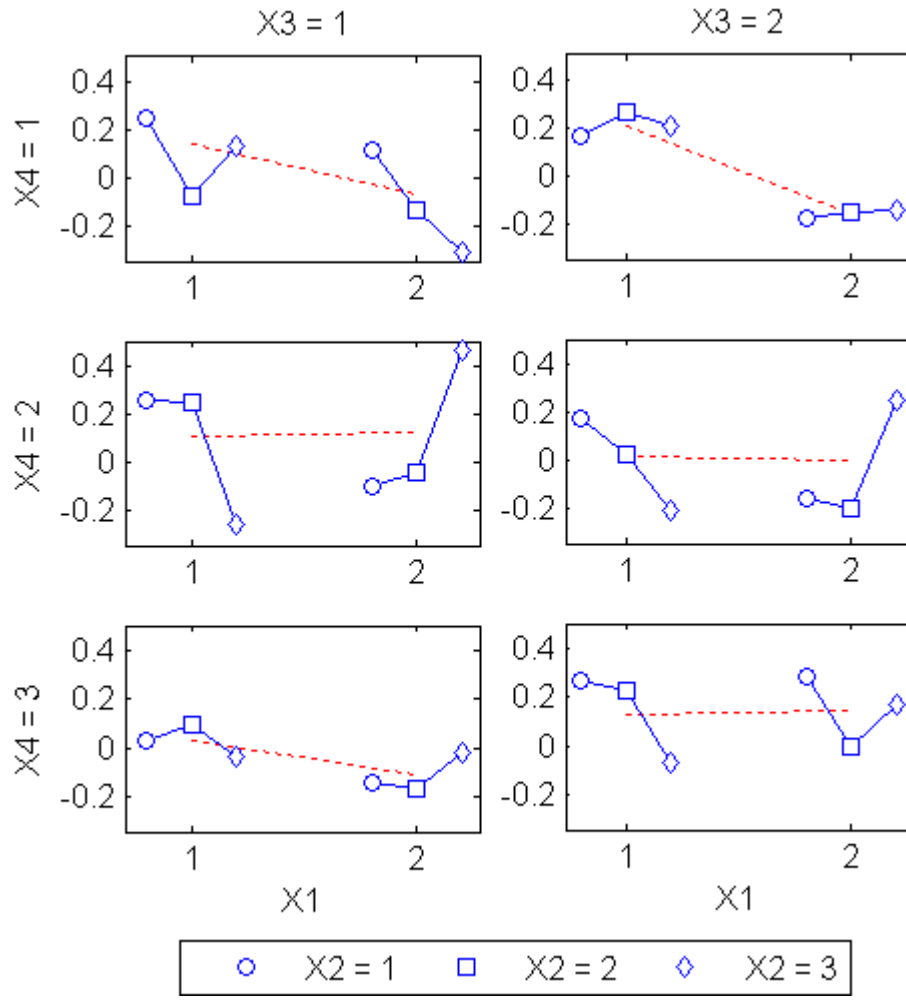
Display a multivari chart for data with two grouping variables:

```
y = randn(100,1); % response
group = [ceil(3*rand(100,1)) ceil(2*rand(100,1))];
multivarichart(y,group)
```



Display a multivari chart for data with four grouping variables:

```
y = randn(1000,1); % response
group = {ceil(2*rand(1000,1)),ceil(3*rand(1000,1)), ...
         ceil(2*rand(1000,1)),ceil(3*rand(1000,1))};
multivarichart(y,group)
```



See Also `maineffectsplot` | `interactionplot`

How To

- “Grouped Data” on page 2-34

Purpose

Multivariate normal cumulative distribution function

Syntax

```
y = mvncdf(X)
y = mvncdf(X,mu,SIGMA)
y = mvncdf(xl,xu,mu,SIGMA)
[y,err] = mvncdf(...)
[...] = mvncdf(...,options)
```

Description

`y = mvncdf(X)` returns the cumulative probability of the multivariate normal distribution with zero mean and identity covariance matrix, evaluated at each row of `X`. Rows of the n-by-d matrix `X` correspond to observations or points, and columns correspond to variables or coordinates. `y` is an n-by-1 vector.

`y = mvncdf(X,mu,SIGMA)` returns the cumulative probability of the multivariate normal distribution with mean `mu` and covariance `SIGMA`, evaluated at each row of `X`. `mu` is a 1-by-d vector, and `SIGMA` is a d-by-d symmetric, positive definite matrix. `mu` can also be a scalar value, which `mvncdf` replicates to match the size of `X`. If the covariance matrix is diagonal, containing variances along the diagonal and zero covariances off the diagonal, `SIGMA` may also be specified as a 1-by-d vector containing just the diagonal. Pass in the empty matrix `[]` for `mu` to use as its default value when you want to only specify `SIGMA`.

The multivariate normal cumulative probability at `X` is defined as the probability that a random vector `V`, distributed as multivariate normal, will fall within the semi-infinite rectangle with upper limits defined by `X`, for example, $\Pr\{V(1) \le X(1), V(2) \le X(2), \ldots, V(d) \le X(d)\}$.

`y = mvncdf(xl,xu,mu,SIGMA)` returns the multivariate normal cumulative probability evaluated over the rectangle with lower and upper limits defined by `xl` and `xu`, respectively.

`[y,err] = mvncdf(...)` returns an estimate of the error in `y`. For bivariate and trivariate distributions, `mvncdf` uses adaptive quadrature on a transformation of the t density, based on methods developed by Drezner and Wesolowsky and by Genz, as described in the references. The default absolute error tolerance for these cases is `1e-8`. For four or more dimensions, `mvncdf` uses a quasi-Monte Carlo integration

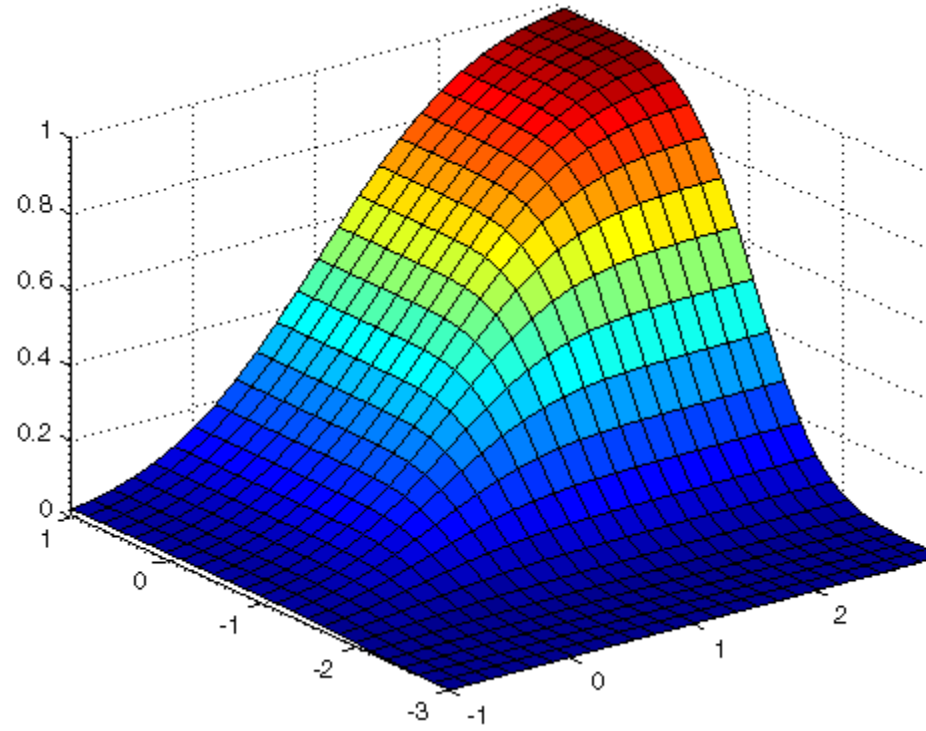
algorithm based on methods developed by Genz and Bretz, as described in the references. The default absolute error tolerance for these cases is `1e-4`.

`[...] = mvncdf(...,options)` specifies control parameters for the numerical integration used to compute `y`. This argument can be created by a call to `statset`. Choices of `statset` parameters:

- `'TolFun'` — Maximum absolute error tolerance. Default is `1e-8` when $d < 4$, or `1e-4` when $d \geq 4$.
- `'MaxFunEvals'` — Maximum number of integrand evaluations allowed when $d \geq 4$. Default is `1e7`. `'MaxFunEvals'` is ignored when $d < 4$.
- `'Display'` — Level of display output. Choices are `'off'` (the default), `'iter'`, and `'final'`. `'Display'` is ignored when $d < 4$.

Examples

```
mu = [1 -1]; SIGMA = [.9 .4; .4 .3];
[X1,X2] = meshgrid(linspace(-1,3,25)',linspace(-3,1,25)');
X = [X1(:) X2(:)];
p = mvncdf(X,mu,SIGMA);
surf(X1,X2,reshape(p,25,25));
```



References

[1] Drezner, Z. "Computation of the Trivariate Normal Integral." *Mathematics of Computation*. Vol. 63, 1994, pp. 289–294.

[2] Drezner, Z., and G. O. Wesolowsky. "On the Computation of the Bivariate Normal Integral." *Journal of Statistical Computation and Simulation*. Vol. 35, 1989, pp. 101–107.

[3] Genz, A. "Numerical Computation of Rectangular Bivariate and Trivariate Normal and t Probabilities." *Statistics and Computing*. Vol. 14, No. 3, 2004, pp. 251–260.

[4] Genz, A., and F. Bretz. "Numerical Computation of Multivariate t Probabilities with Application to Power Calculation of Multiple

Contrasts." *Journal of Statistical Computation and Simulation*. Vol. 63, 1999, pp. 361–378.

[5] Genz, A., and F. Bretz. "Comparison of Methods for the Computation of Multivariate t Probabilities." *Journal of Computational and Graphical Statistics*. Vol. 11, No. 4, 2002, pp. 950–971.

See Also

`mvnpdf` | `mvnrnd`

How To

- "Multivariate Normal Distribution" on page B-58

Purpose

Multivariate normal probability density function

Syntax

```
y = mvnpdf(X)
y = mvnpdf(X,MU)
y = mvnpdf(X,MU,SIGMA)
```

Description

`y = mvnpdf(X)` returns the n-by-`1` vector `y`, containing the probability density of the multivariate normal distribution with zero mean and identity covariance matrix, evaluated at each row of the n-by-d matrix `X`. Rows of `X` correspond to observations and columns correspond to variables or coordinates.

`y = mvnpdf(X,MU)` returns the density of the multivariate normal distribution with mean `mu` and identity covariance matrix, evaluated at each row of `X`. `MU` is a `1`-by-d vector, or an n-by-d matrix. If `MU` is a matrix, the density is evaluated for each row of `X` with the corresponding row of `MU`. `MU` can also be a scalar value, which `mvnpdf` replicates to match the size of `X`.

`y = mvnpdf(X,MU,SIGMA)` returns the density of the multivariate normal distribution with mean `MU` and covariance `SIGMA`, evaluated at each row of `X`. `SIGMA` is a d-by-d matrix, or a d-by-d-by-n array, in which case the density is evaluated for each row of `X` with the corresponding page of `SIGMA`, i.e., `mvnpdf` computes `y(i)` using `X(i,:)` and `SIGMA(:,:,i)`. If the covariance matrix is diagonal, containing variances along the diagonal and zero covariances off the diagonal, `SIGMA` may also be specified as a `1`-by-d vector or a 1-by-d-by-n array, containing just the diagonal. Specify `[]` for `MU` to use its default value when you want to specify only `SIGMA`.

If `X` is a 1-by-d vector, `mvnpdf` replicates it to match the leading dimension of `mu` or the trailing dimension of `SIGMA`.

Examples

```
mu = [1 -1];
SIGMA = [.9 .4; .4 .3];
X = mvnrnd(mu,SIGMA,10);
p = mvnpdf(X,mu,SIGMA);
```

See Also `mvncdf` | `mvnrnd` | `normpdf`

How To

- "Multivariate Normal Distribution" on page B-58

Purpose

Multivariate linear regression

Syntax

```
beta = mvregress(X,Y)
[beta,SIGMA] = mvregress(X,Y)
[beta,SIGMA,RESID] = mvregress(X,Y)
[beta,SIGMA,RESID,COVB] = mvregress(...)
[beta,SIGMA,RESID,COVB,objective] = mvregress(...)
[...] = mvregress(X,Y,param1,val1,param2,val2,...)
```

Description

`beta = mvregress(X,Y)` returns a vector `beta` of coefficient estimates for a multivariate regression of the d-dimensional responses in `Y` on the predictors in `X`. If $d = 1$, `X` can be an n-by-p matrix of p predictors at each of n observations. If $d \geq 1$, `X` can be a cell array of length n, with each cell containing a d-by-p design matrix for one multivariate observation. If all observations have the same d-by-p design matrix, `X` can be a single cell. `Y` is n-by-d. `beta` is p-by-1.

Note To include a constant term in a model, a matrix `X` should contain a column of 1s. If `X` is a cell array `X`, each cell should contain a matrix with a column of 1s.

`mvregress` treats `NaN`s in `X` or `Y` as missing values. Missing values in `X` are ignored. Missing values in `Y` are handled according to the value of the `'algorithm'` parameter described below.

`[beta,SIGMA] = mvregress(X,Y)` also returns a d-by-d matrix `SIGMA` for the estimated covariance of `Y`.

`[beta,SIGMA,RESID] = mvregress(X,Y)` also returns an n-by-d matrix `RESID` of residuals.

The `RESID` values corresponding to missing values in `Y` are the differences between the conditionally imputed values for `Y` and the fitted values. The `SIGMA` estimate is not the sample covariance matrix of the `RESID` matrix.

`[beta,SIGMA,RESID,COVB] = mvregress(...)` also returns a matrix `COVB` for the estimated covariance of the coefficients. By default, or if the `'varformat'` parameter is `'beta'` (see below), `COVB` is the estimated covariance matrix of `beta`. If the `'varformat'` parameter is `'full'`, `COVB` is the combined estimated covariance matrix for `beta` and `SIGMA`.

`[beta,SIGMA,RESID,COVB,objective] = mvregress(...)` also returns the value of the objective function, or log likelihood, `objective`, after the last iteration.

`[...] = mvregress(X,Y,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` specifies additional parameter name/value pairs chosen from the following:

- `'algorithm'` — Either `'ecm'` to compute the maximum likelihood estimates via the ECM algorithm, `'cwls'` to perform least squares (optionally conditionally weighted by an input covariance matrix), or `'mvn'` to omit observations with missing data and compute the ordinary multivariate normal estimates. The default is `'mvn'` for complete data, `'ecm'` for missing data when the sample size is sufficient to estimate all parameters, and `'cwls'` otherwise.
- `'covar0'` — A d-by-d matrix to be used as the initial estimate for `SIGMA`. The default is the identity matrix. For the `'cwls'` algorithm, this matrix is usually a diagonal matrix used as a weighting at each iteration. The `'cwls'` algorithm uses the initial value of `SIGMA` at each iteration, without changing it.
- `'covtype'` — Either `'full'`, to allow a full covariance matrix, or `'diagonal'`, to restrict the covariance matrix to be diagonal. The default is `'full'`.
- `'maxiter'` — Maximum number of iterations. The default is `100`.
- `'outputfcn'` — An output function called with three arguments:

  1. A vector of current parameter estimates.

  2. A structure with fields `'Covar'` for the current value of the covariance matrix, `'iteration'` for the current iteration number, and `'fval'` for the current value of the objective function.

3. A text string that is `'init'` when called during initialization, `'iter'` when called after an iteration, and `'done'` when called after completion.

The function should return logical `true` if the iterations should stop, or logical `false` if they should continue.

- `'param0'` — A vector of p elements to be used as the initial estimate for `beta`. Default is a zero vector. Not used for the `'mvn'` algorithm.
- `'tolbeta'` — Convergence tolerance for `beta`. The default is `sqrt(eps)`. Iterations continue until the `tolbeta` and `tolobj` conditions are met. The test for convergence at iteration `k` is

```
norm(beta(k)-beta(k-1))<sqrt(p)*tolbeta*(1+norm(beta(k)))
```

where `p = length(beta)`.

- `'tolobj'` — Convergence tolerance for changes in the objective function. The default is `eps^(3/4)`. The test is

```
abs(obj(k)-obj(k-1)) < tolobj*(1+abs(obj(k)))
```

where `obj` is the objective function. If both `tolobj` and `tolbeta` are `0`, the function performs `maxiter` iterations with no convergence test.

- `'beta0'` — A vector of p elements to be used as the initial estimate for `beta`. Default is a zero vector. Not used for the `'mvn'` algorithm.
- `'covar0'` — A d-by-d matrix to be used as the initial estimate for `SIGMA`. Default is the identity matrix. For the `'cwls'` algorithm, this matrix is usually a diagonal matrix and it is not changed during the iterations, so the input value is used as the weighting matrix at each iteration.
- `'outputfcn'` — An output function.
- `'varformat'` — Either `'beta'` to compute `COVB` for `beta` only (default), or `'full'` to compute `COVB` for both `beta` and `SIGMA`.
- `'vartype'` — Either `'hessian'` to compute `COVB` using the Hessian or observed information (default), or `'fisher'` to compute `COVB` using

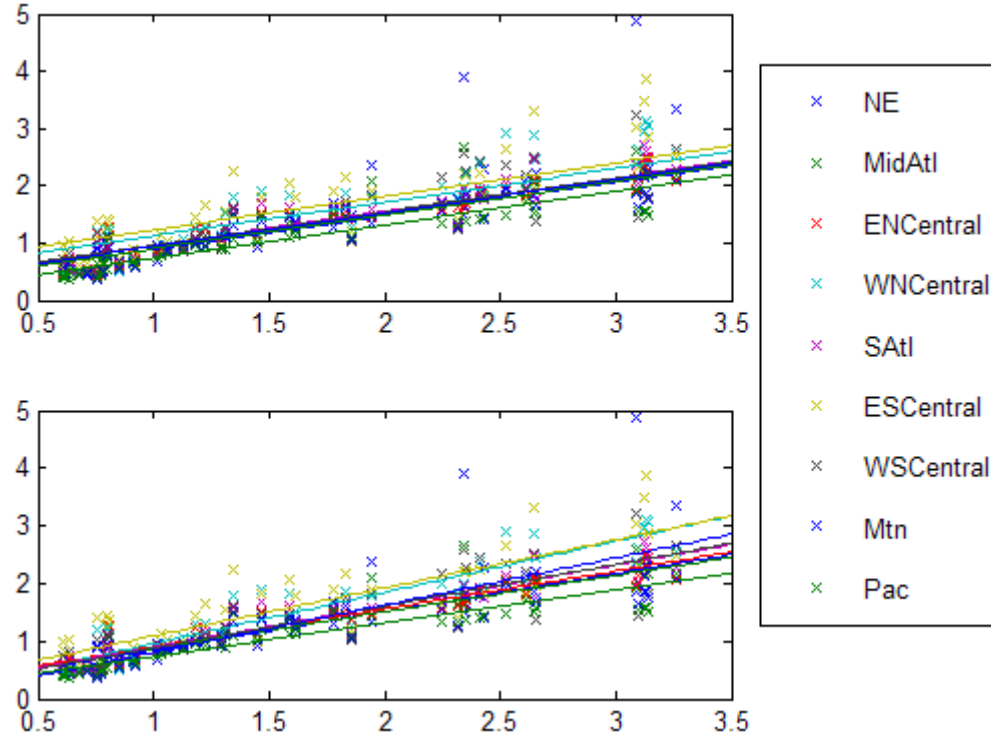
the complete-data Fisher or expected information. The `'hessian'` method takes into account the increased uncertainties due to missing data, while the `'fisher'` method does not.

Examples

Predict regional flu estimates based on Google™ queries using the national CDC estimates as a predictor:

```
load flu

% response: regional queries
y = double(flu(:,2:end-1));

% predictor: national CDC estimates
x = flu.WtdILI;
[nobs,nregions] = size(y);

% Create and fit model with separate intercepts but
% common slope
X = cell(nobs,1);
for j=1:nobs
    X{j} = [eye(nregions), repmat(x(j),nregions,1)];
end
[beta,sig,resid,vars,loglik] = mvregress(X,y);

% Plot raw data with fitted lines
B = [beta(1:nregions)';repmat(beta(end),1,nregions)]
axes1 = axes('Position',[0.13 0.5838 0.6191 0.3412]);
xx = linspace(.5,3.5)';
h = plot(x,y,'x', xx, [ones(size(xx)),xx]*B,'-');
for j=1:nregions;
  set(h(nregions+j),'color',get(h(j),'color'));
end
regions = flu.Properties.VarNames;
legend1 = legend(regions{2:end-1});
set(legend1,'Position', [0.7733 0.1967 0.2161 0.6667]);

% Create and fit model with separate intercepts and slopes
```

```
for j=1:nobs
   X{j} = [eye(nregions), x(j)*eye(nregions)];
end
[beta,sig,resid,vars,loglik2] = mvregress(X,y);

% Plot raw data with fitted lines
B = [beta(1:nregions)';beta(nregions+1:end)']
axes2 = axes('Parent',gcf,'Position',...
  [0.13 0.11 0.6191 0.3412]);
h = plot(x,y,'x', xx, [ones(size(xx)),xx]*B,'-');

for j=1:nregions;
   set(h(nregions+j),'color',get(h(j),'color'));
end

% Likelihood ratio test for significant difference
chisq = 2*(loglik2-loglik)
p = 1-chi2cdf(chisq, nregions-1)

chisq =

   96.4556


p =

     0
```



References

[1] Little, Roderick J. A., and Donald B. Rubin. *Statistical Analysis with Missing Data*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 2002.

[2] Meng, Xiao-Li, and Donald B. Rubin. "Maximum Likelihood Estimation via the ECM Algorithm." *Biometrika*. Vol. 80, No. 2, 1993, pp. 267–278.

[3] Sexton, Joe, and A. R. Swensen. "ECM Algorithms that Converge at the Rate of EM." *Biometrika*. Vol. 87, No. 3, 2000, pp. 651–662.

[4] Dempster, A. P., N. M. Laird, and D. B. Rubin. "Maximum Likelihood from Incomplete Data via the EM Algorithm." *Journal of the Royal Statistical Society*. Series B, Vol. 39, No. 1, 1977, pp. 1–37.

See Also

`mvregresslike` | `manova1`

How To

- "Multivariate Normal Distribution" on page B-58

mvregresslike

Purpose

Negative log-likelihood for multivariate regression

Syntax

```
nlogL = mvregresslike(X,Y,b,SIGMA,alg)
[nlogL,COVB] = mvregresslike(...)
[nlogL,COVB] = mvregresslike(...,type,format)
```

Description

`nlogL = mvregresslike(X,Y,b,SIGMA,alg)` computes the negative log-likelihood `nlogL` for a multivariate regression of the d-dimensional multivariate observations in the n-by-d matrix `Y` on the predictor variables in the matrix or cell array `X`, evaluated for the p-by-1 column vector `b` of coefficient estimates and the d-by-d matrix `SIGMA` specifying the covariance of a row of `Y`. If $d = 1$, `X` can be an n-by-p design matrix of predictor variables. For any value of d, `X` can also be a cell array of length n, with each cell containing a d-by-p design matrix for one multivariate observation. If all observations have the same d-by-p design matrix, `X` can be a single cell.

`NaN` values in `X` or `Y` are taken as missing. Observations with missing values in `X` are ignored. Treatment of missing values in `Y` depends on the algorithm specified by *`alg`*.

`alg` should match the algorithm used by `mvregress` to obtain the coefficient estimates `b`, and must be one of the following:

- `'ecm'` — ECM algorithm
- `'cwls'` — Least squares conditionally weighted by `SIGMA`
- `'mvn'` — Multivariate normal estimates computed after omitting rows with any missing values in `Y`

`[nlogL,COVB] = mvregresslike(...)` also returns an estimated covariance matrix `COVB` of the parameter estimates `b`.

`[nlogL,COVB] = mvregresslike(...,type,format)` specifies the type and format of `COVB`.

`type` is either:

- `'hessian'` — To use the Hessian or observed information. This method takes into account the increased uncertainties due to missing data. This is the default.
- `'fisher'` — To use the Fisher or expected information. This method uses the complete data expected information, and does not include uncertainty due to missing data.

`format` is either:

- `'beta'` — To compute `COVB` for `b` only. This is the default.
- `'full'` — To compute `COVB` for both `b` and `SIGMA`.

See Also

`mvregress | manova1`

How To

- "Multivariate Normal Distribution" on page B-58

mvnrnd

Purpose

Multivariate normal random numbers

Syntax

```
R = mvnrnd(MU,SIGMA)
r = mvnrnd(MU,SIGMA,cases)
```

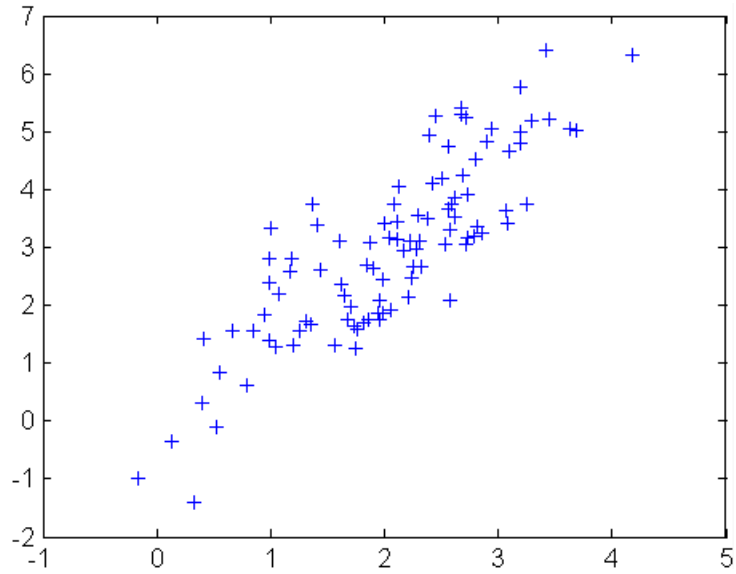
Description

`R = mvnrnd(MU,SIGMA)` returns an n-by-d matrix `R` of random vectors chosen from the multivariate normal distribution with mean `MU`, and covariance `SIGMA`. `MU` is an n-by-d matrix, and `mvnrnd` generates each row of `R` using the corresponding row of `mu`. `SIGMA` is a d-by-d symmetric positive semi-definite matrix, or a d-by-d-by-n array. If `SIGMA` is an array, `mvnrnd` generates each row of `R` using the corresponding page of `SIGMA`, i.e., `mvnrnd` computes `R(i,:)` using `MU(i,:)` and `SIGMA(:,:,i)`. If the covariance matrix is diagonal, containing variances along the diagonal and zero covariances off the diagonal, `SIGMA` may also be specified as a `1`-by-d vector or a 1-by-d-by-n array, containing just the diagonal. If `MU` is a `1`-by-d vector, `mvnrnd` replicates it to match the trailing dimension of `SIGMA`.

`r = mvnrnd(MU,SIGMA,cases)` returns a `cases`-by-d matrix `R` of random vectors chosen from the multivariate normal distribution with a common `1`-by-`d` mean vector `MU`, and a common `d`-by-`d` covariance matrix `SIGMA`.

Examples

```
mu = [2 3];
SIGMA = [1 1.5; 1.5 3];
r = mvnrnd(mu,SIGMA,100);
plot(r(:,1),r(:,2),'+')
```



See Also

`mvnpdf` | `mvncdf` | `normrnd`

How To

- "Multivariate Normal Distribution" on page B-58

mvtcdf

Purpose

Multivariate t cumulative distribution function

Syntax

```
y = mvtcdf(X,C,DF)
y = mvtcdf(xl,xu,C,DF)
[y,err] = mvtcdf(...)
[...] = mvntdf(...,options)
```

Description

`y = mvtcdf(X,C,DF)` returns the cumulative probability of the multivariate t distribution with correlation parameters `C` and degrees of freedom `DF`, evaluated at each row of `X`. Rows of the n-by-d matrix `X` correspond to observations or points, and columns correspond to variables or coordinates. `y` is an `n`-by-`1` vector.

`C` is a symmetric, positive definite, d-by-d matrix, typically a correlation matrix. If its diagonal elements are not 1, `mvtcdf` scales `C` to correlation form. `mvtcdf` does not rescale `X`. `DF` is a scalar, or a vector with n elements.

The multivariate t cumulative probability at `X` is defined as the probability that a random vector `T`, distributed as multivariate t, will fall within the semi-infinite rectangle with upper limits defined by `X`, i.e., $\Pr\{T(1)\le X(1), T(2)\le X(2), \ldots T(d)\le X(d)\}$.

`y = mvtcdf(xl,xu,C,DF)` returns the multivariate t cumulative probability evaluated over the rectangle with lower and upper limits defined by `xl` and `xu`, respectively.

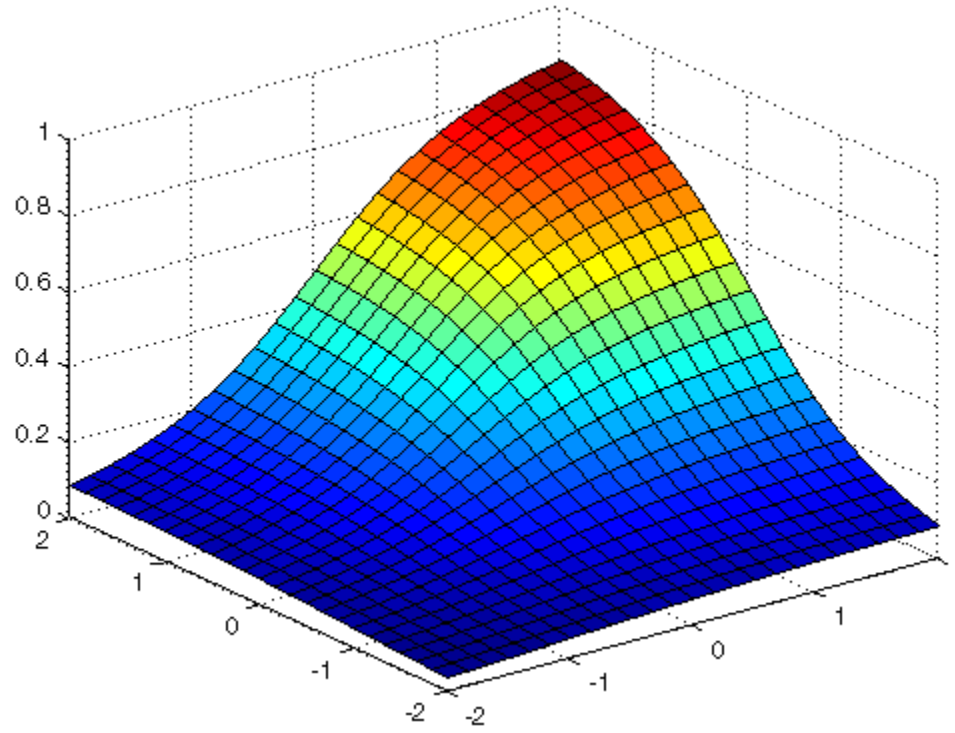
`[y,err] = mvtcdf(...)` returns an estimate of the error in `y`. For bivariate and trivariate distributions, `mvtcdf` uses adaptive quadrature on a transformation of the t density, based on methods developed by Genz, as described in the references. The default absolute error tolerance for these cases is `1e-8`. For four or more dimensions, `mvtcdf` uses a quasi-Monte Carlo integration algorithm based on methods developed by Genz and Bretz, as described in the references. The default absolute error tolerance for these cases is `1e-4`.

`[...] = mvntdf(...,options)` specifies control parameters for the numerical integration used to compute `y`. This argument can be created by a call to `statset`. Choices of `statset` parameters are:

- `'TolFun'` — Maximum absolute error tolerance. Default is `1e-8` when $d < 4$, or `1e-4` when $d \geq 4$.
- `'MaxFunEvals'` — Maximum number of integrand evaluations allowed when $d \geq 4$. Default is `1e7`. `'MaxFunEvals'` is ignored when $d < 4$.
- `'Display'` — Level of display output. Choices are `'off'` (the default), `'iter'`, and `'final'`. `'Display'` is ignored when $d < 4$.

Examples

```
C = [1 .4; .4 1]; df = 2;
[X1,X2] = meshgrid(linspace(-2,2,25)',linspace(-2,2,25)');
X = [X1(:) X2(:)];
p = mvtcdf(X,C,df);
surf(X1,X2,reshape(p,25,25));
```



References

[1] Genz, A. "Numerical Computation of Rectangular Bivariate and Trivariate Normal and t Probabilities." *Statistics and Computing*. Vol. 14, No. 3, 2004, pp. 251–260.

[2] Genz, A., and F. Bretz. "Numerical Computation of Multivariate t Probabilities with Application to Power Calculation of Multiple Contrasts." *Journal of Statistical Computation and Simulation*. Vol. 63, 1999, pp. 361–378.

[3] Genz, A., and F. Bretz. "Comparison of Methods for the Computation of Multivariate t Probabilities." *Journal of Computational and Graphical Statistics*. Vol. 11, No. 4, 2002, pp. 950–971.

See Also

`mvtpdf` | `mvtrnd`

How To

- “Multivariate t Distribution” on page B-64

mvtpdf

Purpose

Multivariate t probability density function

Syntax

```
y = mvtpdf(X,C,df)
```

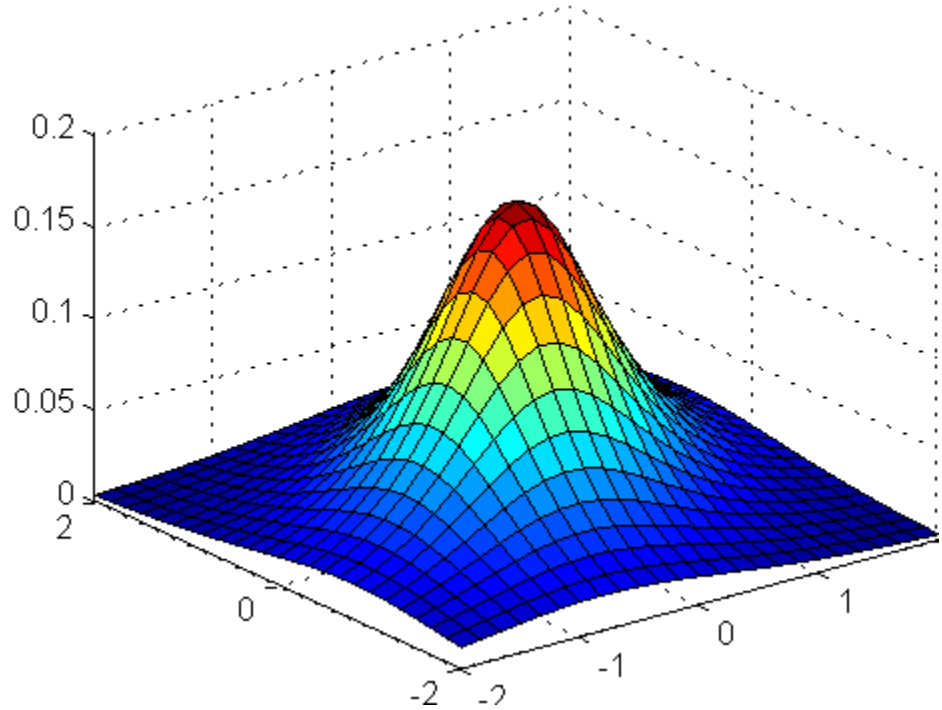
Description

`y = mvtpdf(X,C,df)` returns the probability density of the multivariate t distribution with correlation parameters `C` and degrees of freedom `df`, evaluated at each row of `X`. Rows of the n-by-d matrix `X` correspond to observations or points, and columns correspond to variables or coordinates. `C` is a symmetric, positive definite, d-by-d matrix, typically a correlation matrix. If its diagonal elements are not 1, `mvtpdf` scales `C` to correlation form. `mvtcdf` does not rescale `X`. `df` is a scalar, or a vector with n elements. `y` is an n-by-1 vector.

Examples

Visualize a multivariate t distribution:

```
[X1,X2] = meshgrid(linspace(-2,2,25)',linspace(-2,2,25)');
X = [X1(:) X2(:)];
C = [1 .4; .4 1];
df = 2;
p = mvtpdf(X,C,df);
surf(X1,X2,reshape(p,25,25))
```



See Also

`mvtcdf` | `mvtrnd`

How To

- "Multivariate t Distribution" on page B-64

mvtrnd

Purpose

Multivariate *t* random numbers

Syntax

```
R = mvtrnd(C,df,cases)
R = mvtrnd(C,df)
```

Description

`R = mvtrnd(C,df,cases)` returns a matrix of random numbers chosen from the multivariate *t* distribution, where `C` is a correlation matrix. `df` is the degrees of freedom and is either a scalar or is a vector with `cases` elements. If `p` is the number of columns in `C`, then the output `R` has `cases` rows and `p` columns.

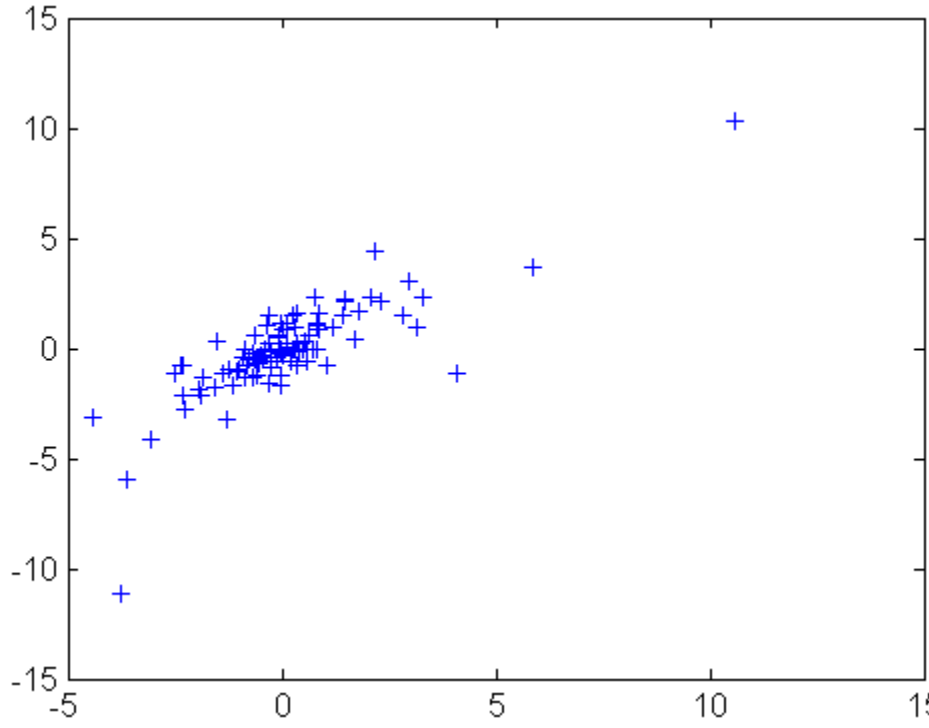
Let `t` represent a row of `R`. Then the distribution of `t` is that of a vector having a multivariate normal distribution with mean 0, variance 1, and covariance matrix `C`, divided by an independent chi-square random value having `df` degrees of freedom. The rows of `R` are independent.

`C` must be a square, symmetric and positive definite matrix. If its diagonal elements are not all 1 (that is, if `C` is a covariance matrix rather than a correlation matrix), `mvtrnd` rescales `C` to transform it to a correlation matrix before generating the random numbers.

`R = mvtrnd(C,df)` returns a single random number from the multivariate *t* distribution.

Examples

```
SIGMA = [1 0.8;0.8 1];
R = mvtrnd(SIGMA,3,100);
plot(R(:,1),R(:,2),'+')
```



See Also

`mvtpdf` | `mvtcdf`

How To

- “Multivariate t Distribution” on page B-64

cvpartition.N property

Purpose

Number of observations (including observations with missing `group` values)

Description

Number of observations (including observations with missing `group` values).

Purpose

Naive Bayes classifier

Description

A `NaiveBayes` object defines a Naive Bayes classifier. A Naive Bayes classifier assigns a new observation to the most probable class, assuming the features are conditionally independent given the class value.

Construction

NaiveBayes	Create NaiveBayes object

Methods

disp	Display `NaiveBayes` classifier object
display	Display `NaiveBayes` classifier object
fit	Create Naive Bayes classifier object by fitting training data
posterior	Compute posterior probability of each class for test data
predict	Predict class label for test data
subsasgn	Subscripted reference for `NaiveBayes` object
subsref	Subscripted reference for `NaiveBayes` object

Properties

CIsNonEmpty	Flag for non-empty classes
CLevels	Class levels
CNames	Class names
CPrior	Class priors

Dist	Distribution names
NClasses	Number of classes
NDims	Number of dimensions
Params	Parameter estimates

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

Examples

Predict the class label using the Naive Bayes classifier

```
load fisheriris
```

Use the default Gaussian distribution and a confusion matrix:

```
O1 = NaiveBayes.fit(meas,species);
C1 = O1.predict(meas);
cMat1 = confusionmat(species,C1)
```

This returns:

```
cMat1 =

    50     0     0
     0    47     3
     0     3    47
```

Use the Gaussian distribution for features 1 and 3 and use the kernel density estimation for features 2 and 4:

```
O2 = NaiveBayes.fit(meas,species,'dist',...
{'normal','kernel','normal','kernel'});
C2 = O2.predict(meas);
cMat2 = confusionmat(species,C2)
```

This returns:

```
cMat2 =

    50     0     0
     0    47     3
     0     3    47
```

References

[1] Mitchell, T. (1997) Machine Learning, McGraw Hill.

[2] Vangelis M., Ion A., and Geogios P. Spam Filtering with Naive Bayes - Which Naive Bayes? (2006) Third Conference on Email and Anti-Spam.

[3] George H. John and Pat Langley. Estimating continuous distributions in bayesian classifiers (1995) the Eleventh Conference on Uncertainty in Artificial Intelligence.

How To

- "Naive Bayes Classification" on page 12-29
- "Grouped Data" on page 2-34

NaiveBayes

Purpose

Create NaiveBayes object

Description

You cannot create a `NaiveBayes` classifier by calling the constructor. Use `NaiveBayes.fit` to create a `NaiveBayes` classifier by fitting the object to training data.

See Also

`fit`

Purpose

Covariance ignoring NaN values

Syntax

```
Y = nancov(X)
Y = nancov(X1,X2)
Y = nancov(...,1)
Y = nancov(...,'pairwise')
```

Description

`Y = nancov(X)` is the covariance `cov` of `X`, computed after removing observations with `NaN` values.

For vectors `x`, `nancov(x)` is the sample variance of the remaining elements, once `NaN` values are removed. For matrices `X`, `nancov(X)` is the sample covariance of the remaining observations, once observations (rows) containing any `NaN` values are removed.

`Y = nancov(X1,X2)`, where `X1` and `X2` are matrices with the same number of elements, is equivalent to `nancov(X)`, where `X = [X1(:) X2(:)]`.

`nancov` removes the mean from each variable (column for matrix `X`) before calculating `Y`. If n is the number of remaining observations after removing observations with `NaN` values, `nancov` normalizes `Y` by either $n - 1$ or n , depending on whether $n > 1$ or $n = 1$, respectively. To specify normalization by n, use `Y = nancov(...,1)`.

`Y = nancov(...,'pairwise')` computes `Y(i,j)` using rows with no `NaN` values in columns `i` or `j`. The result `Y` may not be a positive definite matrix.

Examples

Generate random data for two variables (columns) with random missing values:

```
X = rand(10,2);
p = randperm(numel(X));
X(p(1:5)) = NaN
X =
    0.8147    0.1576
       NaN       NaN
    0.1270    0.9572
```

```
    0.9134       NaN
    0.6324       NaN
    0.0975    0.1419
    0.2785    0.4218
    0.5469    0.9157
    0.9575    0.7922
    0.9649       NaN
```

Establish a correlation between a third variable and the other two variables:

```
X(:,3) = sum(X,2)
X =
    0.8147    0.1576    0.9723
       NaN       NaN       NaN
    0.1270    0.9572    1.0842
    0.9134       NaN       NaN
    0.6324       NaN       NaN
    0.0975    0.1419    0.2394
    0.2785    0.4218    0.7003
    0.5469    0.9157    1.4626
    0.9575    0.7922    1.7497
    0.9649       NaN       NaN
```

Compute the covariance matrix for the three variables after removing observations (rows) with `NaN` values:

```
Y = nancov(X)
Y =
    0.1311    0.0096    0.1407
    0.0096    0.1388    0.1483
    0.1407    0.1483    0.2890
```

See Also

`NaN` | `cov` | `var` | `nanvar`

Purpose

Maximum ignoring NaN values

Syntax

```
y = nanmax(X)
Y = nanmax(X1,X2)
y = nanmax(X,[],dim)
[y,indices] = nanmax(...)
```

Description

`y = nanmax(X)` is the maximum `max` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanmax(x)` is the maximum of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanmax(X)` is a row vector of column maxima, once `NaN` values are removed. For multidimensional arrays `X`, `nanmax` operates along the first nonsingleton dimension.

`Y = nanmax(X1,X2)` returns an array `Y` the same size as `X1` and `X2` with `Y(i,j) = nanmax(X1(i,j),X2(i,j))`. Scalar inputs are expanded to an array of the same size as the other input.

`y = nanmax(X,[],dim)` operates along the dimension `dim` of `X`.

`[y,indices] = nanmax(...)` also returns the row indices of the maximum values for each column in the vector `indices`.

Examples

Find column maxima and their indices for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
[y,indices] = nanmax(X)
y =
     4     5   NaN
indices =
     3     2     1
```

See Also

`NaN` | `max` | `nanmin`

nanmean

Purpose

Mean ignoring NaN values

Syntax

```
y = nanmean(X)
y = nanmean(X,dim)
```

Description

`y = nanmean(X)` is the `mean` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanmean(x)` is the mean of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanmean(X)` is a row vector of column means, once `NaN` values are removed. For multidimensional arrays `X`, `nanmean` operates along the first nonsingleton dimension.

`y = nanmean(X,dim)` takes the mean along dimension `dim` of `X`.

Note If `X` contains a vector of all `NaN` values along some dimension, the vector is empty once the `NaN` values are removed, so the sum of the remaining elements is `0`. Since the mean involves division by `0`, its value is `NaN`. The output `NaN` is not a mean of `NaN` values.

Examples

Find column means for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
y = nanmean(X)
y =
   3.5000  3.0000  NaN
```

See Also

`NaN` | `mean` | `nanmedian`

Purpose

Median ignoring NaN values

Syntax

```
y = nanmedian(X)
y = nanmedian(X,dim)
```

Description

`y = nanmedian(X)` is the `median` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanmedian(x)` is the median of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanmedian(X)` is a row vector of column medians, once `NaN` values are removed. For multidimensional arrays `X`, `nanmedian` operates along the first nonsingleton dimension.

`y = nanmedian(X,dim)` takes the mean along dimension `dim` of `X`.

Examples

Find column medians for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
y = nanmedian(X)
y =
   3.5000  3.0000  NaN
```

See Also

`NaN` | `median` | `nanmean`

nanmin

Purpose

Minimum ignoring NaN values

Syntax

```
y = nanmin(X)
Y = nanmin(X1,X2)
y = nanmin(X,[],dim)
[y,indices] = nanmin(...)
```

Description

`y = nanmin(X)` is the minimum `min` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanmin(x)` is the minimum of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanmin(X)` is a row vector of column minima, once `NaN` values are removed. For multidimensional arrays `X`, `nanmin` operates along the first nonsingleton dimension.

`Y = nanmin(X1,X2)` returns an array `Y` the same size as `X1` and `X2` with `Y(i,j) = nanmin(X1(i,j),X2(i,j))`. Scalar inputs are expanded to an array of the same size as the other input.

`y = nanmin(X,[],dim)` operates along the dimension `dim` of `X`.

`[y,indices] = nanmin(...)` also returns the row indices of the minimum values for each column in the vector `indices`.

Examples

Find column minima and their indices for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
[y,indices] = nanmin(X)
y =
     3     1   NaN
indices =
     2     1     1
```

See Also

NaN | min | nanmax

Purpose

Standard deviation ignoring NaN values

Syntax

```
y = nanstd(X)
y = nanstd(X,1)
y = nanstd(X,flag,dim)
```

Description

`y = nanstd(X)` is the standard deviation `std` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanstd(x)` is the sample standard deviation of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanstd(X)` is a row vector of column sample standard deviations, once `NaN` values are removed. For multidimensional arrays `X`, `nanstd` operates along the first nonsingleton dimension.

If n is the number of remaining observations after removing observations with `NaN` values, `nanstd` normalizes `y` by n–1. To specify normalization by n, use `y = nanstd(X,1)`.

`y = nanstd(X,flag,dim)` takes the standard deviation along the dimension `dim` of `X`. The `flag` is `0` or `1` to specify normalization by n – 1 or n, respectively, where n is the number of remaining observations after removing observations with `NaN` values.

Examples

Find column standard deviations for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
y = nanstd(X)
y =
   0.7071  2.8284  NaN
```

See Also

`NaN` | `std` | `nanvar` | `nanmean`

nansum

Purpose

Sum ignoring NaN values

Syntax

```
y = nansum(X)
y = nansum(X,dim)
```

Description

`y = nansum(X)` is the `sum` of `X`, computed after removing `NaN` values.

For vectors `x`, `nansum(x)` is the sum of the remaining elements, once `NaN` values are removed. For matrices `X`, `nansum(X)` is a row vector of column sums, once `NaN` values are removed. For multidimensional arrays `X`, `nansum` operates along the first nonsingleton dimension.

`y = nansum(X,dim)` takes the sum along dimension `dim` of `X`.

Note If `X` contains a vector of all `NaN` values along some dimension, the vector is empty once the `NaN` values are removed, so the sum of the remaining elements is `0`. The output `0` is not a sum of `NaN` values.

Examples

Find column sums for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
y = nansum(X)
y =
     7     6     0
```

See Also

`NaN` | `sum`

Purpose

Variance, ignoring NaN values

Syntax

```
y = nanvar(X)
y = nanvar(X,1)
y = nanvar(X,w)
y = nanvar(X,w,dim)
```

Description

`y = nanvar(X)` is the variance `var` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanvar(x)` is the sample variance of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanvar(X)` is a row vector of column sample variances, once `NaN` values are removed. For multidimensional arrays `X`, `nanvar` operates along the first nonsingleton dimension.

`nancov` removes the mean from each variable (column for matrix `X`) before calculating `Y`. If n is the number of remaining observations after removing observations with `NaN` values, `nanvar` normalizes `y` by either $n - 1$ or n , depending on whether $n > 1$ or $n = 1$, respectively. To specify normalization by n, use `y = nanvar(X,1)`.

`y = nanvar(X,w)` computes the variance using the weight vector `w`. The length of `w` must equal the length of the dimension over which `nanvar` operates, and its elements must be nonnegative. Elements of `X` corresponding to `NaN` values of `w` are ignored.

`y = nanvar(X,w,dim)` takes the variance along the dimension `dim` of `X`. Set `w` to `[]` to use the default normalization by $n - 1$.

Examples

Find column standard deviations for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
y = nanvar(X)
```

```
y =
   0.5000  8.0000  NaN
```

See Also

NaN | var | nanstd | nanmean

Purpose

Negative binomial cumulative distribution function

Syntax

```
Y = nbincdf(X,R,P)
```

Description

`Y = nbincdf(X,R,P)` computes the negative binomial cdf at each of the values in `X` using the corresponding number of successes, `R` and probability of success in a single trial, `P`. `X`, `R`, and `P` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `Y`. A scalar input for `X`, `R`, or `P` is expanded to a constant array with the same dimensions as the other inputs.

The negative binomial cdf is

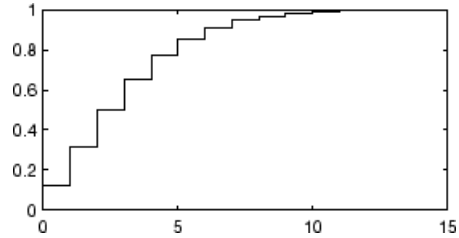
$$y = F(x \mid r, p) = \sum_{i=0}^{x} \binom{r+i-1}{i} p^r q^i I_{(0,1,\ldots)}(i)$$

The simplest motivation for the negative binomial is the case of successive random trials, each having a constant probability `P` of success. The number of *extra* trials you must perform in order to observe a given number `R` of successes has a negative binomial distribution. However, consistent with a more general interpretation of the negative binomial, `nbincdf` allows `R` to be any positive value, including nonintegers. When `R` is noninteger, the binomial coefficient in the definition of the cdf is replaced by the equivalent expression

$$\frac{\Gamma(r+i)}{\Gamma(r)\Gamma(i+1)}$$

Examples

```
x = (0:15);
p = nbincdf(x,3,0.5);
stairs(x,p)
```



See Also

`cdf` | `nbinpdf` | `nbininv` | `nbinstat` | `nbinfit` | `nbinrnd`

How To

- "Negative Binomial Distribution" on page B-72

Purpose

Negative binomial parameter estimates

Syntax

```
parmhat = nbinfit(data)
[parmhat,parmci] = nbinfit(data,alpha)
[...] = nbinfit(data,alpha,options)
```

Description

`parmhat = nbinfit(data)` returns the maximum likelihood estimates (MLEs) of the parameters of the negative binomial distribution given the data in the vector `data`.

`[parmhat,parmci] = nbinfit(data,alpha)` returns MLEs and `100(1-alpha)` percent confidence intervals. By default, `alpha = 0.05`, which corresponds to 95% confidence intervals.

`[...] = nbinfit(data,alpha,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates. The negative binomial fit function accepts an `options` structure which you can create using the function `statset`. Enter `statset('nbinfit')` to see the names and default values of the parameters that `nbinfit` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

Note The variance of a negative binomial distribution is greater than its mean. If the sample variance of the data in `data` is less than its sample mean, `nbinfit` cannot compute MLEs. You should use the `poissfit` function instead.

See Also

`nbincdf` | `nbininv` | `nbinpdf` | `nbinrnd` | `nbinstat` | `mle` | `statset`

How To

- "Negative Binomial Distribution" on page B-72

nbininv

Purpose

Negative binomial inverse cumulative distribution function

Syntax

```
X = nbininv(Y,R,P)
```

Description

`X = nbininv(Y,R,P)` returns the inverse of the negative binomial cdf with corresponding number of successes, `R` and probability of success in a single trial, `P`. Since the binomial distribution is discrete, `nbininv` returns the least integer `X` such that the negative binomial cdf evaluated at `X` equals or exceeds `Y`. `Y`, `R`, and `P` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `X`. A scalar input for `Y`, `R`, or `P` is expanded to a constant array with the same dimensions as the other inputs.

The simplest motivation for the negative binomial is the case of successive random trials, each having a constant probability `P` of success. The number of *extra* trials you must perform in order to observe a given number `R` of successes has a negative binomial distribution. However, consistent with a more general interpretation of the negative binomial, `nbininv` allows `R` to be any positive value, including nonintegers.

Examples

How many times would you need to flip a fair coin to have a 99% probability of having observed 10 heads?

```
flips = nbininv(0.99,10,0.5) + 10
flips =
  33
```

Note that you have to flip at least 10 times to get 10 heads. That is why the second term on the right side of the equals sign is a 10.

See Also

`icdf` | `nbincdf` | `nbinpdf` | `nbinstat` | `nbinfit` | `nbinrnd`

How To

- "Negative Binomial Distribution" on page B-72

Purpose

Negative binomial probability density function

Syntax

```
Y = nbinpdf(X,R,P)
```

Description

`Y = nbinpdf(X,R,P)` returns the negative binomial pdf at each of the values in `X` using the corresponding number of successes, `R` and probability of success in a single trial, `P`. `X`, `R`, and `P` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `Y`. A scalar input for `X`, `R`, or `P` is expanded to a constant array with the same dimensions as the other inputs. Note that the density function is zero unless the values in `X` are integers.

The negative binomial pdf is

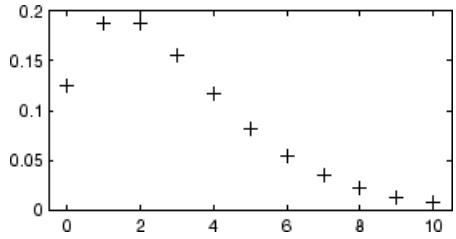
$$y = f(x \mid r, p) = \binom{r+x-1}{x} p^r q^x I_{(0,1,\ldots)}(x)$$

The simplest motivation for the negative binomial is the case of successive random trials, each having a constant probability `P` of success. The number of *extra* trials you must perform in order to observe a given number `R` of successes has a negative binomial distribution. However, consistent with a more general interpretation of the negative binomial, `nbinpdf` allows `R` to be any positive value, including nonintegers. When `R` is noninteger, the binomial coefficient in the definition of the pdf is replaced by the equivalent expression

$$\frac{\Gamma(r+x)}{\Gamma(r)\Gamma(x+1)}$$

Examples

```
x = (0:10);
y = nbinpdf(x,3,0.5);
plot(x,y,'+')
set(gca,'Xlim',[-0.5,10.5])
```



See Also

pdf | nbincdf | nbininv | nbinstat | nbinfit | nbinrnd

How To

- “Negative Binomial Distribution” on page B-72

Purpose

Negative binomial random numbers

Syntax

```
RND = nbinrnd(R,P)
RND = nbinrnd(R,P,m,n,...)
RND = nbinrnd(R,P,[m,n,...])
```

Description

`RND = nbinrnd(R,P)` is a matrix of random numbers chosen from a negative binomial distribution with corresponding number of successes, `R` and probability of success in a single trial, `P`. `R` and `P` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `RND`. A scalar input for `R` or `P` is expanded to a constant array with the same dimensions as the other input.

`RND = nbinrnd(R,P,m,n,...)` or `RND = nbinrnd(R,P,[m,n,...])` generates an `m`-by-`n`-by-... array. The `R`, `P` parameters can each be scalars or arrays of the same size as `R`.

The simplest motivation for the negative binomial is the case of successive random trials, each having a constant probability `P` of success. The number of *extra* trials you must perform in order to observe a given number `R` of successes has a negative binomial distribution. However, consistent with a more general interpretation of the negative binomial, `nbinrnd` allows `R` to be any positive value, including nonintegers.

Examples

Suppose you want to simulate a process that has a defect probability of 0.01. How many units might Quality Assurance inspect before finding three defective items?

```
r = nbinrnd(3,0.01,1,6)+3
r =
  496  142  420  396  851  178
```

See Also

`random` | `nbinpdf` | `nbincdf` | `nbininv` | `nbinstat` | `nbinfit`

How To

- "Negative Binomial Distribution" on page B-72

nbinstat

Purpose

Negative binomial mean and variance

Syntax

```
[M,V] = nbinstat(R,P)
```

Description

`[M,V] = nbinstat(R,P)` returns the mean of and variance for the negative binomial distribution with corresponding number of successes, `R` and probability of success in a single trial, `P`. `R` and `P` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `R` or `P` is expanded to a constant array with the same dimensions as the other input.

The mean of the negative binomial distribution with parameters r and p is rq / p, where $q = 1 - p$. The variance is rq / p^2.

The simplest motivation for the negative binomial is the case of successive random trials, each having a constant probability `P` of success. The number of *extra* trials you must perform in order to observe a given number `R` of successes has a negative binomial distribution. However, consistent with a more general interpretation of the negative binomial, `nbinstat` allows `R` to be any positive value, including nonintegers.

Examples

```
p = 0.1:0.2:0.9;
r = 1:5;
[R,P] = meshgrid(r,p);
[M,V] = nbinstat(R,P)
M =
  9.0000  18.0000  27.0000  36.0000  45.0000
  2.3333  4.6667  7.0000  9.3333  11.6667
  1.0000  2.0000  3.0000  4.0000  5.0000
  0.4286  0.8571  1.2857  1.7143  2.1429
  0.1111  0.2222  0.3333  0.4444  0.5556

V =
  90.0000 180.0000 270.0000 360.0000 450.0000
  7.7778  15.5556  23.3333  31.1111  38.8889
  2.0000  4.0000  6.0000  8.0000  10.0000
```

```
    0.6122   1.2245   1.8367   2.4490   3.0612
    0.1235   0.2469   0.3704   0.4938   0.6173
```

See Also

nbinpdf | nbincdf | nbininv | nbinfit | nbinrnd

How To

- “Negative Binomial Distribution” on page B-72

ncfcdf

Purpose

Noncentral F cumulative distribution function

Syntax

```
P = ncfcdf(X,NU1,NU2,DELTA)
```

Description

`P = ncfcdf(X,NU1,NU2,DELTA)` computes the noncentral F cdf at each of the values in `X` using the corresponding numerator degrees of freedom in `NU1`, denominator degrees of freedom in `NU2`, and positive noncentrality parameters in `DELTA`. `NU1`, `NU2`, and `DELTA` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `P`. A scalar input for `X`, `NU1`, `NU2`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

The noncentral F cdf is

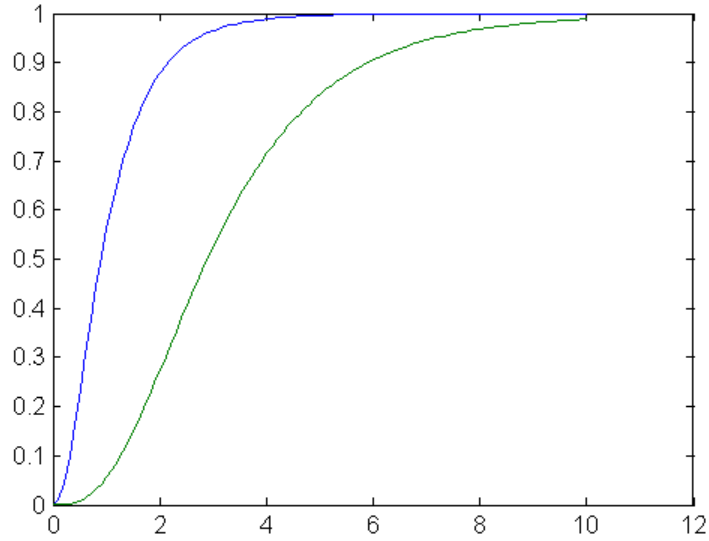
$$F(x \mid \nu_1,\nu_2,\delta) = \sum_{j=0}^{\infty}\left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!}e^{\frac{-\delta}{2}}\right) I\left(\frac{\nu_1 \cdot x}{\nu_2 + \nu_1 \cdot x}\middle|\frac{\nu_1}{2}+j,\frac{\nu_2}{2}\right)$$

where $I(x \mid a,b)$ is the incomplete beta function with parameters a and b.

Examples

Compare the noncentral F cdf with $\delta = 10$ to the F cdf with the same number of numerator and denominator degrees of freedom (5 and 20 respectively).

```
x = (0.01:0.1:10.01)';
p1 = ncfcdf(x,5,20,10);
p = fcdf(x,5,20);
plot(x,p,'-',x,p1,'-')
```



References

[1] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 189–200.

See Also

`cdf` | `ncfpdf` | `ncfinv` | `ncfstat` | `ncfrnd`

How To

- “Noncentral F Distribution” on page B-78

ncfinv

Purpose

Noncentral F inverse cumulative distribution function

Syntax

```
X = ncfinv(P,NU1,NU2,DELTA)
```

Description

`X = ncfinv(P,NU1,NU2,DELTA)` returns the inverse of the noncentral F cdf with numerator degrees of freedom `NU1`, denominator degrees of freedom `NU2`, and positive noncentrality parameter `DELTA` for the corresponding probabilities in `P`. `P`, `NU1`, `NU2`, and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `X`. A scalar input for `P`, `NU1`, `NU2`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

Examples

One hypothesis test for comparing two sample variances is to take their ratio and compare it to an F distribution. If the numerator and denominator degrees of freedom are 5 and 20 respectively, then you reject the hypothesis that the first variance is equal to the second variance if their ratio is less than that computed below.

```
critical = finv(0.95,5,20)
critical =
  2.7109
```

Suppose the truth is that the first variance is twice as big as the second variance. How likely is it that you would detect this difference?

```
prob = 1 - ncfcdf(critical,5,20,2)
prob =
  0.1297
```

If the true ratio of variances is 2, what is the typical (median) value you would expect for the F statistic?

```
ncfinv(0.5,5,20,2)
ans =
    1.2786
```

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions.* Hoboken, NJ: Wiley-Interscience, 2000.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2.* Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 189–200.

See Also

`icdf` | `ncfcdf` | `ncfpdf` | `ncfstat` | `ncfrnd`

How To

- "Noncentral F Distribution" on page B-78

ncfpdf

Purpose

Noncentral *F* probability density function

Syntax

```
Y = ncfpdf(X,NU1,NU2,DELTA)
```

Description

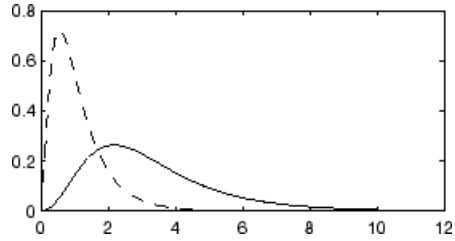
`Y = ncfpdf(X,NU1,NU2,DELTA)` computes the noncentral *F* pdf at each of the values in `X` using the corresponding numerator degrees of freedom in `NU1`, denominator degrees of freedom in `NU2`, and positive noncentrality parameters in `DELTA`. `X`, `NU1`, `N2`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `Y`. A scalar input for `P`, `NU1`, `NU2`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

The *F* distribution is a special case of the noncentral *F* where $\delta = 0$. As δ increases, the distribution flattens like the plot in the example.

Examples

Compare the noncentral *F* pdf with $\delta = 10$ to the F pdf with the same number of numerator and denominator degrees of freedom (5 and 20 respectively).

```
x = (0.01:0.1:10.01)';
p1 = ncfpdf(x,5,20,10);
p = fpdf(x,5,20);
plot(x,p,'-',x,p1,'-')
```



References

[1] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2.* Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 189–200.

See Also

`pdf` | `ncfcdf` | `ncfinv` | `ncfstat` | `ncfrnd`

How To

- "Noncentral F Distribution" on page B-78

ncfrnd

Purpose

Noncentral F random numbers

Syntax

```
R = ncfrnd(NU1,NU2,DELTA)
R = ncfrnd(NU1,NU2,DELTA,m,n,...)
R = ncfrnd(NU1,NU2,DELTA,[m,n,...])
```

Description

`R = ncfrnd(NU1,NU2,DELTA)` returns a matrix of random numbers chosen from the noncentral F distribution with corresponding numerator degrees of freedom in `NU1`, denominator degrees of freedom in `NU2`, and positive noncentrality parameters in `DELTA`. `NU1`, `NU2`, and `DELTA` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `NU1`, `NU2`, or `DELTA` is expanded to a constant matrix with the same dimensions as the other inputs.

`R = ncfrnd(NU1,NU2,DELTA,m,n,...)` or `R = ncfrnd(NU1,NU2,DELTA,[m,n,...])` generates an `m`-by-`n`-by-... array. The `NU1`, `NU2`, `DELTA` parameters can each be scalars or arrays of the same size as `R`.

Examples

Compute six random numbers from a noncentral F distribution with 10 numerator degrees of freedom, 100 denominator degrees of freedom and a noncentrality parameter, δ, of 4.0. Compare this to the F distribution with the same degrees of freedom.

```
r = ncfrnd(10,100,4,1,6)
r =
  2.5995  0.8824  0.8220  1.4485  1.4415  1.4864

r1 = frnd(10,100,1,6)
r1 =
  0.9826  0.5911  1.0967  0.9681  2.0096  0.6598
```

References

[1] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2.* Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 189–200.

See Also

`random` | `ncfpdf` | `ncfcdf` | `ncfinv` | `ncfstat`

How To

- “Noncentral F Distribution” on page B-78

Purpose

Noncentral F mean and variance

Syntax

```
[M,V] = ncfstat(NU1,NU2,DELTA)
```

Description

`[M,V] = ncfstat(NU1,NU2,DELTA)` returns the mean of and variance for the noncentral F pdf with corresponding numerator degrees of freedom in `NU1`, denominator degrees of freedom in `NU2`, and positive noncentrality parameters in `DELTA`. `NU1`, `NU2`, and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `NU1`, `NU2`, or `DELTA` is expanded to a constant array with the same dimensions as the other input.

The mean of the noncentral F distribution with parameters ν_1, ν_2, and δ is

$$\frac{\nu_2(\delta+\nu_1)}{\nu_1(\nu_2-2)}$$

where $\nu_2 > 2$.

The variance is

$$2\left(\frac{\nu_2}{\nu_1}\right)^2\left[\frac{(\delta+\nu_1)^2+(2\delta+\nu_1)(\nu_2-2)}{(\nu_2-2)^2(\nu_2-4)}\right]$$

where $\nu_2 > 4$.

Examples

```
[m,v]= ncfstat(10,100,4)
m =
  1.4286
v =
  0.4252
```

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 73–74.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 189–200.

See Also

`ncfpdf` | `ncfcdf` | `ncfinv` | `ncfrnd`

How To

- "Noncentral F Distribution" on page B-78

NaiveBayes.NClasses property

Purpose

Number of classes

Description

The `NClasses` property specifies the number of classes in the grouping variable used to create the Naive Bayes classifier.

Purpose

Number k of mixture components

Description

The number k of mixture components.

Purpose

Noncentral *t* cumulative distribution function

Syntax

```
P = nctcdf(X,NU,DELTA)
```

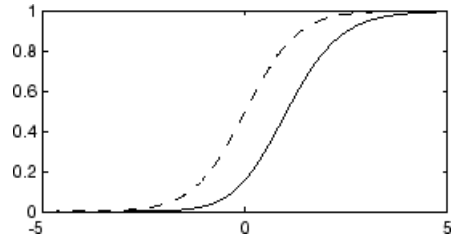
Description

`P = nctcdf(X,NU,DELTA)` computes the noncentral *t* cdf at each of the values in `X` using the corresponding degrees of freedom in `NU` and noncentrality parameters in `DELTA`. `X`, `NU`, and `DELTA` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `P`. A scalar input for `X`, `NU`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

Examples

Compare the noncentral *t* cdf with `DELTA = 1` to the *t* cdf with the same number of degrees of freedom (10).

```
x = (-5:0.1:5)';
p1 = nctcdf(x,10,1);
p = tcdf(x,10);
plot(x,p,'-',x,p1,'-')
```



References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 147–148.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 201–219.

See Also

`cdf` | `nctpdf` | `nctinv` | `nctstat` | `nctrnd`

How To

- "Noncentral t Distribution" on page B-80

nctinv

Purpose

Noncentral *t* inverse cumulative distribution function

Syntax

```
X = nctinv(P,NU,DELTA)
```

Description

`X = nctinv(P,NU,DELTA)` returns the inverse of the noncentral *t* cdf with `NU` degrees of freedom and noncentrality parameter `DELTA` for the corresponding probabilities in `P`. `P`, `NU`, and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `X`. A scalar input for `P`, `NU`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

Examples

```
x = nctinv([0.1 0.2],10,1)
x =
  -0.2914  0.1618
```

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 147–148.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 201–219.

See Also

`icdf` | `nctcdf` | `nctpdf` | `nctstat` | `nctrnd`

How To

- "Noncentral t Distribution" on page B-80

Purpose

Noncentral *t* probability density function

Syntax

```
Y = nctpdf(X,V,DELTA)
```

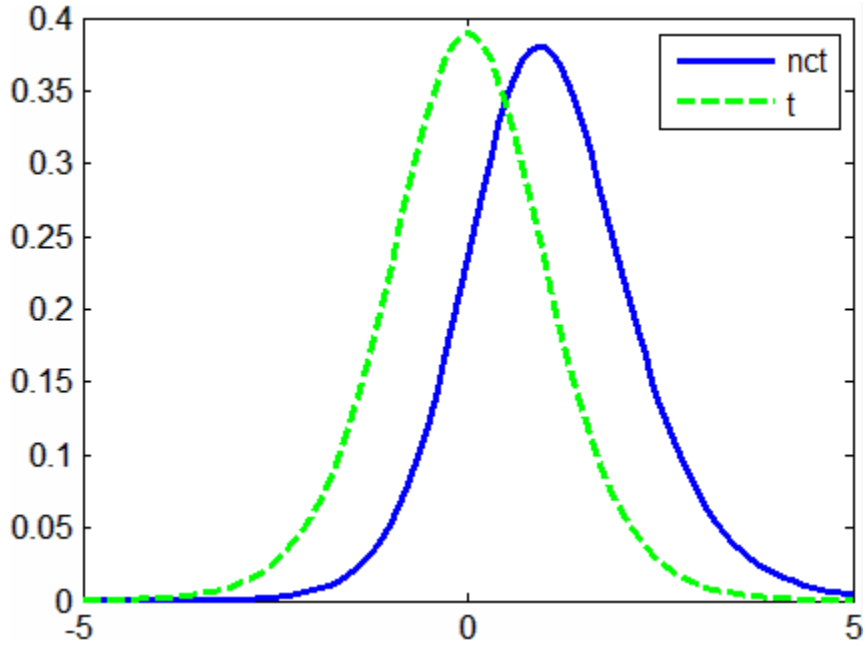
Description

`Y = nctpdf(X,V,DELTA)` computes the noncentral *t* pdf at each of the values in `X` using the corresponding degrees of freedom in `V` and noncentrality parameters in `DELTA`. Vector or matrix inputs for `X`, `V`, and `DELTA` must have the same size, which is also the size of `Y`. A scalar input for `X`, `V`, or `DELTA` is expanded to a constant matrix with the same dimensions as the other inputs.

Examples

Compare the noncentral *t* pdf with `DELTA = 1` to the *t* pdf with the same number of degrees of freedom (10):

```
x = (-5:0.1:5)';
nct = nctpdf(x,10,1);
t = tpdf(x,10);

plot(x,nct,'b-','LineWidth',2)
hold on
plot(x,t,'g--','LineWidth',2)
legend('nct','t')
```



References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 147–148.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 201–219.

See Also

`pdf` | `nctcdf` | `nctinv` | `nctstat` | `nctrnd`

How To

- “Noncentral t Distribution” on page B-80

Purpose

Noncentral *t* random numbers

Syntax

```
R = nctrnd(V,DELTA)
R = nctrnd(V,DELTA,m,n,...)
R = nctrnd(V,DELTA,[m,n,...])
```

Description

`R = nctrnd(V,DELTA)` returns a matrix of random numbers chosen from the noncentral T distribution using the corresponding degrees of freedom in `V` and noncentrality parameters in `DELTA`. `V` and `DELTA` can be vectors, matrices, or multidimensional arrays. A scalar input for `V` or `DELTA` is expanded to a constant array with the same dimensions as the other input.

`R = nctrnd(V,DELTA,m,n,...)` or `R = nctrnd(V,DELTA,[m,n,...])` generates an `m`-by-`n`-by-... array. The `V`, `DELTA` parameters can each be scalars or arrays of the same size as `R`.

Examples

```
nctrnd(10,1,5,1)
ans =
  1.6576
  1.0617
  1.4491
  0.2930
  3.6297
```

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 147–148.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 201–219.

See Also

`random` | `nctpdf` | `nctcdf` | `nctinv` | `nctstat`

How To

- "Noncentral t Distribution" on page B-80

Purpose

Noncentral t mean and variance

Syntax

```
[M,V] = nctstat(NU,DELTA)
```

Description

`[M,V] = nctstat(NU,DELTA)` returns the mean of and variance for the noncentral t pdf with `NU` degrees of freedom and noncentrality parameter `DELTA`. `NU` and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `NU` or `DELTA` is expanded to a constant array with the same dimensions as the other input.

The mean of the noncentral t distribution with parameters ν and δ is

$$\frac{\delta(\nu/2)^{1/2}\Gamma((\nu-1)/2)}{\Gamma(\nu/2)}$$

where $\nu > 1$.

The variance is

$$\frac{\nu}{(\nu-2)}(1+\delta^2)-\frac{\nu}{2}\delta^2\left[\frac{\Gamma((\nu-1)/2)}{\Gamma(\nu/2)}\right]^2$$

where $\nu > 2$.

Examples

```
[m,v] = nctstat(10,1)

m =
  1.0837

v =
  1.3255
```

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 147–148.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 201–219.

See Also

`nctpdf` | `nctcdf` | `nctinv` | `nctrnd`

How To

- "Noncentral t Distribution" on page B-80

ncx2cdf

Purpose

Noncentral chi-square cumulative distribution function

Syntax

```
P = ncx2cdf(X,V,DELTA)
```

Description

`P = ncx2cdf(X,V,DELTA)` computes the noncentral chi-square cdf at each of the values in `X` using the corresponding degrees of freedom in `V` and positive noncentrality parameters in `DELTA`. `X`, `V`, and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `P`. A scalar input for `X`, `V`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

Some texts refer to this distribution as the generalized Rayleigh, Rayleigh-Rice, or Rice distribution.

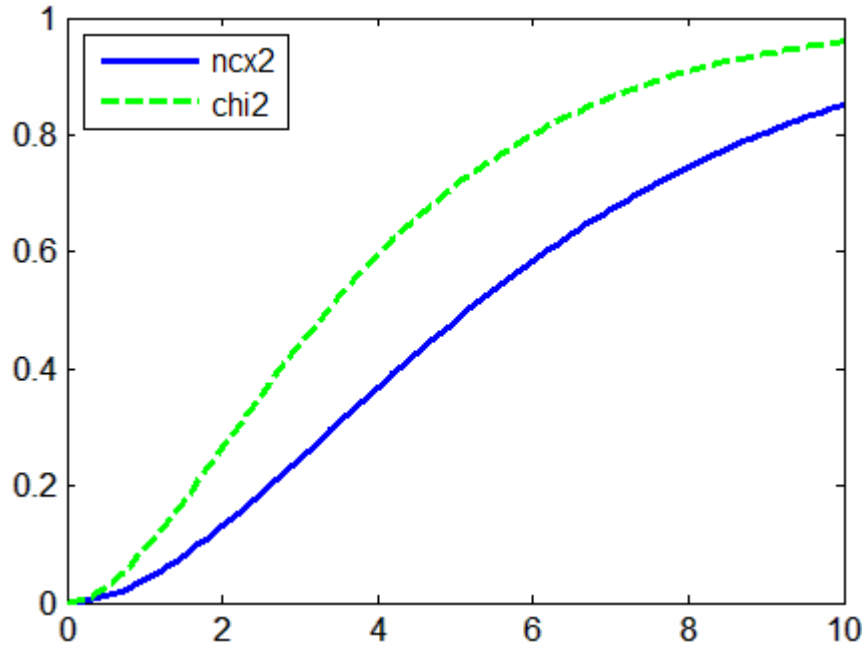
The noncentral chi-square cdf is

$$F(x \mid \nu,\delta) = \sum_{j=0}^{\infty} \left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!} e^{\frac{-\delta}{2}} \right) \Pr\left[\chi^2_{\nu+2j} \le x \right]$$

Examples

Compare the noncentral chi-square cdf with `DELTA = 2` to the chi-square cdf with the same number of degrees of freedom (4):

```
x = (0:0.1:10)';
ncx2 = ncx2cdf(x,4,2);
chi2 = chi2cdf(x,4);

plot(x,ncx2,'b-','LineWidth',2)
hold on
plot(x,chi2,'g--','LineWidth',2)
legend('ncx2','chi2','Location','NW')
```



References

[1] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 130–148.

See Also

`cdf` | `ncx2pdf` | `ncx2inv` | `ncx2stat` | `ncx2rnd`

How To

- "Noncentral Chi-Square Distribution" on page B-76

ncx2inv

Purpose

Noncentral chi-square inverse cumulative distribution function

Syntax

```
X = ncx2inv(P,V,DELTA)
```

Description

`X = ncx2inv(P,V,DELTA)` returns the inverse of the noncentral chi-square cdf using the corresponding degrees of freedom in `V` and positive noncentrality parameters in `DELTA`, at the corresponding probabilities in `P`. `P`, `V`, and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `X`. A scalar input for `P`, `V`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

Algorithms

`ncx2inv` uses Newton's method to converge to the solution.

Examples

```
ncx2inv([0.01 0.05 0.1],4,2)
ans =
  0.4858  1.1498  1.7066
```

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions.* 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 50–52.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2.* Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 130–148.

See Also

`icdf` | `ncx2cdf` | `ncx2pdf` | `ncx2stat` | `ncx2rnd`

How To

- "Noncentral Chi-Square Distribution" on page B-76

Purpose

Noncentral chi-square probability density function

Syntax

```
Y = ncx2pdf(X,V,DELTA)
```

Description

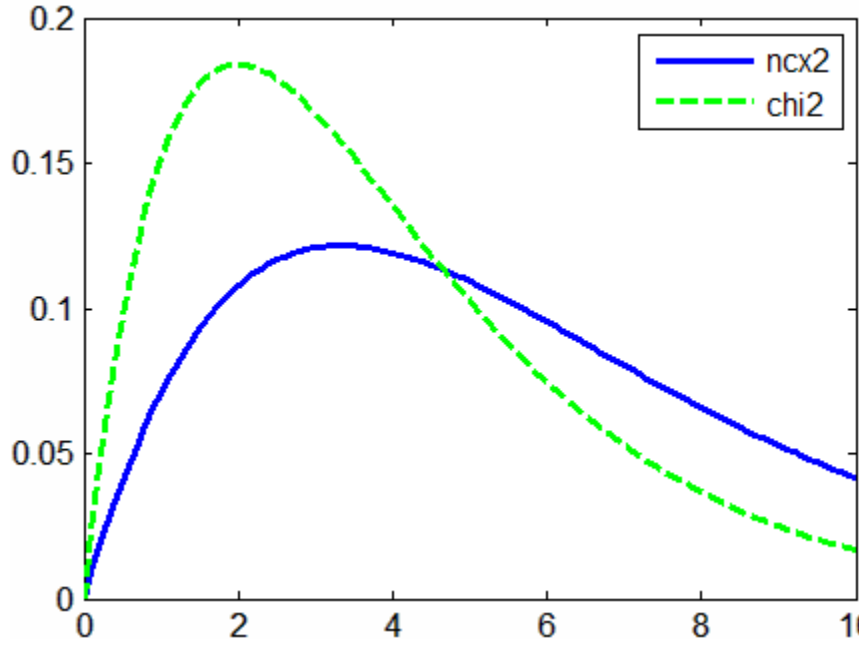
`Y = ncx2pdf(X,V,DELTA)` computes the noncentral chi-square pdf at each of the values in `X` using the corresponding degrees of freedom in `V` and positive noncentrality parameters in `DELTA`. Vector or matrix inputs for `X`, `V`, and `DELTA` must have the same size, which is also the size of `Y`. A scalar input for `X`, `V`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

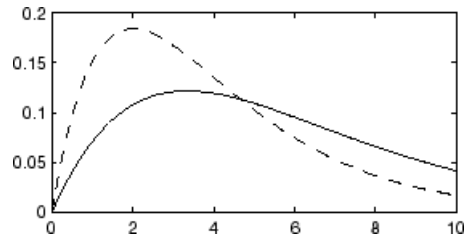
Some texts refer to this distribution as the generalized Rayleigh, Rayleigh-Rice, or Rice distribution.

Examples

Compare the noncentral chi-square pdf with `DELTA = 2` to the chi-square pdf with the same number of degrees of freedom (4):

```
x = (0:0.1:10)';
ncx2 = ncx2pdf(x,4,2);
chi2 = chi2pdf(x,4);

plot(x,ncx2,'b-','LineWidth',2)
hold on
plot(x,chi2,'g--','LineWidth',2)
legend('ncx2','chi2')
```





References

[1] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2.* Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 130–148.

See Also

`pdf` | `ncx2cdf` | `ncx2inv` | `ncx2stat` | `ncx2rnd`

How To

- “Noncentral Chi-Square Distribution” on page B-76

Purpose

Noncentral chi-square random numbers

Syntax

```
R = ncx2rnd(V,DELTA)
R = ncx2rnd(V,DELTA,m,n,...)
R = ncx2rnd(V,DELTA,[m,n,...])
```

Description

`R = ncx2rnd(V,DELTA)` returns a matrix of random numbers chosen from the noncentral chi-square distribution using the corresponding degrees of freedom in `V` and positive noncentrality parameters in `DELTA`. `V` and `DELTA` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `V` or `DELTA` is expanded to a constant array with the same dimensions as the other input.

`R = ncx2rnd(V,DELTA,m,n,...)` or `R = ncx2rnd(V,DELTA,[m,n,...])` generates an `m`-by-`n`-by-... array. The `V`, `DELTA` parameters can each be scalars or arrays of the same size as `R`.

Examples

```
ncx2rnd(4,2,6,3)
ans =
  6.8552  5.9650  11.2961
  5.2631  4.2640  5.9495
  9.1939  6.7162  3.8315
 10.3100  4.4828  7.1653
  2.1142  1.9826  4.6400
  3.8852  5.3999  0.9282
```

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 50–52.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 130–148.

See Also

`random` | `ncx2pdf` | `ncx2cdf` | `ncx2inv` | `ncx2stat`

How To

- "Noncentral Chi-Square Distribution" on page B-76

ncx2stat

Purpose

Noncentral chi-square mean and variance

Syntax

```
[M,V] = ncx2stat(NU,DELTA)
```

Description

`[M,V] = ncx2stat(NU,DELTA)` returns the mean of and variance for the noncentral chi-square pdf with `NU` degrees of freedom and noncentrality parameter `DELTA`. `NU` and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `NU` or `DELTA` is expanded to a constant array with the same dimensions as the other input.

The mean of the noncentral chi-square distribution with parameters `v` and δ is $v+\delta$, and the variance is $2(v+2\delta)$.

Examples

```
[m,v] = ncx2stat(4,2)
m =
   6
v =
  16
```

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 50–52.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 130–148.

See Also

`ncx2pdf` | `ncx2cdf` | `ncx2inv` | `ncx2rnd`

How To

- "Noncentral Chi-Square Distribution" on page B-76

Purpose

Number of dimensions of categorical array

Syntax

```
n = ndims(A)
```

Description

`n = ndims(A)` returns the number of dimensions in the categorical array `A`. The number of dimensions in an array is always greater than or equal to 2. Trailing singleton dimensions are ignored. Put simply, `ndims(A)` is `length(size(A))`.

See Also

`size`

gmdistribution.NDimensions property

Purpose

Dimension d of multivariate Gaussian distributions

Description

The dimension d of the multivariate Gaussian distributions.

Purpose

Number of dimensions of dataset array

Syntax

```
n = ndims(A)
```

Description

`n = ndims(A)` returns the number of dimensions in the dataset `A`. The number of dimensions in an array is always 2.

See Also

`size`

qrandset.ndims

Purpose

Number of dimensions in matrix

Syntax

```
n = ndims(p)
```

Description

`n = ndims(p)` returns the number of dimensions in the matrix that is created by the syntax `p(:,:)`. Since this is always a 2-D matrix, `n` is always equal to 2.

See Also

`qrandset | size`

Purpose

Number of dimensions

Description

The `NDims` property specifies the number of dimensions, which is equal to the number of features in the training data used to create the Naive Bayes classifier.

qrandstream.ne

Purpose

Not equal relation for handles

Syntax

```
h1 ~= h2
```

Description

Handles are equal if they are handles for the same object and are unequal otherwise.

`h1 ~= h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise ~= result.

If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = ne(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream | eq | ge | gt | le | lt`

Purpose

Nearest neighbor search object

Description

`NeighborSearcher` is an abstract class used for nearest neighbor search. You cannot create instances of this class directly. Instead, create an instance of a derived class such as `ExhaustiveSearcher` or `KDTreeSearcher` either by calling the derived class constructor or by calling the function `createns`.

Construction

`NeighborSearcher` is an abstract class. You cannot create instances of this class directly. You can construct an object in a subclass, such as `KDTreeSearcher` or `ExhaustiveSearcher`, either by calling the subclass constructors or by using the `createns` function.

Properties

`X`

A matrix used to create the object.

`Distance`

A string specifying a built-in distance metric (applies to both `ExhaustiveSearcher` and `KDTreeSearcher`) or a function handle (only applies to `ExhaustiveSearcher`) that you provide when you create the object. This property is the default distance metric used when you call the `knnsearch` method to find nearest neighbors for future query points.

`DistParameter`

Specifies the additional parameter for the chosen distance metric. The value is:

- If `'Distance'` is `'minkowski'`: A positive scalar indicating the exponent of the Minkowski distance. (Applies for both `ExhaustiveSearcher` and `KDTreeSearcher`.)
- If `'Distance'` is `'mahalanobis'`: A positive definite matrix representing the covariance matrix used for computing the Mahalanobis distance. (Only applies for `ExhaustiveSearcher`.)

- If `'Distance'` is `'seuclidean'`: A vector representing the scale value of the data when computing the `'seuclidean'` distance. (Only applies for `ExhaustiveSearcher`.)
- Otherwise: Empty.

See Also

`createns` | `KDTreeSearcher` | `ExhaustiveSearcher`

Purpose

Generate quasi-random point set

Syntax

```
X = net(p,n)
```

Description

`X = net(p,n)` returns the first `n` points `X` from the point set `p` of the `qrandset` class. `X` is `n`-by-d, where d is the dimension of the point set.

Objects `p` of the `@qrandset` class encapsulate properties of a specified quasi-random sequence. Values of the point set are not generated and stored in memory until `p` is accessed using `net` or parenthesis indexing.

Examples

Use `haltonset` to generate a 3-D Halton point set, skip the first 1000 values, and then retain every 101st point:

```
p = haltonset(3,'Skip',1e3,'Leap',1e2)
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none
```

Use `scramble` to apply reverse-radix scrambling:

```
p = scramble(p,'RR2')
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : RR2
```

Use `net` to generate the first four points:

```
X0 = net(p,4)
X0 =
    0.0928    0.6950    0.0029
    0.6958    0.2958    0.8269
```

```
    0.3013    0.6497    0.4141
    0.9087    0.7883    0.2166
```

Use parenthesis indexing to generate every third point, up to the 11th point:

```
X = p(1:3:11,:)
X =
    0.0928    0.6950    0.0029
    0.9087    0.7883    0.2166
    0.3843    0.9840    0.9878
    0.6831    0.7357    0.7923
```

See Also

`haltonset` | `sobolset` | `qrandstream`

Purpose

Nonlinear regression

Syntax

```
beta = nlinfit(X,y,fun,beta0)
[beta,r] = nlinfit(X,y,fun,beta0)
[beta,r,J] = nlinfit(X,y,fun,beta0)
[beta,r,J,COVB] = nlinfit(X,y,fun,beta0)
[beta,r,J,COVB,mse] = nlinfit(X,y,fun,beta0)
[beta,...] = nlinfit(X,y,fun,beta0,options)
```

Description

`beta = nlinfit(X,y,fun,beta0)` returns a vector `beta` of coefficient estimates for a nonlinear regression of the responses in `y` on the predictors in `X` using the model specified by `fun`.

`[beta,r] = nlinfit(X,y,fun,beta0)` returns the residuals of the fit.

`[beta,r,J] = nlinfit(X,y,fun,beta0)` returns the Jacobian of `fun`.

`[beta,r,J,COVB] = nlinfit(X,y,fun,beta0)` returns an estimated covariance matrix of the fitted coefficients.

`[beta,r,J,COVB,mse] = nlinfit(X,y,fun,beta0)` returns an estimated variance of the error term.

`[beta,...] = nlinfit(X,y,fun,beta0,options)` specifies control parameters for the `nlinfit` algorithm.

Tips

- To produce error estimates on predictions, use `nlpredci` with its optional outputs `r`, `J`, `COVB`, or `mse`.
- To produce error estimates on the estimated coefficients `beta`, use `nlparci` with its optional outputs `r`, `J`, `COVB`, or `mse`.
- If you use the robust fitting option (see `options` in "Input Arguments" on page 20-1180), you must use `COVB` and may need `mse` as input to `nlpredci` or `nlparci` to ensure that the confidence intervals take the robust fit properly into account.

Input Arguments

`X`

Typically, `X` is a design matrix of predictor (independent variable) values, with one row for each value in `Y` and one column for each coefficient. However, `X` can be any array that `fun` accepts.

`y`

Vector of response (dependent variable) values.

`nlinfit` treats `NaN`s in `y` as missing data and ignores the corresponding rows.

`fun`

Function specified using `@` that accepts two arguments:

- A coefficient vector, say `b`
- The array `X`

For example, `fun = @modelfun`, where `modelfun.m` is a file such as:

```
function yhat = modelfun(b,X)
...
```

`fun(b,X)` returns a vector of fitted response values, matching `Y` as closely as possible in the least-squares sense.

`nlinfit` treats `NaN`s in `fun(b,X)` as missing data and ignores the corresponding rows.

`beta0`

Vector containing initial coefficient values. The number of elements in `beta0` equals the number of elements in the `beta` output. A poor value of `beta0` can lead to a poor solution `beta`, meaning one with large residual error.

`options`

Structure you can create using `statset`. Applicable `statset` parameters:

- `'DerivStep'` — Relative difference used in finite difference gradient calculation. May be a scalar, or a vector the same size as `beta0`. The default is `eps^(1/3)`.
- `'Display'` — Level of display output during estimation. The choices are
  - `'off'` (default) — Displays no information
  - `'final'` — Displays information after the final iteration
  - `'iter'` — Displays information at each iteration
- `'FunValCheck'` — Check for invalid values, such as `NaN` or `Inf`, from the objective function. Values are `'off'` or `'on'` (the default).
- `'MaxIter'` — Maximum number of iterations allowed. The default is `100`.
- `'Robust'` — Invoke robust fitting option. Values are `'off'` (the default) or `'on'`.
- `'TolFun'` — Termination tolerance on the residual sum of squares. The default is `1e-8`.
- `'TolX'` — Termination tolerance on the estimated coefficients `beta`. The default is `1e-8`.
- `'Tune'` — The tuning constant used in robust fitting to normalize the residuals before applying the weight function. The value is a positive scalar, with the default value dependent on the weight function. This parameter is required if the weight function is specified as a function handle.
- `'WgtFun'` — A weight function for robust fitting. Valid only when `'Robust'` is `'on'`. It can be `'bisquare'` (the default), `'andrews'`, `'cauchy'`, `'fair'`, `'huber'`, `'logistic'`, `'talwar'`, or `'welsch'`. It can also be a function handle that

accepts a normalized residual as input and returns the robust weights as output.

Output Arguments

`beta`

Vector of coefficients. `beta` minimizes the sum of the squares of `y - fun(beta,X)`.

`r`

Residual vector `y - fun(beta,X)`.

`J`

Estimated Jacobian of `fun` with respect to `beta`.

`COVB`

Estimated covariance matrix of the coefficients `beta`.

`mse`

Mean squared error `norm(r)^2/(n-p)`, where `n` is the number of elements in `r`, and `p` is the number of parameters (the length of `beta`).

Examples

Suppose you have data, and want to fit a model of the form

$$y_i = a_1 + a_2\exp(-a_3 x_i) + \varepsilon_i.$$

Here the a_i are the parameters you want to estimate, x_i are the data points, the y_i are the responses, and the ε_i are noise terms.

1. Write a function handle that represents the model:

```
mdl = @(a,x)(a(1) + a(2)*exp(-a(3)*x));
```

2. Generate synthetic data with parameters `a = [1;3;2]`, with the `x` data points distributed exponentially with parameter `2`, and normally distributed noise with standard deviation `0.1`:

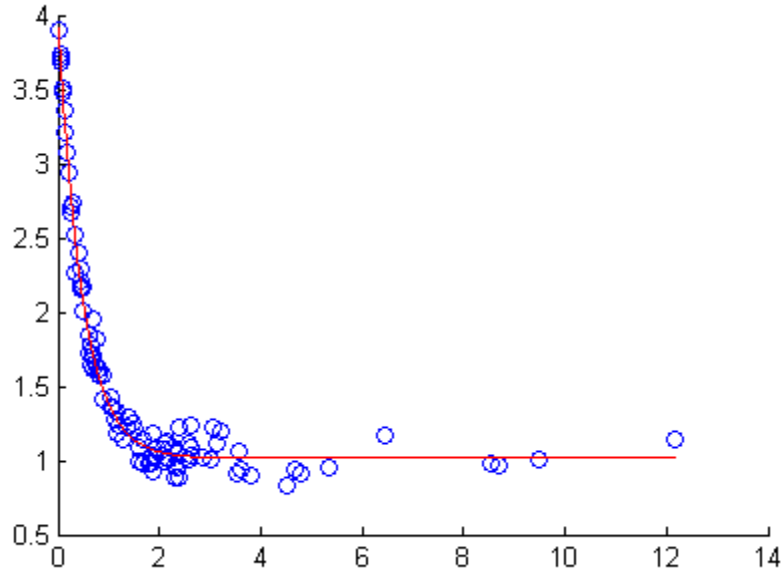
```
rng(9845,'twister') % for reproducibility
a = [1;3;2];
x = exprnd(2,100,1);
epsn = normrnd(0,0.1,100,1);
y = mdl(a,x) + epsn;
```

3 Fit the model to data starting from the arbitrary guess `a0 = [2;2;2]`:

```
a0 = [2;2;2];
[ahat,r,J,cov,mse] = nlinfit(x,y,mdl,a0);
ahat

ahat =
    1.0153
    3.0229
    2.1070
```

4 Examine the fit:

```
xrange = min(x):.01:max(x);
hold on
scatter(x,y)
plot(xrange,mdl(ahat,xrange),'r')
hold off
```



5 Check whether `[1;3;2]` is in a 95% confidence interval using `nlparci`:

```
ci = nlparci(ahat,r,'Jacobian',J)

ci =
    0.9869    1.0438
    2.9401    3.1058
    1.9963    2.2177
```

Algorithms

`nlinfit` uses the Levenberg-Marquardt algorithm [1] for nonlinear least squares to compute non-robust fits.

For robust fits, `nlinfit` uses an algorithm [2] that iteratively refits a weighted nonlinear regression, where the weights at each iteration are based on each observation's residual from the previous iteration. These weights serve to downweight points that are outliers so that their

influence on the fit is decreased. Iterations continue until the weights converge. The computation of weights is identical to the iterative reweighting scheme used by `robustfit` for fitting a robust linear model, and in particular, the possible weighting functions and their tuning parameters are the same. The nonlinear regression at each iteration is a weighted version of the Levenberg-Marquardt algorithm that `nlinfit` uses for non-robust fits.

References

[1] Seber, G. A. F., and C. J. Wild. *Nonlinear Regression*. Hoboken, NJ: Wiley-Interscience, 2003.

[2] DuMouchel, W. H., and F. L. O'Brien. "Integrating a Robust Option into a Multiple Regression Computing Environment." *Computer Science and Statistics: Proceedings of the 21st Symposium on the Interface*. Alexandria, VA: American Statistical Association, 1989.

[3] Holland, P. W., and R. E. Welsch. "Robust Regression Using Iteratively Reweighted Least-Squares." *Communications in Statistics: Theory and Methods*, *A6*, 1977, pp. 813–827.

Alternatives

`nlintool` is a graphical user interface to `nlinfit`.

See Also

`nlparci` | `nlpredci` | `nlintool`

Tutorials

- "Nonlinear Regression" on page 9-72

nlintool

Purpose

Interactive nonlinear regression

Syntax

```
nlintool(X,y,fun,beta0)
nlintool(X,y,fun,beta0,alpha)
nlintool(X,y,fun,beta0,alpha,'xname','yname')
```

Description

`nlintool(X,y,fun,beta0)` is a graphical user interface to the `nlinfit` function, and uses the same input arguments. The interface displays plots of the fitted response against each predictor, with the other predictors held fixed. The fixed values are in the text boxes below each predictor axis. Change the fixed values by typing in a new value or by dragging the vertical lines in the plots to new positions. When you change the value of a predictor, all plots update to display the model at the new point in predictor space. Dashed red curves show 95% simultaneous confidence bands for the function.

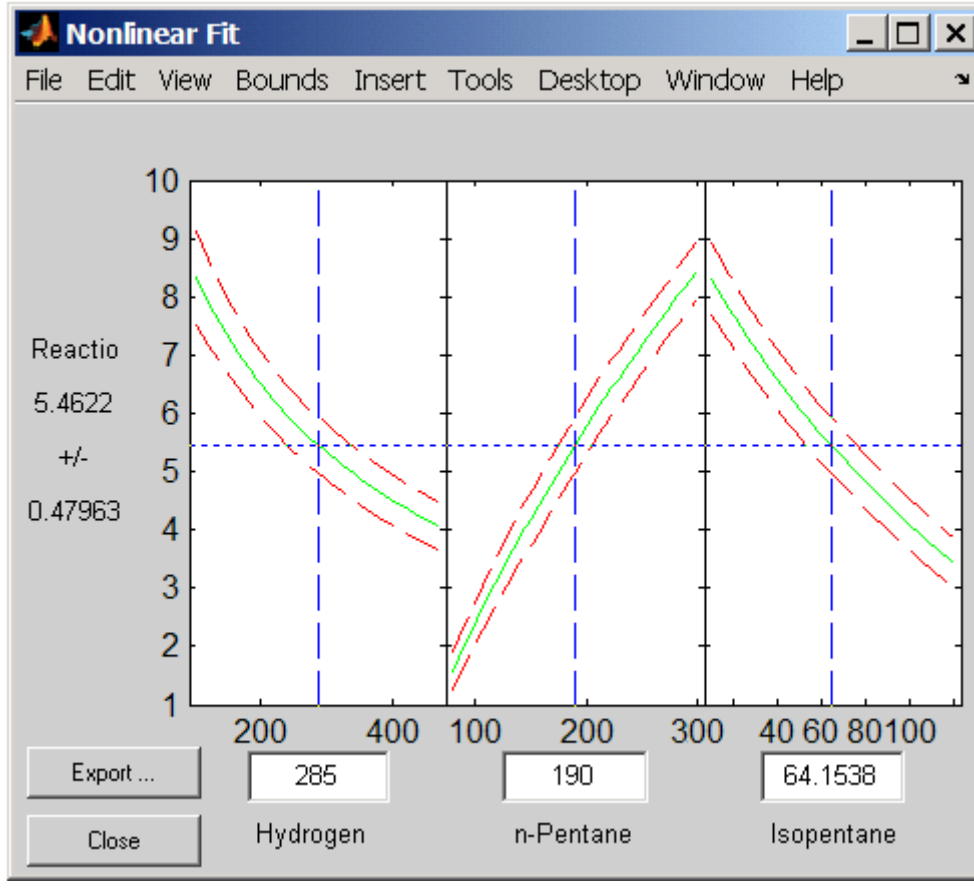
`nlintool(X,y,fun,beta0,alpha)` shows `100(1-alpha)`% confidence bands. These are simultaneous confidence bounds for the function value. Using the **Bounds** menu you can switch between simultaneous and non-simultaneous bounds, and between bounds on the function and bounds for predicting a new observation.

`nlintool(X,y,fun,beta0,alpha,'xname','yname')` labels the plots using the string matrix `'xname'` for the predictors and the string `'yname'` for the response.

Examples

The data in `reaction.mat` are partial pressures of three chemical reactants and the corresponding reaction rates. The function `hougen` implements the nonlinear Hougen-Watson model for reaction rates. The following fits the model to the data:

```
load reaction
nlintool(reactants,rate,@hougen,beta,0.01,xn,yn)
```



See Also

`nlinfit` | `polytool` | `rstool`

nlmefit

Purpose

Nonlinear mixed-effects estimation

Syntax

```
beta = nlmefit(X,y,group,V,fun,beta0)
[beta,PSI] = nlmefit(X,y,group,V,fun,beta0)
[beta,PSI,stats] = nlmefit(X,y,group,V,fun,beta0)
[beta,PSI,stats,B] = nlmefit(X,y,group,V,fun,beta0)
[beta,PSI,stats,B] = nlmefit(X,y,group,V,fun,beta0,'Name',
   value)
```

Description

`beta = nlmefit(X,y,group,V,fun,beta0)` fits a nonlinear mixed-effects regression model and returns estimates of the fixed effects in `beta`. By default, `nlmefit` fits a model in which each parameter is the sum of a fixed and a random effect, and the random effects are uncorrelated (their covariance matrix is diagonal).

`X` is an n-by-h matrix of n observations on h predictors.

`y` is an n-by-1 vector of responses.

`group` is a grouping variable indicating m groups in the observations. `group` is a categorical variable, a numeric vector, a character matrix with rows for group names, or a cell array of strings. For more information on grouping variables, see "Grouped Data" on page 2-34.

`V` is an m-by-g matrix or cell array of g group-specific predictors. These are predictors that take the same value for all observations in a group. The rows of `V` are assigned to groups using `grp2idx`, according to the order specified by `grp2idx(group)`. Use a cell array for `V` if group predictors vary in size across groups. Use `[]` for `V` if there are no group-specific predictors.

`fun` is a handle to a function that accepts predictor values and model parameters and returns fitted values. `fun` has the form

```
yfit = modelfun(PHI,XFUN,VFUN)
```

The arguments are:

- `PHI` — A 1-by-p vector of model parameters.

- `XFUN` — A k-by-h array of predictors, where:
  - k = 1 if `XFUN` is a single row of `X`.
  - $k = n_i$ if `XFUN` contains the rows of `X` for a single group of size n_i.
  - $k = n$ if `XFUN` contains all rows of `X`.
- `VFUN` — Group-specific predictors given by one of:
  - A 1-by-g vector corresponding to a single group and a single row of `V`.
  - An n-by-g array, where the jth row is V(`I`,:) if the jth observation is in group `I`.

  If `V` is empty, `nlmefit` calls `modelfun` with only two inputs.
- `yfit` — A k-by-1 vector of fitted values

When either `PHI` or `VFUN` contains a single row, it corresponds to all rows in the other two input arguments.

Note If `modelfun` can compute `yfit` for more than one vector of model parameters per call, use the `'Vectorization'` parameter (described later) for improved performance.

`beta0` is a q-by-1 vector with initial estimates for q fixed effects. By default, q is the number of model parameters p.

`nlmefit` fits the model by maximizing an approximation to the marginal likelihood with random effects integrated out, assuming that:

- Random effects are multivariate normally distributed and independent between groups.
- Observation errors are independent, identically normally distributed, and independent of the random effects.

`[beta,PSI] = nlmefit(X,y,group,V,fun,beta0)` also returns `PSI`, an *r*-by-*r* estimated covariance matrix for the random effects. By default, *r* is equal to the number of model parameters *p*.

`[beta,PSI,stats] = nlmefit(X,y,group,V,fun,beta0)` also returns `stats`, a structure with fields:

- `dfe` — The error degrees of freedom for the model
- `logl` — The maximized log-likelihood for the fitted model
- `rmse` — The square root of the estimated error variance (computed on the log scale for the `exponential` error model)
- `errorparam` — The estimated parameters of the error variance model
- `aic` — The Akaike information criterion, calculated as `aic` = `-2 * logl + 2 * numParam`, where `numParam` is the number of fitting parameters, including the degree of freedom for covariance matrix of the random effects, the number of fixed effects and the number of parameters of the error model, and `logl` is a field in the `stats` structure
- `bic` — The Bayesian information criterion, calculated as `bic` = `–2*logl + log(M) * numParam`
  - `M` is the number of groups.
  - `numParam` and `logl` are defined as in `aic`.

  Note that some literature suggests that the computation of `bic` should be , `bic` = `–2*logl + log(N) * numParam`, where `N` is the number of observations.
- `covb` — The estimated covariance matrix of the parameter estimates
- `sebeta` — The standard errors for `beta`
- `ires` — The population residuals `(y-y_population)`, where `y_population` is the individual predicted values
- `pres` — The population residuals `(y-y_population)`, where `y_population` is the population predicted values
- `iwres` — The individual weighted residuals

- `pwres` — The population weighted residuals
- `cwres` — The conditional weighted residuals

`[beta,PSI,stats,B] = nlmefit(X,y,group,V,fun,beta0)` also returns `B`, an *r*-by-*m* matrix of estimated random effects for the *m* groups. By default, *r* is equal to the number of model parameters *p*.

`[beta,PSI,stats,B] = nlmefit(X,y,group,V,fun,beta0,'Name',value)` specifies one or more optional parameter name/value pairs. Specify *`Name`* inside single quotes.

Use the following parameters to fit a model different from the default. (The default model is obtained by setting both `FEConstDesign` and `REConstDesign` to `eye(p)`, or by setting both `FEParamsSelect` and `REParamsSelect` to `1:p`.) Use at most one parameter with an `'FE'` prefix and one parameter with an `'RE'` prefix. The `nlmefit` function requires you to specify at least one fixed effect and one random effect.

Parameter	Value
`FEParamsSelect`	A vector specifying which elements of the parameter vector `PHI` include a fixed effect, given as a numeric vector of indices from `1` to `p` or as a 1-by-*p* logical vector. If *q* is the specified number of elements, then the model includes *q* fixed effects.
`FEConstDesign`	A *p*-by-*q* design matrix `ADESIGN`, where `ADESIGN*beta` are the fixed components of the *p* elements of `PHI`.
`FEGroupDesign`	A *p*-by-*q*-by-*m* array specifying a different *p*-by-*q* fixed-effects design matrix for each of the *m* groups.
`FEObsDesign`	A *p*-by-*q*-by-*n* array specifying a different *p*-by-*q* fixed-effects design matrix for each of the *n* observations.

Parameter	Value
`REParamsSelect`	A vector specifying which elements of the parameter vector `PHI` include a random effect, given as a numeric vector of indices from `1` to `p` or as a 1-by-*p* logical vector. The model includes *r* random effects, where *r* is the specified number of elements.
`REConstDesign`	A *p*-by-*r* design matrix `BDESIGN`, where `BDESIGN*B` are the random components of the *p* elements of `PHI`.
`REGroupDesign`	A *p*-by-*r*-by-*m* array specifying a different *p*-by-*r* random-effects design matrix for each of *m* groups.
`REObsDesign`	A *p*-by-*r*-by-*n* array specifying a different *p*-by-*r* random-effects design matrix for each of *n* observations.

Use the following parameters to control the iterative algorithm for maximizing the likelihood:

Parameter	Value
`RefineBeta0`	Determines whether `nlmefit` makes an initial refinement of `beta0` by first fitting `modelfun` without random effects and replacing `beta0` with `beta`. Choices are `'on'` and `'off'`. The default value is `'on'`.
`ErrorModel`	A string specifying the form of the error term. Default is `'constant'`. Each model defines the error using a standard normal (Gaussian) variable *e*, the function value *f*, and one or two parameters *a* and *b*. Choices are: • `'constant'`: $y = f + a*e$

Parameter	Value
	• `'proportional'`: $y = f + b*f*e$ • `'combined'`: $y = f + (a+b*f)*e$ • `'exponential'`: $y = f*\exp(a*e)$, or equivalently $\log(y) = \log(f) + a*e$ If this parameter is given, the output `stats.errorparam` field has the value • a for `'constant'` and `'exponential'` • b for `'proportional'` • [a b] for `'combined'`
`ApproximationType`	The method used to approximate the likelihood of the model. Choices are: • `'LME'` — Use the likelihood for the linear mixed-effects model at the current conditional estimates of `beta` and `B`. This is the default. • `'RELME'` — Use the restricted likelihood for the linear mixed-effects model at the current conditional estimates of `beta` and `B`. • `'FO'` — First-order Laplacian approximation without random effects. • `'FOCE'` — First-order Laplacian approximation at the conditional estimates of `B`.

Parameter	Value
`Vectorization`	Indicates acceptable sizes for the `PHI`, `XFUN`, and `VFUN` input arguments to `modelfun`. Choices are: • `'SinglePhi'` — `modelfun` can only accept a single set of model parameters at a time, so `PHI` must be a single row vector in each call. `nlmefit` calls `modelfun` in a loop, if necessary, with a single `PHI` vector and with `XFUN` containing rows for a single observation or group at a time. `VFUN` may be a single row that applies to all rows of `XFUN`, or a matrix with rows corresponding to rows in `XFUN`. This is the default. • `'SingleGroup'` — `modelfun` can only accept inputs corresponding to a single group in the data, so `XFUN` must contain rows of `X` from a single group in each call. Depending on the model, `PHI` is a single row that applies to the entire group or a matrix with one row for each observation. `VFUN` is a single row. • `'Full'` — `modelfun` can accept inputs for multiple parameter vectors and multiple groups in the data. Either `PHI` or `VFUN` may be a single row that applies to all rows of `XFUN` or a matrix with rows corresponding to rows in `XFUN`. This option can improve performance by reducing the number of calls to `modelfun`, but may require `modelfun` to perform singleton expansion on `PHI` or `V`.

Parameter	Value
`CovParameterization`	Specifies the parameterization used internally for the scaled covariance matrix. Choices are `'chol'` for the Cholesky factorization or `'logm'` the matrix logarithm. The default is `'logm'`.
`CovPattern`	Specifies an *r*-by-*r* logical or numeric matrix `P` that defines the pattern of the random-effects covariance matrix `PSI`. `nlmefit` estimates the variances along the diagonal of `PSI` and the covariances specified by nonzeroes in the off-diagonal elements of `P`. Covariances corresponding to zero off-diagonal elements in `P` are constrained to be zero. If `P` does not specify a row-column permutation of a block diagonal matrix, `nlmefit` adds nonzero elements to `P` as needed. The default value of `P` is `eye(r)`, corresponding to uncorrelated random effects. Alternatively, `P` may be a 1-by-*r* vector containing values in `1:r`, with equal values specifying groups of random effects. In this case, `nlmefit` estimates covariances only within groups, and constrains covariances across groups to be zero.

Parameter	Value
ParamTransform	A vector of P values specifying a transformation function *f*() for each of the P parameters: XB = ADESIGN*BETA + BDESIGN*B PHI = *f*(XB)Each element of the vector must be one of the following integer codes specifying the transformation for the corresponding value of PHI: • 0: PHI = XB (default for all parameters) • 1: log(PHI) = XB • 2: probit(PHI) = XB • 3: logit(PHI) = XB

Options	A structure of the form returned by statset. nlmefit uses the following statset parameters:
	• 'DerivStep' — Relative difference used in finite difference gradient calculation. May be a scalar, or a vector whose length is the number of model parameters *p*. The default is eps^(1/3).
	• 'Display' — Level of iterative display during estimation. Choices are:
	  - 'off' (default) — Displays no information
	  - 'final' — Displays information after the final iteration
	  - 'iter' — Displays information at each iteration
	• 'FunValCheck' — Check for invalid values, such as NaN or Inf, from

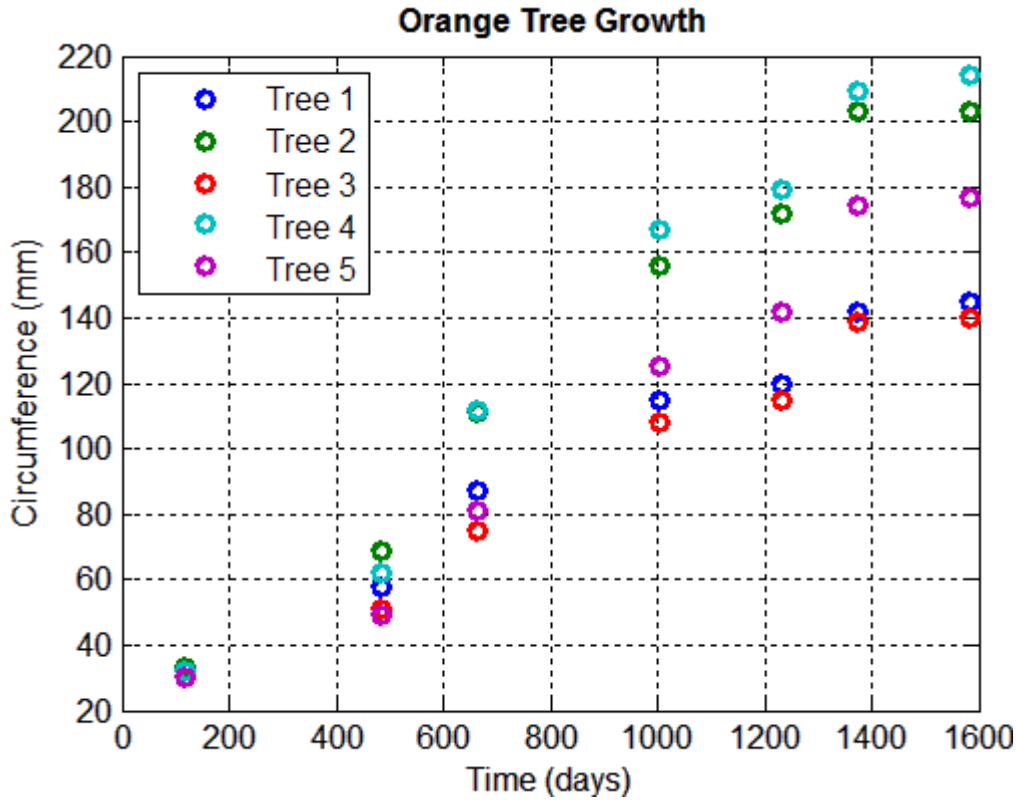
Parameter	Value
	`modelfun`. Choices are `'on'` and `'off'`. The default is `'on'`. • `'MaxIter'` — Maximum number of iterations allowed. The default is `200`. • `'OutputFcn'` — Function handle specified using @, a cell array with function handles or an empty array (default). The solver calls all output functions after each iteration. • `'TolFun'` — Termination tolerance on the log-likelihood function. The default is `1e-4`. • `'TolX'` — Termination tolerance on the estimated fixed and random effects. The default is `1e-4`.
`OptimFun`	Specifies the optimization function used in maximizing the likelihood. Choices are `'fminsearch'` to use `fminsearch` or `'fminunc'` to use `fminunc`. The default is `'fminsearch'`. You can specify `'fminunc'` only if Optimization Toolbox software is installed.

Examples

Display data on the growth of five orange trees:

```
CIRC = [30 58 87 115 120 142 145;
        33 69 111 156 172 203 203;
        30 51 75 108 115 139 140;
        32 62 112 167 179 209 214;
        30 49 81 125 142 174 177];
time = [118 484 664 1004 1231 1372 1582];

h = plot(time,CIRC','o','LineWidth',2);
```

```
xlabel('Time (days)')
ylabel('Circumference (mm)')
title('{\bf Orange Tree Growth}')
legend([repmat('Tree ',5,1),num2str((1:5)')],...
       'Location','NW')
grid on
hold on
```



Use an anonymous function to specify a logistic growth model:

```
model=@(PHI,t)(PHI(:,1))./(1+exp(-(t-PHI(:,2))./PHI(:,3)));
```

Fit the model using `nlmefit` with default settings (that is, assuming each parameter is the sum of a fixed and a random effect, with no correlation among the random effects):

```
TIME = repmat(time,5,1);
NUMS = repmat((1:5)',size(time));

beta0 = [100 100 100];
[beta1,PSI1,stats1] = nlmefit(TIME(:),CIRC(:),NUMS(:),...
                              [],model,beta0)
beta1 =
  191.3189
  723.7608
  346.2517

PSI1 =
  962.1534         0         0
         0    0.0000         0
         0         0  297.9881

stats1 =
           dfe: 28
          logl: -131.5457
           mse: 59.7882
          rmse: 7.9016
    errorparam: 7.7323
           aic: 277.0913
           bic: 274.3574
          covb: [3x3 double]
        sebeta: [15.2249 33.1579 26.8235]
          ires: [35x1 double]
          pres: [35x1 double]
         iwres: [35x1 double]
         pwres: [35x1 double]
         cwres: [35x1 double]
```

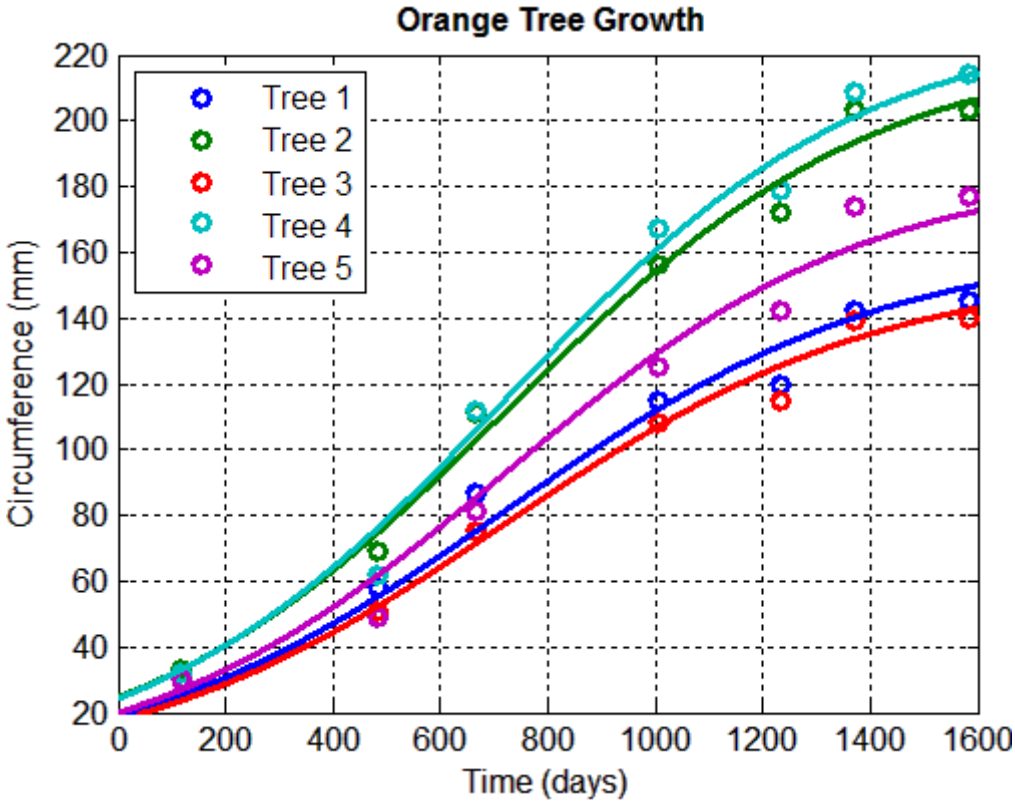
The negligible variance of the second random effect, `PSI1(2,2)`, suggests that it can be removed to simplify the model:

```
[beta2,PSI2,stats2,b2] = nlmefit(TIME(:),CIRC(:),...
    NUMS(:),[],model,beta0,'REParamsSelect',[1 3])

beta2 =
  191.3194
  723.7628
  346.2548

PSI2 =
  962.2114         0
         0  298.3989

stats2 =
           dfe: 29
          logl: -131.5456
           mse: 59.7851
          rmse: 7.7640
    errorparam: 7.7321
           aic: 275.0913
           bic: 272.7479
          covb: [3x3 double]
        sebeta: [15.2252 33.1572 26.8246]
          ires: [35x1 double]
          pres: [35x1 double]
         iwres: [35x1 double]
         pwres: [35x1 double]
         cwres: [35x1 double]

b2 =
  -28.5250   31.6063  -36.5070   39.0735   -5.6479
   10.0097   -0.7638    6.0117   -9.4685   -5.7892
```

The log-likelihood `logl` is unaffected, and both the Akaike and Bayesian information criteria (`aic` and `bic`) are reduced, supporting the decision to drop the second random effect from the model.

Use the estimated fixed effects in `beta2` and the estimated random effects for each tree in `b2` to plot the model through the data:

```
PHI = repmat(beta2,1,5) + ...          % Fixed effects
      [b2(1,:);zeros(1,5);b2(2,:)];    % Random effects

colors = get(h,'Color');
tplot = 0:0.1:1600;
for I = 1:5
  fitted_model=@(t)(PHI(1,I))./(1+exp(-(t-PHI(2,I))./ ...
PHI(3,I)));
  plot(tplot,fitted_model(tplot),'Color',colors{I}, ...
   'LineWidth',2)
end
```



References

[1] Lindstrom, M. J., and D. M. Bates. "Nonlinear mixed-effects models for repeated measures data." *Biometrics*. Vol. 46, 1990, pp. 673–687.

[2] Davidian, M., and D. M. Giltinan. *Nonlinear Models for Repeated Measurements Data*. New York: Chapman & Hall, 1995.

[3] Pinheiro, J. C., and D. M. Bates. "Approximations to the log-likelihood function in the nonlinear mixed-effects model." *Journal of Computational and Graphical Statistics*. Vol. 4, 1995, pp. 12–35.

[4] Demidenko, E. *Mixed Models: Theory and Applications.* Hoboken, NJ: John Wiley & Sons, Inc., 2004.

See Also

`nlinfit` | `nlpredci` | `nlmefitsa`

How To

- "Grouped Data" on page 2-34

nlmefitsa

Purpose

Fit nonlinear mixed effects model with stochastic EM algorithm

Syntax

```
[BETA,PSI,STATS,B] = nlmefitsa(X,Y,GROUP,V,MODELFUN,BETA0)
[BETA,PSI,STATS,B] = nlmefitsa(X,Y,GROUP,V,MODELFUN,BETA0,
   'Name',Value)
```

Description

`[BETA,PSI,STATS,B] = nlmefitsa(X,Y,GROUP,V,MODELFUN,BETA0)` fits a nonlinear mixed-effects regression model and returns estimates of the fixed effects in `BETA`. By default, `nlmefitsa` fits a model where each model parameter is the sum of a corresponding fixed and random effect, and the covariance matrix of the random effects is diagonal, i.e., uncorrelated random effects.

The `BETA`, `PSI`, and other values this function returns are the result of a random (Monte Carlo) simulation designed to converge to the maximum likelihood estimates of the parameters. Because the results are random, it is advisable to examine the plot of simulation to results to be sure that the simulation has converged. It may also be helpful to run the function multiple times, using multiple starting values, or use the `'Replicates'` parameter to perform multiple simulations.

`[BETA,PSI,STATS,B] = nlmefitsa(X,Y,GROUP,V,MODELFUN,BETA0,'Name',Value)` accepts one or more comma-separated parameter name/value pairs. Specify *`Name`* inside single quotes.

Input Arguments

Definitions:

In the following list of arguments, the following variable definitions apply:

- n — number of observations
- h — number of predictor variables
- m — number of groups
- g — number of group-specific predictor variables
- p — number of parameters

- f — number of fixed effects

`X`

An n-by-h matrix of n observations on h predictor variables.

`Y`

An n-by-1 vector of responses.

`GROUP`

A grouping variable indicating to which of m groups each observation belongs. `GROUP` can be a categorical variable, a numeric vector, a character matrix with rows for group names, or a cell array of strings.

`V`

An m-by-g matrix of g group-specific predictor variables for each of the m groups in the data. These are predictor values that take on the same value for all observations in a group. Rows of `V` are ordered according to `GRP2IDX(GROUP)`. Use an m-by-g cell array for `V` if any of the group-specific predictor values vary in size across groups. Specify `[]` for `V` if there are no group predictors.

`MODELFUN`

A handle to a function that accepts predictor values and model parameters, and returns fitted values. `MODELFUN` has the form `YFIT = MODELFUN(PHI,XFUN,VFUN)` with input arguments

- `PHI` — A 1-by-p vector of model parameters.
- `XFUN` — An l-by-h array of predictor variables where
  - l is 1 if `XFUN` is a single row of `X`
  - l is n_i if `XFUN` contains the rows of `X` for a single group of size n_i
  - l is n if `XFUN` contains all rows of `X`.
- `VFUN` — Either

- A 1-by-*g* vector of group-specific predictors for a single group, corresponding to a single row of `V`
- An *n*-by-*g* matrix, where the *k*-th row of `VFUN` is `V`(*i*,:) if the *k*-th observation is in group *i*.

If `V` is empty, `nlmefitsa` calls `MODELFUN` with only two inputs.

`MODELFUN` returns an *l*-by-1 vector of fitted values `YFIT`. When either `PHI` or `VFUN` contains a single row, that one row corresponds to all rows in the other two input arguments. For improved performance, use the `'Vectorization'` parameter name/value pair (described below) if `MODELFUN` can compute `YFIT` for more than one vector of model parameters in one call.

`BETA0`

An *f*-by-1 vector with initial estimates for the *f* fixed effects. By default, *f* is equal to the number of model parameters *p*. `BETA0` can also be an *f*-by-`REPS` matrix, and the estimation is repeated `REPS` times using each column of `BETA0` as a set of starting values.

Name-Value Pair Arguments

By default, `nlmefitsa` fits a model where each model parameter is the sum of a corresponding fixed and random effect. Use the following parameter name/value pairs to fit a model with a different number of or dependence on fixed or random effects. Use at most one parameter name with an `'FE'` prefix and one parameter name with an `'RE'` prefix. Note that some choices change the way `nlmefitsa` calls `MODELFUN`, as described further below.

`FEParamsSelect`

A vector specifying which elements of the model parameter vector `PHI` include a fixed effect, as a numeric vector with elements in 1:*p*, or as a 1-by-*p* logical vector. The model will include *f* fixed effects, where *f* is the specified number of elements.

`FEConstDesign`

A *p*-by-*f* design matrix `ADESIGN`, where `ADESIGN*BETA` are the fixed components of the *p* elements of `PHI`.

`FEGroupDesign`

A *p*-by-*f*-by-*m* array specifying a different *p*-by-*f* fixed effects design matrix for each of the *m* groups.

`REParamsSelect`

A vector specifying which elements of the model parameter vector `PHI` include a random effect, as a numeric vector with elements in 1:*p*, or as a 1-by-*p* logical vector. The model will include *r* random effects, where *r* is the specified number of elements.

`REConstDesign`

A *p*-by-*r* design matrix `BDESIGN`, where `BDESIGN*B` are the random components of the *p* elements of `PHI`. This matrix must consist of 0s and 1s, with at most one 1 per row.

The default model is equivalent to setting both `FEConstDesign` and `REConstDesign` to `eye(p)`, or to setting both `FEParamsSelect` and `REParamsSelect` to 1:*p*.

Additional optional parameter name/value pairs control the iterative algorithm used to maximize the likelihood:

`CovPattern`

Specifies an *r*-by-*r* logical or numeric matrix `PAT` that defines the pattern of the random effects covariance matrix `PSI`. `nlmefitsa` computes estimates for the variances along the diagonal of `PSI` as well as covariances that correspond to non-zeroes in the off-diagonal of `PAT`. `nlmefitsa` constrains the remaining covariances, i.e., those corresponding to off-diagonal zeroes in `PAT`, to be zero. `PAT` must be a row-column permutation of a block diagonal matrix, and `nlmefitsa` adds non-zero elements to `PAT` as needed to produce such a pattern. The default value of `PAT` is `eye(r)`, corresponding to uncorrelated random effects.

Alternatively, specify `PAT` as a 1-by-*r* vector containing values in 1:*r*. In this case, elements of `PAT` with equal values define groups of random effects, `nlmefitsa` estimates covariances only within groups, and constrains covariances across groups to be zero.

`CovO`

Initial value for the covariance matrix `PSI`. Must be an *r*-by-*r* positive definite matrix. If empty, the default value depends on the values of `BETAO`.

`ComputeStdErrors`

`true` to compute standard errors for the coefficient estimates and store them in the output `STATS` structure, or `false` (default) to omit this computation.

`ErrorModel`

A string specifying the form of the error term. Default is `'constant'`. Each model defines the error using a standard normal (Gaussian) variable *e*, the function value *f*, and one or two parameters *a* and *b*. Choices are

- `'constant'` — $y = f + a*e$
- `'proportional'` — $y = f + b*f*e$
- `'combined'` — $y = f + (a+b*f)*e$
- `'exponential'` — $y = f*\exp(a*e)$, or equivalently $\log(y) = \log(f) + a*e$

If this parameter is given, the output `STATS.rmse` field has the value

- *a* for `'constant'` and `'exponential'`
- *b* for `'proportional'`
- [*a b*] for `'combined'`

`ErrorParameters`

A scalar or two-element vector specifying starting values for parameters of the error model. This specifies the a, b, or [a b] values depending on the `ErrorModel` parameter.

`LogLikMethod`

Specifies the method for approximating the log likelihood. Choices are:

- `'is'` — Importance sampling
- `'gq'` — Gaussian quadrature
- `'lin'` — Linearization
- `'none'` — Omit the log likelihood approximation (default)

`NBurnIn`

Number of initial burn-in iterations during which the parameter estimates are not recomputed. Default is 5.

`NChains`

Number c of "chains" simulated. Default is 1. Setting c>1 causes c simulated coefficient vectors to be computed for each group during each iteration. Default depends on the data, and is chosen to provide about 100 groups across all chains.

`NIterations`

Number of iterations. This can be a scalar or a three-element vector. Controls how many iterations are performed for each of three phases of the algorithm:

1 simulated annealing

2 full step size

3 reduced step size

Default is `[150 150 100]`. A scalar is distributed across the three phases in the same proportions as the default.

`NMCMCIterations`

Number of Markov Chain Monte Carlo (MCMC) iterations. This can be a scalar or a three-element vector. Controls how many of three different types of MCMC updates are performed during each phase of the main iteration:

1 full multivariate update

2 single coordinate update

3 multiple coordinate update

Default is `[2 2 2]`. A scalar value is treated as a three-element vector with all elements equal to the scalar.

`OptimFun`

Either `'fminsearch'` or `'fminunc'`, specifying the optimization function to be used during the estimation process. Default is `'fminsearch'`. Use of `'fminunc'` requires Optimization Toolbox.

`Options`

A structure created by a call to `statset`. `nlmefitsa` uses the following `statset` parameters:

- `'DerivStep'` — Relative difference used in finite difference gradient calculation. May be a scalar, or a vector whose length is the number of model parameters *p*. The default is `eps^(1/3)`.
- `Display` — Level of display during estimation.
  - `'off'` (default) — Displays no information
  - `'final'` — Displays information after the final iteration of the estimation algorithm
  - `'iter'` — Displays information at each iteration

- `FunValCheck`
  - `'on'` (sdefault) — Check for invalid values (such as `NaN` or `Inf`) from `MODELFUN`
  - `'off'` — Skip this check
- `OutputFcn` — Function handle specified using `@`, a cell array with function handles or an empty array. `nlmefitsa` calls all output functions after each iteration. See `nlmefitoutputfcn.m` (the default output function for `nlmefitsa`) for an example of an output function.

`ParamTransform`

A vector of *p* values specifying a transformation function `f()` for each of the *p* parameters:

```
XB = ADESIGN*BETA + BDESIGN*B
PHI = f(XB)
```

Each element of the vector must be one of the following integer codes specifying the transformation for the corresponding value of `PHI`:

- 0: `PHI = XB` (default for all parameters)
- 1: `log(PHI) = XB`
- 2: `probit(PHI) = XB`
- 3: `logit(PHI) = XB`

`Replicates`

Number `REPS` of estimations to perform starting from the starting values in the vector `BETA0`. If `BETA0` is a matrix, `REPS` must match the number of columns in `BETA0`. Default is the number of columns in `BETA0`.

`Vectorization`

Determines the possible sizes of the PHI, XFUN, and VFUN input arguments to MODELFUN. Possible values are:

- 'SinglePhi' — MODELFUN is a function (such as an ODE solver) that can only compute YFIT for a single set of model parameters at a time, i.e., PHI must be a single row vector in each call. nlmefitsa calls MODELFUN in a loop if necessary using a single PHI vector and with XFUN containing rows for a single observation or group at a time. VFUN may be a single row that applies to all rows of XFUN, or a matrix with rows corresponding to rows in XFUN.
- 'SingleGroup' — MODELFUN can only accept inputs corresponding to a single group in the data, i.e., XFUN must contain rows of X from a single group in each call. Depending on the model, PHI is a single row that applies to the entire group, or a matrix with one row for each observation. VFUN is a single row.
- 'Full' — MODELFUN can accept inputs for multiple parameter vectors and multiple groups in the data. Either PHI or VFUN may be a single row that applies to all rows of XFUN, or a matrix with rows corresponding to rows in XFUN. Using this option can improve performance by reducing the number of calls to MODELFUN, but may require MODELFUN to perform singleton expansion on PHI or V.

The default for 'Vectorization' is 'SinglePhi'. In all cases, if V is empty, nlmefitsa calls MODELFUN with only two inputs.

Output Arguments

BETA

Estimates of the fixed effects

PSI

An *r*-by-*r* estimated covariance matrix for the random effects. By default, *r* is equal to the number of model parameters *p*.

STATS

A structure with the following fields:

- `logl` — The maximized log-likelihood for the fitted model; empty if the `LogLikMethod` parameter has its default value of `'none'`
- `rmse` — The square root of the estimated error variance (computed on the log scale for the `exponential` error model)
- `errorparam` — The estimated parameters of the error variance model
- `aic` — The Akaike information criterion (empty if `logl` is empty), calculated as `aic` = –2 * `logl` + 2 * `numParam`, where
  - `logl` is the maximized log-likelihood.
  - `numParam` is the number of fitting parameters, including the degree of freedom for covariance matrix of the random effects, the number of fixed effects and the number of parameters of the error model.
- `bic` — The Bayesian information criterion (empty if `logl` is empty), calculated as `bic` = -2*`logl` + log(`M`) * `numParam`
  - `M` is the number of groups.
  - `logl` and `numParam` are defined as in `aic`.

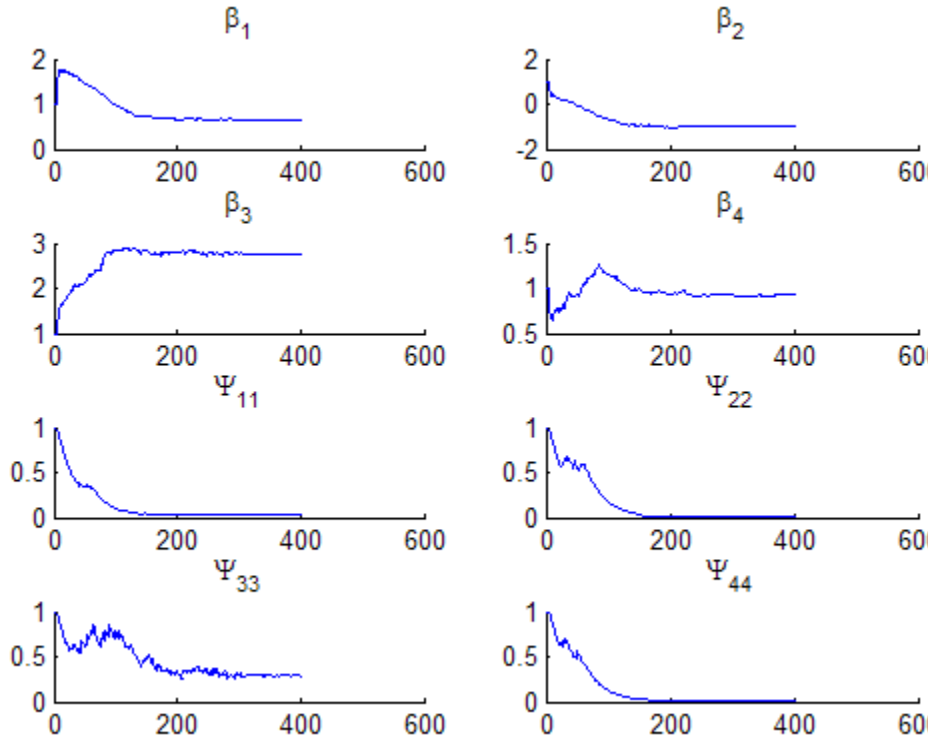
  Note that some literature suggests that the computation of `bic` should be , `bic` = -2*`logl` + log(`N`) * `numParam`, where `N` is the number of observations. To adjust the value of the output you can redefine `bic` as follows: `bic` = `bic` - `numel`(`unique`(`group`)) + `numel`(`Y`)
- `sebeta` — The standard errors for BETA (empty if the `ComputeStdErrors` parameter has its default value of false)
- `covb` — The estimated covariance of the parameter estimates (empty if `ComputeStdErrors` is false)
- `dfe` — The error degrees of freedom

- `pres` — The population residuals (`y-y_population`), where `y_population` is the population predicted values
- `ires` — The population residuals (`y-y_population`), where `y_population` is the individual predicted values
- `pwres` — The population weighted residuals
- `cwres` — The conditional weighted residuals
- `iwres` — The individual weighted residuals

Examples

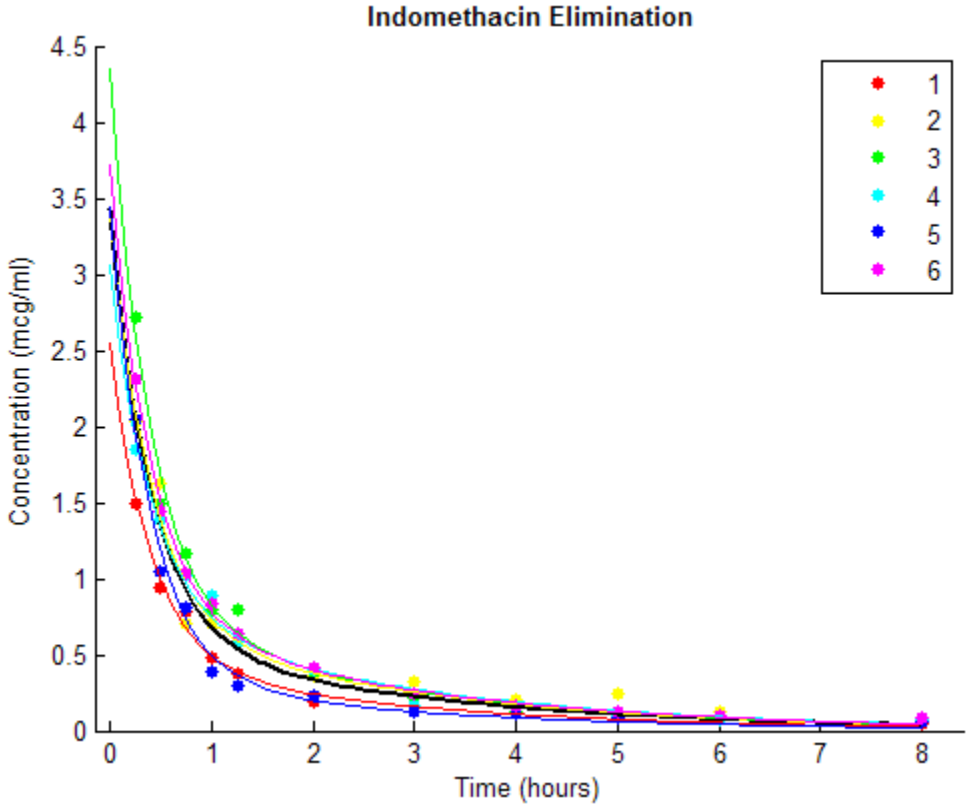
Fit a model to data on concentrations of the drug indomethacin in the bloodstream of six subjects over eight hours:

```
load indomethacin
model = @(phi,t)(phi(:,1).*exp(-phi(:,2).*t)+phi(:,3).*exp(-phi(:,4).*t));
phi0 = [1 1 1 1];
% log transform for 2nd and 4th parameters
xform = [0 1 0 1];
[beta,PSI,stats,br] = nlmefitsa(time,concentration,...
   subject,[],model,phi0,'ParamTransform',xform)
```




```
% Plot the data along with an overall "population" fit
clf
phi = [beta(1), exp(beta(2)), beta(3), exp(beta(4))];
h = gscatter(time,concentration,subject);
xlabel('Time (hours)')
ylabel('Concentration (mcg/ml)')
title('{\bf Indomethacin Elimination}')
xx = linspace(0,8);
line(xx,model(phi,xx),'linewidth',2,'color','k')
```

```
% Plot individual curves based on random effect estimates
for j=1:6
    phir = [beta(1)+br(1,j), exp(beta(2)+br(2,j)), ...
            beta(3)+br(3,j), exp(beta(4)+br(4,j))];
    line(xx,model(phir,xx),'color',get(h(j),'color'))
end
```



Algorithms

In order to estimate the parameters of a nonlinear mixed effects model, we would like to choose the parameter values that maximize a

likelihood function. These values are called the maximum likelihood estimates. The likelihood function can be written in the form

$$p\left(y \mid \beta,\sigma^2,\Sigma\right) = \int p\left(y \mid \beta,b,\sigma^2\right) p(b \mid \Sigma)\, db$$

where

- y is the response data
- ß is the vector of population coefficients
- σ^2 is the residual variance
- $\sum$ is the covariance matrix for the random effects
- b is the set of unobserved random effects

Each $p()$ function on the right-hand-side is a normal (Gaussian) likelihood function that may depend on covariates.

Since the integral does not have a closed form, it is difficult to find parameters that maximize it. Delyon, Lavielle, and Moulines [1] proposed to find the maximum likelihood estimates using an Expectation-Maximization (EM) algorithm in which the E step is replaced by a stochastic procedure. They called their algorithm SAEM, for Stochastic Approximation EM. They demonstrated that this algorithm has desirable theoretical properties, including convergence under practical conditions and convergence to a local maximum of the likelihood function. Their proposal involves three steps:

1. Simulation: Generate simulated values of the random effects b from the posterior density $p(b \mid \Sigma)$ given the current parameter estimates.
2. Stochastic approximation: Update the expected value of the log likelihood function by taking its value from the previous step, and moving part way toward the average value of the log likelihood calculated from the simulated random effects.

3 Maximization step: Choose new parameter estimates to maximize the log likelihood function given the simulated values of the random effects.

References

[1] Delyon, B., M. Lavielle, and E. Moulines, *Convergence of a stochastic approximation version of the EM algorithm*, Annals of Statistics, 27, 94-128, 1999.

[2] Mentré, France, and Marc Lavielle, *Stochastic EM algorithms in population PKPD analyses*, 2008.

See Also

`nlinfit` | `nlmefit`

Purpose

Negative of log-likelihood

Description

The negative of the log-likelihood of the data.

Note This property applies only to gmdistribution objects constructed with `fit`.

ProbDistParametric.NLogL property

Purpose

Read-only value specifying negative log likelihood for input data to ProbDistParametric object

Description

`NLogL` is a read-only property of the `ProbDistParametric` class. `NLogL` is a value specifying the negative log likelihood for input data used to fit a distribution represented by a ProbDistParametric object.

Values

The value is a numeric scalar for a distribution fit to input data, that is, a distribution created using the `fitdist` function. This property is empty for distributions created without fitting to data, that is, by using the `ProbDistUnivParam.ProbDistUnivParam` constructor. Use this information to view and compare the negative log likelihood for input data supplied to create distributions.

Purpose

Read-only value specifying negative log likelihood for input data to ProbDistUnivKernel object

Description

`NLogL` is a read-only property of the `ProbDistUnivKernel` class. `NLogL` is a value specifying the negative log likelihood for input data used to fit a distribution represented by a ProbDistUnivKernel object.

Values

The value is a numeric scalar for a distribution fit to input data, that is, a distribution created using the `fitdist` function. Use this information to view and compare the negative log likelihood for input data used to create distributions.

nlparci

Purpose

Nonlinear regression parameter confidence intervals

Syntax

```
ci = nlparci(beta,resid,'covar',sigma)
ci = nlparci(beta,resid,'jacobian',J)
ci = nlparci(...,'alpha',alpha)
```

Description

`ci = nlparci(beta,resid,'covar',sigma)` returns the 95% confidence intervals `ci` for the nonlinear least squares parameter estimates `beta`. Before calling `nlparci`, use `nlinfit` to fit a nonlinear regression model and get the coefficient estimates `beta`, residuals `resid`, and estimated coefficient covariance matrix `sigma`.

`ci = nlparci(beta,resid,'jacobian',J)` is an alternative syntax that also computes 95% confidence intervals. `J` is the Jacobian computed by `nlinfit`. If the `'robust'` option is used with `nlinfit`, use the `'covar'` input rather than the `'jacobian'` input so that the required `sigma` parameter takes the robust fitting into account.

`ci = nlparci(...,'alpha',alpha)` returns `100(1-alpha)`% confidence intervals.

`nlparci` treats `NaN`s in `resid` or `J` as missing values, and ignores the corresponding observations.

The confidence interval calculation is valid for systems where the length of `resid` exceeds the length of `beta` and `J` has full column rank. When `J` is ill-conditioned, confidence intervals may be inaccurate.

Examples

Fit to exponential decay

Suppose you have data, and want to fit a model of the form

$$y_i = a_1 + a_2\exp(-a_3 x_i) + \varepsilon_i.$$

Here the a_i are the parameters you want to estimate, x_i are the data points, the y_i are the responses, and the ε_i are noise terms.

1 Write a function handle that represents the model:

```
mdl = @(a,x)(a(1) + a(2)*exp(-a(3)*x));
```

2 Generate synthetic data with parameters `a = [1;3;2]`, with the `x` data points distributed exponentially with parameter `2`, and normally distributed noise with standard deviation `0.1`:

```
rng(9845,'twister') % for reproducibility
a = [1;3;2];
x = exprnd(2,100,1);
epsn = normrnd(0,0.1,100,1);
y = mdl(a,x) + epsn;
```

3 Fit the model to data starting from the arbitrary guess `a0 = [2;2;2]`:

```
a0 = [2;2;2];
[ahat,r,J,cov,mse] = nlinfit(x,y,mdl,a0);
ahat

ahat =
    1.0153
    3.0229
    2.1070
```

4 Check whether `[1;3;2]` is in a 95% confidence interval using the Jacobian argument in `nlparci`:

```
ci = nlparci(ahat,r,'Jacobian',J)

ci =
    0.9869    1.0438
    2.9401    3.1058
    1.9963    2.2177
```

5 You can obtain the same result using the covariance argument:

```
ci = nlparci(ahat,r,'covar',cov)

ci =
    0.9869    1.0438
```

```
    2.9401    3.1058
    1.9963    2.2177
```

See Also

nlinfit | nlpredci

Purpose

Nonlinear regression prediction confidence intervals

Syntax

```
[ypred,delta] = nlpredci(modelfun,x,beta,resid,'covar',sigma)
[ypred,delta] = nlpredci(modelfun,x,beta,resid,'jacobian',J)
[...] = nlpredci(...,param1,val1,param2,val2,...)
```

Description

`[ypred,delta] = nlpredci(modelfun,x,beta,resid,'covar',sigma)` returns predictions, `ypred`, and 95% confidence interval half-widths, `delta`, for the nonlinear regression model defined by `modelfun`, at input values `x`. `modelfun` is a function handle, specified using `@`, that accepts two arguments—a coefficient vector and the array `x`—and returns a vector of fitted `y` values. Before calling `nlpredci`, use `nlinfit` to fit `modelfun` by nonlinear least squares and get estimated coefficient values `beta`, residuals `resid`, and estimated coefficient covariance matrix `sigma`.

`[ypred,delta] = nlpredci(modelfun,x,beta,resid,'jacobian',J)` is an alternative syntax that also computes 95% confidence intervals. `J` is the Jacobian computed by `nlinfit`. If the `'robust'` option is used with `nlinfit`, use the `'covar'` input rather than the `'jacobian'` input so that the required `sigma` parameter takes the robust fitting into account.

`[...] = nlpredci(...,param1,val1,param2,val2,...)` accepts optional parameter name/value pairs.

Parameter	Value
`'alpha'`	A value between 0 and 1 that specifies the confidence level as `100(1-alpha)%`. Default is `0.05`.
`'mse'`	The mean squared error returned by `nlinfit`. This is required to predict new observations (see `'predopt'`) if the robust option is used with `nlinfit`; otherwise, the `'mse'` is computed from the residuals and does not take the robust fitting into account.

Parameter	Value
'predopt'	Either 'curve' (the default) to compute confidence intervals for the estimated curve (function value) at x, or 'observation' for prediction intervals for a new observation at x. If 'observation'is specified after using a robust option with nlinfit, the 'mse' parameter must be supplied to specify the robust estimate of the mean squared error.
'simopt'	Either 'on' for simultaneous bounds, or 'off' (the default) for nonsimultaneous bounds.

nlpredci treats NaNs in resid or J as missing values, and ignores the corresponding observations.

The confidence interval calculation is valid for systems where the length of resid exceeds the length of beta and J has full column rank at beta. When J is ill-conditioned, predictions and confidence intervals may be inaccurate.

Examples

Fit to exponential decay

Suppose you have data, and want to fit a model of the form

$$y_i = a_1 + a_2\exp(-a_3 x_i) + \varepsilon_i.$$

Here the a_i are the parameters you want to estimate, x_i are the data points, the y_i are the responses, and the ε_i are noise terms.

1. Write a function handle that represents the model:

```
mdl = @(a,x)(a(1) + a(2)*exp(-a(3)*x));
```

2. Generate synthetic data with parameters a = [1;3;2], with the x data points distributed exponentially with parameter 2, and normally distributed noise with standard deviation 0.1:

```
rng(9845,'twister') % for reproducibility
```

```
a = [1;3;2];
x = exprnd(2,100,1);
epsn = normrnd(0,0.1,100,1);
y = mdl(a,x) + epsn;
```

3 Fit the model to data starting from the arbitrary guess `a0 = [2;2;2]`:

```
a0 = [2;2;2];
[ahat,r,J,cov,mse] = nlinfit(x,y,mdl,a0);
ahat

ahat =
    1.0153
    3.0229
    2.1070
```

4 Find the predicted response `yhat` together with a 95% confidence interval about `yhat`, for the mean of `x`:

```
[ypred dlt] = nlpredci(mdl,mean(x),ahat,r,'Covar',cov)

ypred =
    1.0669

dlt =
    0.0231
```

The 95% confidence interval about `ypred` is:

```
[ypred-dlt,ypred+dlt]

ans =
    1.0438    1.0900
```

See Also

`nlinfit` | `nlparci`

Purpose

Nonnegative matrix factorization

Syntax

```
[W,H] = nnmf(A,k)
[W,H] = nnmf(A,k,param1,val1,param2,val2,...)
[W,H,D] = nnmf(...)
```

Description

`[W,H] = nnmf(A,k)` factors the nonnegative n-by-m matrix `A` into nonnegative factors `W` (n-by-`k`) and `H` (`k`-by-m). The factorization is not exact; `W*H` is a lower-rank approximation to `A`. The factors `W` and `H` are chosen to minimize the root-mean-squared residual `D` between `A` and `W*H`:

```
D = sqrt(norm(A-W*H,'fro')/(N*M))
```

The factorization uses an iterative method starting with random initial values for `W` and `H`. Because the root-mean-squared residual `D` may have local minima, repeated factorizations may yield different `W` and `H`. Sometimes the algorithm converges to a solution of lower rank than k, which may indicate that the result is not optimal.

`W` and `H` are normalized so that the rows of `H` have unit length. The columns of `W` are ordered by decreasing length.

`[W,H] = nnmf(A,k,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs from the following table.

Parameter	Value
`'algorithm'`	Either `'als'` (the default) to use an alternating least-squares algorithm, or `'mult'` to use a multiplicative update algorithm. In general, the `'als'` algorithm converges faster and more consistently. The `'mult'` algorithm is more sensitive to initial values, which makes it a

Parameter	Value
	good choice when using `'replicates'` to find `W` and `H` from multiple random starting values.
`'w0'`	An *n*-by-`k` matrix to be used as the initial value for `W`.
`'h0'`	A `k`-by-*m* matrix to be used as the initial value for `H`.

`'options'`	An options structure as created by the `statset` function. `nnmf` uses the following fields of the options structure:
	• `Display` — Level of display. Choices:
	  - `'off'` (default) — No display
	  - `'final'` — Display final result
	  - `'iter'` — Iterative display of intermediate results
	• `MaxIter` — Maximum number of iterations. Default is `100`. Unlike in optimization settings, reaching `MaxIter` iterations is treated as convergence.
	• `TolFun` — Termination tolerance on change in size of the residual. Default is `1e-4`.
	• `TolX` — Termination tolerance on relative change in the elements of `W` and `H`. Default is `1e-4`.
	• `UseParallel` — Set to `'always'` to compute in parallel. Default is `'never'`.
	• `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. Default is `'never'`. To compute reproducibly, set

Parameter	Value
	`Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. • `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `nnmf` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case - You have an open MATLAB pool - `UseParallel` is `'always'` - `UseSubstreams` is `'never'` In that case, use a cell array the same size as the MATLAB pool. For more information on using parallel computing, see Chapter 17, "Parallel Statistics".
`'replicates'`	The number of times to repeat the factorization, using new random starting values for `W` and `H`, except at the first replication if `'w0'` and `'h0'` are given. This is most beneficial with the `'mult'` algorithm. The default is `1`.

`[W,H,D] = nnmf(...)` also returns `D`, the root mean square residual.

Examples

Example 1

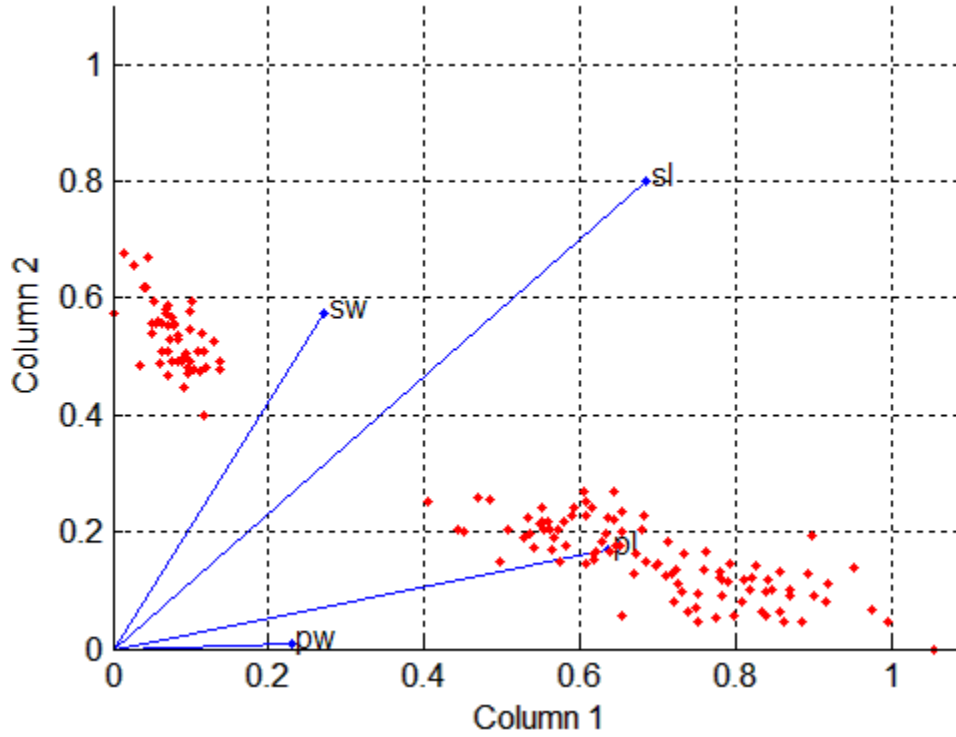
Compute a nonnegative rank-two approximation of the measurements of the four variables in Fisher's iris data:

```
load fisheriris
[W,H] = nnmf(meas,2);
H
H =
    0.6852    0.2719    0.6357    0.2288
    0.8011    0.5740    0.1694    0.0087
```

The first and third variables in `meas` (sepal length and petal length, with coefficients `0.6852` and `0.6357`, respectively) provide relatively strong weights to the first column of `W`. The first and second variables in `meas` (sepal length and sepal width, with coefficients `0.8011`and `0.5740`) provide relatively strong weights to the second column of `W`.

Create a `biplot` of the data and the variables in `meas` in the column space of `W`:

```
biplot(H','scores',W,'varlabels',{'sl','sw','pl','pw'});
axis([0 1.1 0 1.1])
xlabel('Column 1')
ylabel('Column 2')
```



Example 2

Starting from a random array `X` with rank 20, try a few iterations at several replicates using the multiplicative algorithm:

```
X = rand(100,20)*rand(20,50);
opt = statset('MaxIter',5,'Display','final');
[W0,H0] = nnmf(X,5,'replicates',10,...
                   'options',opt,...
                   'algorithm','mult');
    rep iteration    rms resid    |delta x|
      1         5     0.560887    0.0245182
      2         5      0.66418    0.0364471
      3         5     0.609125    0.0358355
      4         5     0.608894    0.0415491
      5         5     0.619291    0.0455135
      6         5     0.621549    0.0299965
      7         5     0.640549    0.0438758
      8         5     0.673015    0.0366856
      9         5     0.606835    0.0318931
     10         5     0.633526    0.0319591
Final root mean square residual = 0.560887
```

Continue with more iterations from the best of these results using alternating least squares:

```
opt = statset('Maxiter',1000,'Display','final');
[W,H] = nnmf(X,5,'w0',W0,'h0',H0,...
                 'options',opt,...
                 'algorithm','als');
    rep iteration    rms resid    |delta x|
      1        80     0.256914 9.78625e-005
Final root mean square residual = 0.256914
```

References

[1] Berry, M. W., et al. “Algorithms and Applications for Approximate Nonnegative Matrix Factorization.” *Computational Statistics and Data Analysis*. Vol. 52, No. 1, 2007, pp. 155–173.

See Also

princomp | factoran | statset

classregtree.nodeclass

Purpose

Class values of nodes of classification tree

Syntax

```
NAME=nodeclass(T)
NAME=nodeclass(T,J)
[NAME,ID]=nodeclass(...)
```

Description

`NAME=nodeclass(T)` returns an n-element cell array with the names of the most probable classes in each node of the tree `T`, where n is the number of nodes in the tree. Every element of this array is a string equal to one of the class names returned by `classname(T)`. For regression trees, `nodeclass` returns an empty cell array.

`NAME=nodeclass(T,J)` takes an array `J` of node numbers and returns the class names for the specified nodes.

`[NAME,ID]=nodeclass(...)` also returns a numeric array with the class index for each node. The class index is determined by the order of classes `classname` returns.

See Also

`classregtree` | `classname` | `numnodes`

Purpose

Return vector of node errors

Syntax

```
e = nodeerr(t)
e = nodeerr(t,nodes)
```

Description

`e = nodeerr(t)` returns an *n*-element vector `e` of the errors of the nodes in the tree `t`, where *n* is the number of nodes. For a regression tree, the error `e(i)` for node `i` is the variance of the observations assigned to node `i`. For a classification tree, `e(i)` is the misclassification probability for node `i`.

`e = nodeerr(t,nodes)` takes a vector `nodes` of node numbers and returns the errors for the specified nodes.

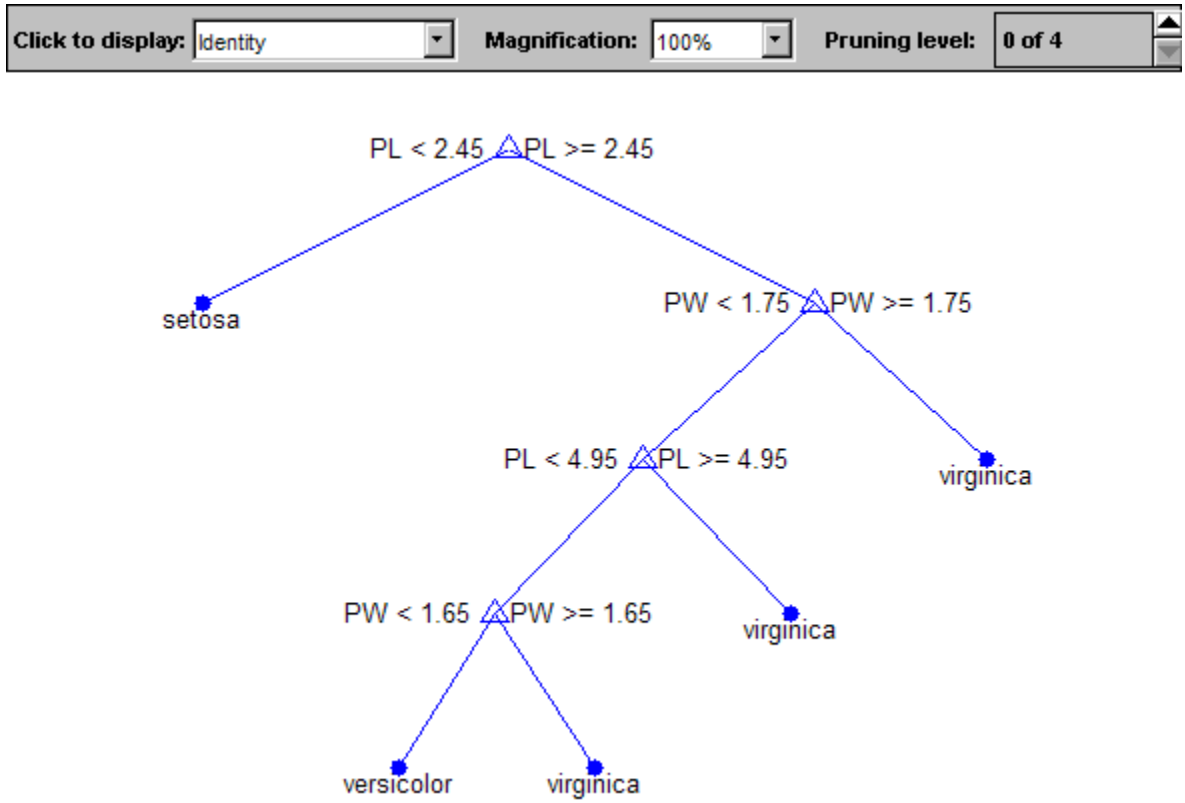
The error `e` is the so-called *resubstitution error* computed by applying the tree to the same data used to create the tree. This error is likely to under estimate the error you would find if you applied the tree to new data. The `test` function provides options to compute the error (or cost) using cross-validation or a test sample.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica
```

```
view(t)
```




```
e = nodeerr(t)
e =
    0.6667
         0
    0.5000
    0.0926
    0.0217
    0.0208
```

```
    0.3333
         0
         0
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes` | `test`

classregtree.nodemean

Purpose

Mean values of nodes of regression tree

Syntax

```
NM = nodemean(T)
NM = nodemean(T,J)
```

Description

`NM = nodemean(T)` returns an n-element numeric array with mean values in each node of the tree `T`, where n is the number of nodes in the tree. Every element of this array is computed by averaging true `Y` values over all observations in the node. For classification trees, `nodemean` returns an empty numeric array.

`NM = nodemean(T,J)` takes an array `J` of node numbers and returns the mean values for the specified nodes.

See Also

`classregtree | numnodes`

Purpose

Node probabilities

Syntax

```
p = nodeprob(t)
p = nodeprob(t,nodes)
```

Description

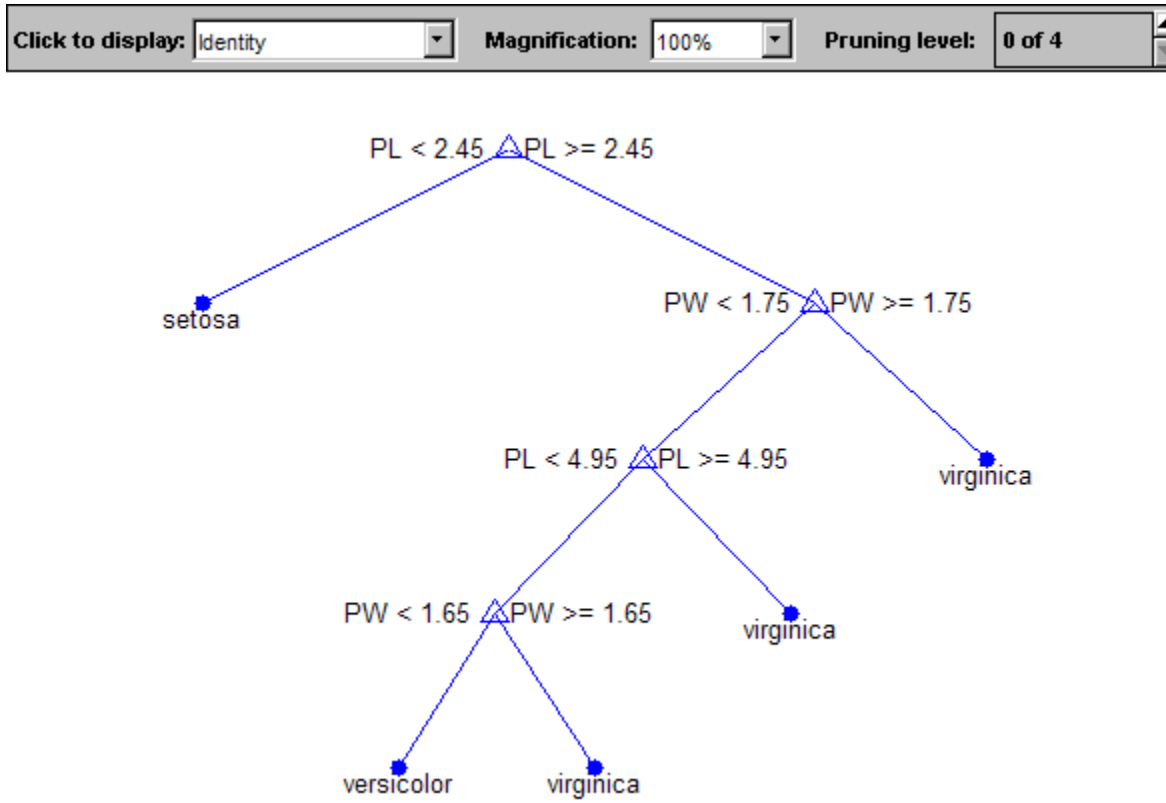
`p = nodeprob(t)` returns an n-element vector `p` of the probabilities of the nodes in the tree `t`, where n is the number of nodes. The probability of a node is computed as the proportion of observations from the original data that satisfy the conditions for the node. For a classification tree, this proportion is adjusted for any prior probabilities assigned to each class.

`p = nodeprob(t,nodes)` takes a vector `nodes` of node numbers and returns the probabilities for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
p = nodeprob(t)
p =
    1.0000
    0.3333
    0.6667
    0.3600
    0.3067
    0.3200
    0.0400
    0.3133
```

```
    0.0067
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `nodesize` | `numnodes`

classregtree.nodesize

Purpose

Return node size

Syntax

```
sizes = nodesize(t)
sizes = nodesize(t,nodes)
```

Description

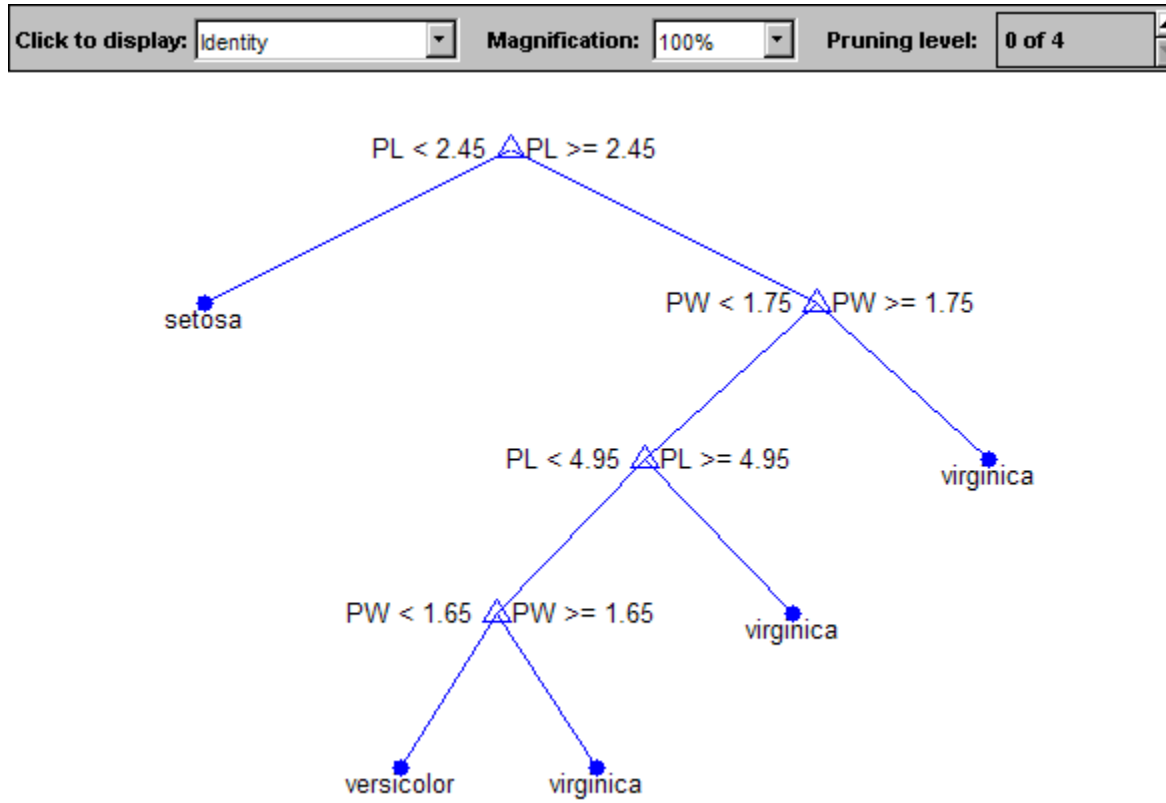
`sizes = nodesize(t)` returns an n-element vector `sizes` of the sizes of the nodes in the tree `t`, where n is the number of nodes. The size of a node is defined as the number of observations from the data used to create the tree that satisfy the conditions for the node.

`sizes = nodesize(t,nodes)` takes a vector `nodes` of node numbers and returns the sizes for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
sizes = nodesize(t)
sizes =
   150
    50
   100
    54
    46
    48
     6
    47
```

1

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes`

Purpose

Notify listeners of event

Syntax

```
notify(h,'eventname')
notify(h,'eventname',data)
```

Description

`notify(h,'eventname')` notifies listeners added to the event named `eventname` on handle object array `h` that the event is taking place. `h` is the array of handles to objects triggering the event, and `eventname` must be a string.

`notify(h,'eventname',data)` provides a way of encapsulating information about an event which can then be accessed by each registered listener. `data` must belong to the `event.eventdata` class.

See Also

`addlistener` | `event.EventData` | `events` | `qrandstream`

nominal

Superclasses

categorical

Purpose

Arrays for nominal categorical data

Description

Nominal arrays are used to store discrete values that are not numeric and that do not have an ordering. A nominal array provides efficient storage and convenient manipulation of such data, while also maintaining meaningful labels for the values. Nominal arrays are often used as grouping variables.

You can subscript, concatenate, reshape, etc. nominal arrays much like ordinary numeric arrays. You can test equality between elements of two nominal arrays, or between a nominal array and a single string representing a nominal value.

Construction

Use the `nominal` constructor to create a nominal array from a numeric, logical, or character array, or from a cell array of strings.

nominal	Construct nominal categorical array

Methods

Each nominal array carries along a list of possible values that it can store, known as its levels. The list is created when you create a nominal array, and you can access it using the `getlevels` method, or modify it using the `addlevels`, `mergelevels`, or `droplevels` methods. Assignment to the array will also add new levels automatically if the values assigned are not already levels of the array.

You can change the order of the list of levels for a nominal array using the `reorderlevels` method, however, that order has no significance for the values in the array. The order is used only for display purposes, or when you convert the nominal array to numeric values using methods such as `double` or `subsindex`, or compare two arrays using `isequal`. If you need to work with values that have a mathematical ordering, you should use an `ordinal` array instead.

Inherited Methods

Methods in the following table are inherited from `categorical`.

addlevels	Add levels to categorical array
cat	Concatenate categorical arrays
cellstr	Convert categorical array to cell array of strings
char	Convert categorical array to character array
circshift	Shift categorical array circularly
ctranspose	Transpose categorical matrix
disp	Display categorical array
display	Display categorical array
double	Convert categorical array to double array
droplevels	Drop levels
end	Last index in indexing expression for categorical array
flipdim	Flip categorical array along specified dimension
fliplr	Flip categorical matrix in left/right direction
flipud	Flip categorical matrix in up/down direction
getlabels	Access categorical array labels
getlevels	Get categorical array levels
hist	Plot histogram of categorical data

horzcat	Horizontal concatenation for categorical arrays
int16	Convert categorical array to signed 16-bit integer array
int32	Convert categorical array to signed 32-bit integer array
int64	Convert categorical array to signed 64-bit integer array
int8	Convert categorical array to signed 8-bit integer array
intersect	Set intersection for categorical arrays
ipermute	Inverse permute dimensions of categorical array
isempty	True for empty categorical array
isequal	True if categorical arrays are equal
islevel	Test for levels
ismember	True for elements of categorical array in set
isscalar	True if categorical array is scalar
isundefined	Test for undefined elements
isvector	True if categorical array is vector
length	Length of categorical array
levelcounts	Element counts by level
ndims	Number of dimensions of categorical array
numel	Number of elements in categorical array

permute	Permute dimensions of categorical array
reorderlevels	Reorder levels
repmat	Replicate and tile categorical array
reshape	Resize categorical array
rot90	Rotate categorical matrix 90 degrees
setdiff	Set difference for categorical arrays
setlabels	Label levels
setxor	Set exclusive-or for categorical arrays
shiftdim	Shift dimensions of categorical array
single	Convert categorical array to single array
size	Size of categorical array
squeeze	Squeeze singleton dimensions from categorical array
subsasgn	Subscripted assignment for categorical array
subsindex	Subscript index for categorical array
subsref	Subscripted reference for categorical array
summary	Summary statistics for categorical array
times	Product of categorical arrays

transpose	Transpose categorical matrix
uint16	Convert categorical array to unsigned 16-bit integers
uint32	Convert categorical array to unsigned 32-bit integers
uint64	Convert categorical array to unsigned 64-bit integers
uint8	Convert categorical array to unsigned 8-bit integers
union	Set union for categorical arrays
unique	Unique values in categorical array
vertcat	Vertical concatenation for categorical arrays

Properties

Inherited Properties

Properties in the following table are inherited from `categorical`.

labels	Text labels for levels
undeflabel	Text label for undefined levels

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

Examples

Create a nominal array from string data in a cell array:

```
colors = nominal({'r' 'b' 'g';'g' 'r' 'b';'b' 'r' 'g'},...
   {'blue' 'green' 'red'})

% Find elements meeting a criterion
colors == 'red'
```

```
ismember(colors,{'red' 'blue'})

% Compare two nominal arrays
colors2 = fliplr(colors)
colors == colors2
```

See Also

histc | ordinal

nominal

Purpose

Construct nominal categorical array

Syntax

```
B = nominal(A)
B = nominal(A,labels)
B = nominal(A,labels,levels)
B = nominal(A,labels,[],edges)
```

Description

`B = nominal(A)` creates a nominal array `B` from the array `A`. `A` can be numeric, logical, character, categorical, or a cell array of strings. `nominal` creates the levels of `B` from the sorted unique values in `A`, and creates default labels for them.

`B = nominal(A,labels)` labels the levels in `B` using the character array or cell array of strings `labels`. `nominal` assigns labels to levels in `B` in order according to the sorted unique values in `A`.

`B = nominal(A,labels,levels)` creates a nominal array with possible levels defined by `levels`. `levels` is a vector whose values can be compared to those in `A` using the equality operator. `nominal` assigns labels to each level from the corresponding elements of `labels`. If `A` contains any values not present in `levels`, the levels of the corresponding elements of `B` are undefined.

`B = nominal(A,labels,[],edges)` creates a nominal array by binning the numeric array `A` with bin edges given by the numeric vector `edges`. The uppermost bin includes values equal to the right-most edge. `nominal` assigns labels to each level in `B` from the corresponding elements of `labels`. `edges` must have one more element than `labels`.

By default, an element of `B` is undefined if the corresponding element of `A` is `NaN` (when `A` is numeric), an empty string (when `A` is character), or undefined (when `A` is categorical). `nominal` treats such elements as "undefined" or "missing" and does not include entries for them among the possible levels for `B`. To create an explicit level for such elements instead of treating them as undefined, you must use the `levels` input, and include `NaN`, the empty string, or an undefined element.

You may include duplicate labels in `labels` in order to merge multiple values in `A` into a single level in `B`.

Examples

Create a nominal array from Fisher's iris data:

```
load fisheriris
species = nominal(species);
summary(species)
     setosa      versicolor      virginica
         50              50             50
```

Create a nominal array from characters, and provide explicit labels:

```
colors1 = nominal({'r' 'b' 'g'; 'g' 'r' 'b'; 'b' 'r' 'g'},...
   {'blue' 'green' 'red'})
```

Create a nominal array from characters, and provide both explicit labels and an explicit order for display:

```
colors2 = nominal({'r' 'b' 'g'; 'g' 'r' 'b'; 'b' 'r' 'g'}, ...
           {'red' 'green' 'blue'},{'r' 'g' 'b'})
```

Create a nominal array from integer data, merging odd and even values into only two nominal levels. Provide explicit labels:

```
toss = nominal(randi([1 4],5,2),{'odd' 'even' 'odd' 'even'},1:4)
```

---

1 Load patient data from the CSV file `hospital.dat` and store the information in a dataset array with observation names given by the first column in the data (patient identification):

```
patients = dataset('file','hospital.dat',...
                   'delimiter',',',...
                   'ReadObsNames',true);
```

2 Make the {0,1}-valued variable `smoke` nominal, and change the labels to `'No'` and `'Yes'`:

```
patients.smoke = nominal(patients.smoke,{'No','Yes'});
```

3 Add new levels to `smoke` as placeholders for more detailed histories of smokers:

```
patients.smoke = addlevels(patients.smoke,...
                 {'0-5 Years','5-10 Years','LongTerm'});
```

4 Assuming the nonsmokers have never smoked, relabel the `'No'` level:

```
patients.smoke = setlabels(patients.smoke,'Never','No');
```

5 Drop the undifferentiated `'Yes'` level from `smoke`:

```
patients.smoke = droplevels(patients.smoke,'Yes');

Warning: OLDLEVELS contains categorical levels that
were present in A, caused some array elements to have
undefined levels.
```

Note that smokers now have an undefined level.

6 Set each smoker to one of the new levels, by observation name:

```
patients.smoke('YPL-320') = '5-10 Years';
```

See Also

`histc` | `ordinal`

Purpose

Normal cumulative distribution function

Syntax

```
P = normcdf(X,mu,sigma)
[P,PLO,PUP] = normcdf(X,mu,sigma,pcov,alpha)
```

Description

`P = normcdf(X,mu,sigma)` computes the normal cdf at each of the values in `X` using the corresponding mean `mu` and standard deviation `sigma`. `X`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `sigma` must be positive.

`[P,PLO,PUP] = normcdf(X,mu,sigma,pcov,alpha)` produces confidence bounds for `P` when the input parameters `mu` and `sigma` are estimates. `pcov` is the covariance matrix of the estimated parameters. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is 0.05. `PLO` and `PUP` are arrays of the same size as `P` containing the lower and upper confidence bounds.

The function `normdf` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\frac{X-\hat{\mu}}{\hat{\sigma}}$$

and then transforming those bounds to the scale of the output `P`. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The normal cdf is

$$p = F(x \mid \mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}}\int_{-\infty}^{x} e^{\frac{-(t-\mu)^2}{2\sigma^2}}\,dt$$

The result, p, is the probability that a single observation from a normal distribution with parameters μ and σ will fall in the interval $(-\infty\ x]$.

The *standard normal* distribution has μ = 0 and σ = 1.

Examples

What is the probability that an observation from a standard normal distribution will fall on the interval [-1 1]?

```
p = normcdf([-1 1]);
p(2)-p(1)
ans =
  0.6827
```

More generally, about 68% of the observations from a normal distribution fall within one standard deviation, σ, of the mean, μ.

See Also

`cdf` | `normpdf` | `norminv` | `normstat` | `normfit` | `normlike` | `normrnd`

How To

- "Normal Distribution" on page B-83

Purpose

Normal parameter estimates

Syntax

```
[muhat,sigmahat] = normfit(data)
[muhat,sigmahat,muci,sigmaci] = normfit(data)
[muhat,sigmahat,muci,sigmaci] = normfit(data,alpha)
[...] = normfit(data,alpha,censoring)
[...] = normfit(data,alpha,censoring,freq)
[...] = normfit(data,alpha,censoring,freq,options)
```

Description

`[muhat,sigmahat] = normfit(data)` returns estimates of the mean, μ, and standard deviation, σ, of the normal distribution given the data in `data`.

`[muhat,sigmahat,muci,sigmaci] = normfit(data)` returns 95% confidence intervals for the parameter estimates on the mean and standard deviation in the arrays `muci` and `sigmaci`, respectively. The first row of `muci` contains the lower bounds of the confidence intervals for μ the second row contains the upper bounds. The first row of `sigmaci` contains the lower bounds of the confidence intervals for σ, and the second row contains the upper bounds.

`[muhat,sigmahat,muci,sigmaci] = normfit(data,alpha)` returns 100(1 - `alpha`) % confidence intervals for the parameter estimates, where `alpha` is a value in the range `[0 1]` specifying the width of the confidence intervals. By default, `alpha` is `0.05`, which corresponds to 95% confidence intervals.

`[...] = normfit(data,alpha,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is `1` for observations that are right-censored and `0` for observations that are observed exactly. `data` must be a vector in order to pass in the argument `censoring`.

`[...] = normfit(data,alpha,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. Typically, `freq` contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `alpha`, `censoring`, or `freq` to use their default values.

`[...] = normfit(data,alpha,censoring,freq,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates when there is censoring. The normal fit function accepts an `options` structure which you can create using the function `statset`. Enter `statset('normfit')` to see the names and default values of the parameters that `normfit` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

Examples

In this example the data is a two-column random normal matrix. Both columns have $\mu = 10$ and $\sigma = 2$. Note that the confidence intervals below contain the "true values."

```
data = normrnd(10,2,100,2);
[mu,sigma,muci,sigmaci] = normfit(data)
mu =
  10.1455  10.0527
sigma =
  1.9072  2.1256
muci =
  9.7652  9.6288
  10.5258  10.4766
sigmaci =
  1.6745  1.8663
  2.2155  2.4693
```

See Also

`mle` | `normlike` | `normpdf` | `normcdf` | `norminv` | `normstat` | `normrnd`

How To

- “Normal Distribution” on page B-83

Purpose

Normal inverse cumulative distribution function

Syntax

```
X = norminv(P,mu,sigma)
[X,XLO,XUP] = norminv(P,mu,sigma,pcov,alpha)
```

Description

`X = norminv(P,mu,sigma)` computes the inverse of the normal cdf using the corresponding mean `mu` and standard deviation `sigma` at the corresponding probabilities in `P`. `P`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `sigma` must be positive, and the values in `P` must lie in the interval [0 1].

`[X,XLO,XUP] = norminv(P,mu,sigma,pcov,alpha)` produces confidence bounds for `X` when the input parameters `mu` and `sigma` are estimates. `pcov` is the covariance matrix of the estimated parameters. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is `0.05`. `XLO` and `XUP` are arrays of the same size as `X` containing the lower and upper confidence bounds.

The function `norminv` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\hat{\mu} + \hat{\sigma} q$$

where q is the `P`th quantile from a normal distribution with mean 0 and standard deviation 1. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds may be more accurate.

The normal inverse function is defined in terms of the normal cdf as

$$x = F^{-1}(p \mid \mu,\sigma) = \{x : F(x \mid \mu,\sigma) = p\}$$

where

$$p = F(x \mid \mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}} \int_{-\infty}^{x} e^{\frac{-(t-\mu)^2}{2\sigma^2}} dt$$

The result, x, is the solution of the integral equation above where you supply the desired probability, p.

Examples

Find an interval that contains 95% of the values from a standard normal distribution.

```
x = norminv([0.025 0.975],0,1)
x =
  -1.9600  1.9600
```

Note that the interval `x` is not the only such interval, but it is the shortest.

```
xl = norminv([0.01 0.96],0,1)
xl =
  -2.3263  1.7507
```

The interval `xl` also contains 95% of the probability, but it is longer than `x`.

See Also

`icdf` | `normcdf` | `normpdf` | `normstat` | `normfit` | `normlike` | `normrnd`

How To

- "Normal Distribution" on page B-83

Purpose

Normal negative log-likelihood

Syntax

```
nlogL = normlike(params,data)
[nlogL,AVAR] = normlike(params,data)
[...] = normlike(param,data,censoring)
[...] = normlike(param,data,censoring,freq)
```

Description

`nlogL = normlike(params,data)` returns the negative of the normal log-likelihood function. `params(1)` is the mean, `mu`, and `params(2)` is the standard deviation, `sigma`.

`[nlogL,AVAR] = normlike(params,data)` also returns the inverse of Fisher's information matrix, `AVAR`. If the input parameter values in `params` are the maximum likelihood estimates, the diagonal elements of `AVAR` are their asymptotic variances. `AVAR` is based on the observed Fisher's information, not the expected information.

`[...] = normlike(param,data,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = normlike(param,data,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. The vector `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `censoring` to use its default value.

`normlike` is a utility function for maximum likelihood estimation.

See Also

`normfit` | `normpdf` | `normcdf` | `norminv` | `normstat` | `normrnd`

How To

- "Normal Distribution" on page B-83

normpdf

Purpose

Normal probability density function

Syntax

```
Y = normpdf(X,mu,sigma)
Y = normpdf(X)
Y = normpdf(X,mu)
```

Description

`Y = normpdf(X,mu,sigma)` computes the pdf at each of the values in `X` using the normal distribution with mean `mu` and standard deviation `sigma`. `X`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `sigma` must be positive.

The normal pdf is

$$y = f(x \mid \mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{\frac{-(x-\mu)^2}{2\sigma^2}}$$

The *likelihood function* is the pdf viewed as a function of the parameters. Maximum likelihood estimators (MLEs) are the values of the parameters that maximize the likelihood function for a fixed value of `x`.

The *standard normal* distribution has $\mu = 0$ and $\sigma = 1$.

If x is standard normal, then $x\sigma + \mu$ is also normal with mean μ and standard deviation σ. Conversely, if y is normal with mean μ and standard deviation σ, then $x = (y-\mu) / \sigma$ is standard normal.

`Y = normpdf(X)` uses the standard normal distribution (`mu = 0`, `sigma = 1`).

`Y = normpdf(X,mu)` uses the normal distribution with unit standard deviation (`sigma = 1`).

Examples

```
mu = [0:0.1:2];
[y i] = max(normpdf(1.5,mu,1));
MLE = mu(i)
MLE =
```

```
    1.5000
```

See Also

pdf | normcdf | norminv | normstat | normfit | normlike | normrnd | mvnpdf

How To

- “Normal Distribution” on page B-83

normplot

Purpose

Normal probability plot

Syntax

```
h = normplot(X)
```

Description

`h = normplot(X)` displays a normal probability plot of the data in `X`. For matrix `X`, normplot displays a line for each column of `X`. `h` is a handle to the plotted lines.

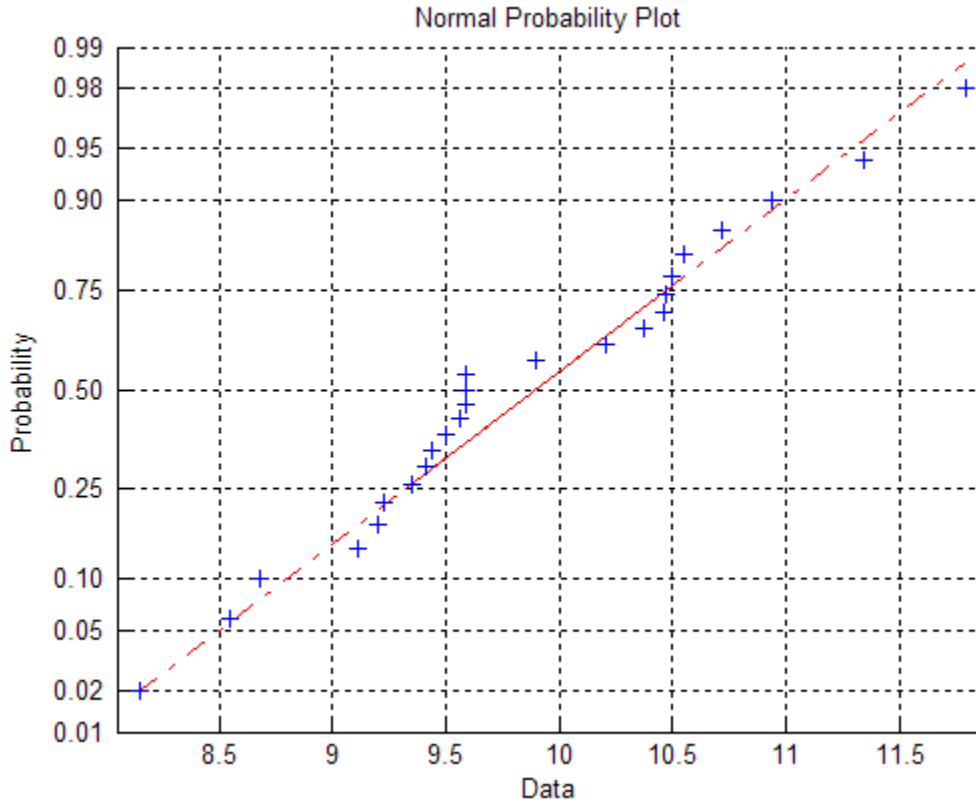
The plot has the sample data displayed with the plot symbol `'+'`. Superimposed on the plot is a line joining the first and third quartiles of each column of `X` (a robust linear fit of the sample order statistics.) This line is extrapolated out to the ends of the sample to help evaluate the linearity of the data.

The purpose of a normal probability plot is to graphically assess whether the data in `X` could come from a normal distribution. If the data are normal the plot will be linear. Other distribution types will introduce curvature in the plot. `normplot` uses midpoint probability plotting positions. Use `probplot` when the data included censored observations.

Examples

Generate a normal sample and a normal probability plot of the data.

```
x = normrnd(10,1,25,1);
normplot(x)
```



See Also

`cdfplot` | `wblplot` | `probplot` | `hist` | `normfit` | `norminv` | `normpdf` | `normspec` | `normstat` | `normcdf` | `normrnd` | `normlike`

How To

- “Normal Distribution” on page B-83

normrnd

Purpose

Normal random numbers

Syntax

```
R = normrnd(mu,sigma)
R = normrnd(mu,sigma,m,n,...)
R = normrnd(mu,sigma,[m,n,...])
```

Description

`R = normrnd(mu,sigma)` generates random numbers from the normal distribution with mean parameter `mu` and standard deviation parameter `sigma`. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `mu` or `sigma` is expanded to a constant array with the same dimensions as the other input.

`R = normrnd(mu,sigma,m,n,...)` or `R = normrnd(mu,sigma,[m,n,...])` generates an `m`-by-`n`-by-... array. The `mu`, `sigma` parameters can each be scalars or arrays of the same size as `R`.

Examples

```
n1 = normrnd(1:6,1./(1:6))
n1 =
  2.1650  2.3134  3.0250  4.0879  4.8607  6.2827

n2 = normrnd(0,1,[1 5])
n2 =
  0.0591  1.7971  0.2641  0.8717  -1.4462

n3 = normrnd([1 2 3;4 5 6],0.1,2,3)
n3 =
  0.9299  1.9361  2.9640
  4.1246  5.0577  5.9864
```

See Also

`random` | `normpdf` | `normcdf` | `norminv` | `normstat` | `normfit` | `normlike` | `mvnrnd` | `lognrnd`

How To

- "Normal Distribution" on page B-83

Purpose

Normal density plot between specifications

Syntax

```
normspec(specs)
normspec(specs,mu,sigma)
normspec(specs,mu,sigma,region)
p = normspec(...)
[p,h] = normspec(...)
```

Description

`normspec(specs)` plots the standard normal density, shading the portion inside the specification limits given by the two-element vector `specs`. Set `specs(1)` to `-Inf` if there is no lower limit; set `specs(2)` to `Inf` if there is no upper limit.

`normspec(specs,mu,sigma)` shades the portion inside the specification limits of a normal density with parameters `mu` and `sigma`. The defaults are `mu = 0` and `sigma = 1`.

`normspec(specs,mu,sigma,region)` shades the *`region`* either `'inside'` or `'outside'` the specification limits. The default is `'inside'`.

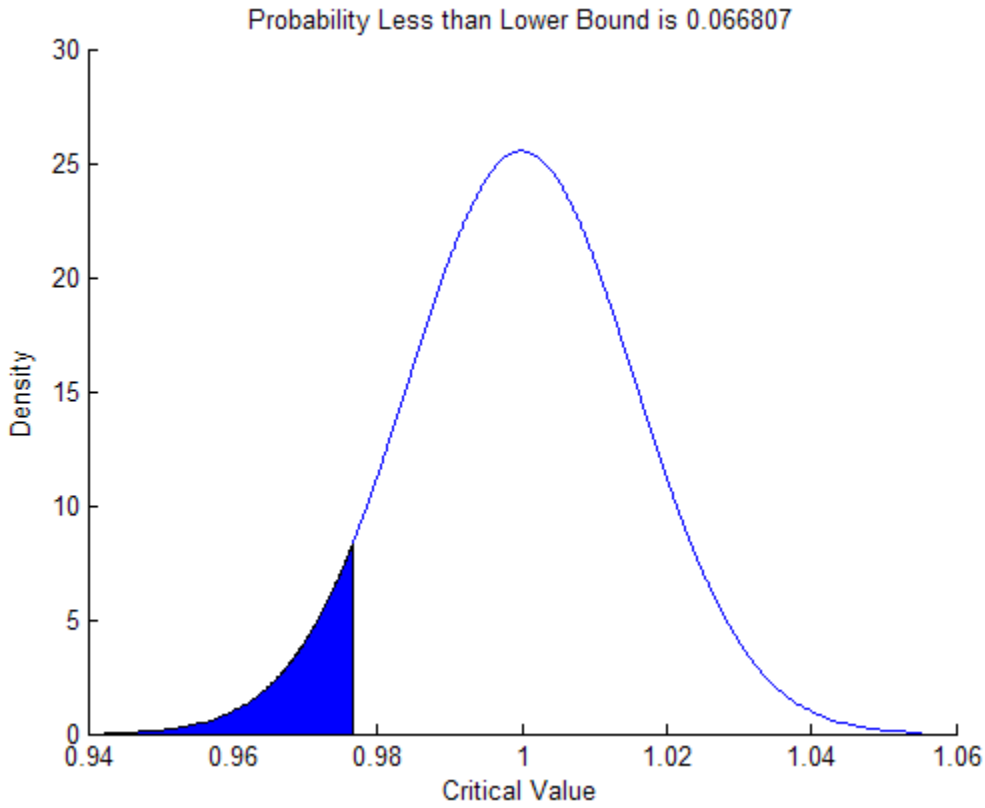
`p = normspec(...)` also returns the probability, `p`, of the shaded area.

`[p,h] = normspec(...)` also returns a handle `h` to the line objects.

Examples

A production process fills cans of paint. The average amount of paint in any can is 1 gallon, but variability in the process produces a standard deviation of 2 ounces (2/128 gallons). What is the probability that cans will be filled under specification by 3 or more ounces?

```
p = normspec([1-3/128,Inf],1,2/128,'outside')
p =
    0.0668
```



See Also `capaplot | histfit`

How To

- “Normal Distribution” on page B-83

Purpose

Normal mean and variance

Syntax

```
[M,V] = normstat(mu,sigma)
```

Description

`[M,V] = normstat(mu,sigma)` returns the mean of and variance for the normal distribution using the corresponding mean `mu` and standard deviation `sigma`. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `mu` or `sigma` is expanded to a constant array with the same dimensions as the other input.

The mean of the normal distribution with parameters μ and σ is μ, and the variance is σ^2.

Examples

```
n = 1:5;
[m,v] = normstat(n'*n,n'*n)
m =
   1   2   3   4   5
   2   4   6   8  10
   3   6   9  12  15
   4   8  12  16  20
   5  10  15  20  25

v =
   1   4   9  16  25
   4  16  36  64 100
   9  36  81 144 225
  16  64 144 256 400
  25 100 225 400 625
```

See Also

`normpdf` | `normcdf` | `norminv` | `normfit` | `normlike` | `normrnd`

How To

- "Normal Distribution" on page B-83

piecewisedistribution.nsegments

Purpose

Number of segments

Syntax

```
n = nsegments(obj)
```

Description

`n = nsegments(obj)` returns the number of segments `n` in the piecewise distribution object `obj`.

Examples

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);

n = nsegments(obj)
n =
     3
```

See Also

`paretotails` | `boundary` | `segment`

Purpose

Number of decision trees in ensemble

Description

The `NTrees` property is a scalar equal to the number of decision trees in the ensemble.

See Also

`Trees`

ProbDistParametric.NumParams property

Purpose

Read-only value specifying number of parameters of ProbDistParametric object

Description

`NumParams` is a read-only property of the `ProbDistParametric` class. `NumParams` is a value specifying the number of parameters of a distribution represented by a ProbDistParametric object.

Values

This value is an integer that counts both the specified parameters and parameters that are fit to the data. Use this information to view and compare the number of parameters supplied to create distributions.

Purpose

Number of elements in dataset array

Syntax

```
n = numel(A)
n = numel(A, varargin)
```

Description

`n = numel(A)` returns 1. To find the number of elements, `n`, in the dataset array `A`, use `prod(size(A))` or `numel(A,':',':')`.

`n = numel(A, varargin)` returns the number of subscripted elements, `n`, in `A(index1, index2, ..., indexn)`, where `varargin` is a cell array whose elements are `index1, index2, ... indexn`.

See Also

`length` | `size`

categorical.numel

Purpose

Number of elements in categorical array

Syntax

```
n = numel(A)
n = numel(A, varargin)
```

Description

`n = numel(A)` returns the number of elements in the categorical array `A`.

`n = numel(A, varargin)` returns the number of subscripted elements, `n`, in `A(index1, index2, ..., indexN)`, where `varargin` is a cell array whose elements are `index1, index2, ... indexN`.

See Also

`size`

Purpose

Number of nodes

Syntax

```
n = numnodes(t)
```

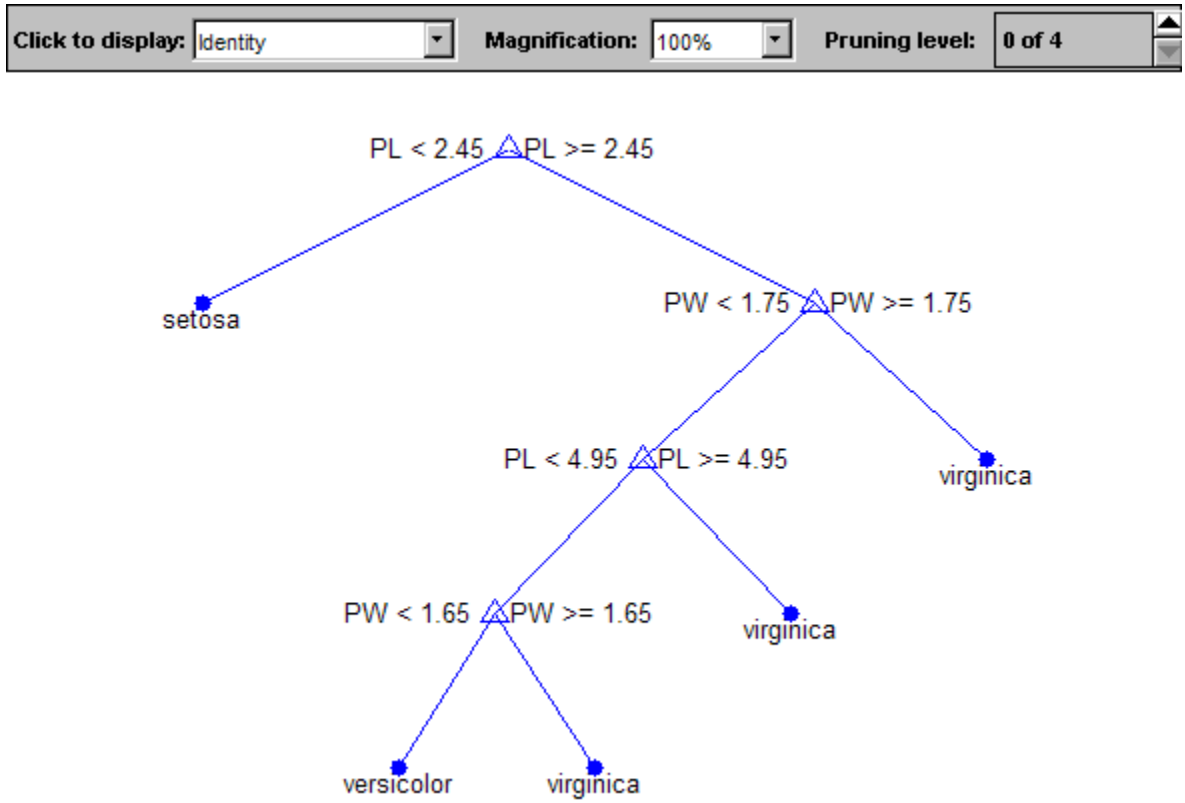
Description

`n = numnodes(t)` returns the number of nodes `n` in the tree `t`.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t=
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica
view(t)
```




```
n = numnodes(t)
n =
     9
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree`

Purpose

Number of test sets

Description

Value is the number of folds in partitions of type `'kfold'` and `'leaveout'`.

Value is `1` in partitions of type `'holdout'` and `'resubstitution'`.

TreeBagger.NVarToSample property

Purpose

Number of variables for random feature selection

Description

The `NVarToSample` property specifies the number of predictor or feature variables to select at random for each decision split. By default, it is set to the square root of the total number of variables for classification and one third of the total number of variables for regression. Setting this argument to any valid value except `'all'` invokes Breiman's "random forest" algorithm.

See Also

`classregtree`

Purpose

Cell array of nonempty, distinct strings giving names of observations in data set

Description

A cell array of nonempty, distinct strings giving the names of the observations in the data set. This property may be empty, but if not empty, the number of strings must equal the number of observations.

ClassificationBaggedEnsemble.oobEdge

Purpose

Out-of-bag classification edge

Syntax

```
edge = oobEdge(ens)
edge = oobEdge(ens,Name,Value)
```

Description

`edge = oobEdge(ens)` returns out-of-bag classification edge for `ens`.

`edge = oobEdge(ens,Name,Value)` computes classification edge with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A classification bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `ens.NTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NTrained`

`mode`

String representing the meaning of the output `L`:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.

- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`edge`

Classification edge, a weighted average of the classification margin.

Definitions

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in `ens.Prior`.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `ens.X`.

Out of Bag

Bagging, which stands for “bootstrap aggregation”, is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses

against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Examples

Find the out-of-bag edge for a bagged ensemble from the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'Bag',100,...
    'Tree','type','classification');
edge = oobEdge(ens)

edge =
    0.8730
```

See Also

`oobMargin` | `oobPredict` | `oobLoss`

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- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Out-of-bag error

Syntax

```
err = oobError(B)
err = oobError(B,'param1',val1,'param2',val2,...)
```

Description

`err = oobError(B)` computes the misclassification probability (for classification trees) or mean squared error (for regression trees) for out-of-bag observations in the training data, using the trained bagger `B`. `err` is a vector of length `NTrees`, where `NTrees` is the number of trees in the ensemble.

`err = oobError(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how `oobError` computes errors. If set to `'cumulative'` (default), the method computes cumulative errors and `err` is a vector of length `NTrees`, where the first element gives error from `trees(1)`, second element gives error from `trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `err` is a vector of length `NTrees`, where each element is an error from each tree in the ensemble. If set to `'ensemble'`, `err` is a scalar showing the cumulative error for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the

	first element gives error from `trees(1)`, the second element gives error from `trees(1:2)` etc.
`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. `oobError` uses these weights to combine output from the specified trees by taking a weighted average instead of the simple nonweighted majority vote. You cannot use this argument in the `'individual'` mode.

See Also

`CompactTreeBagger.error`

Purpose

Indicator matrix for out-of-bag observations

Description

The `OOBIndices` property is a logical array of size `Nobs`-by-`NTrees` where `Nobs` is the number of observations in the training data and `NTrees` is the number of trees in the ensemble. The `(I,J)` element is true if observation `I` is out-of-bag for tree `J` and false otherwise. In other words, a true value means observation `I` was not selected for the training data used to grow tree `J`.

See Also

`classregtree`

TreeBagger.OOBInstanceWeight property

Purpose

Count of out-of-bag trees for each observation

Description

The `OOBInstanceWeight` property is a numeric array of size `Nobs`-by-1 containing the number of trees used for computing out-of-bag response for each observation. `Nobs` is the number of observations in the training data used to create the ensemble.

Purpose

Out-of-bag classification error

Syntax

```
L = oobloss(ens)
L = oobloss(ens,Name,Value)
```

Description

`L = oobloss(ens)` returns the classification error for `ens` computed for out-of-bag data.

`L = oobloss(ens,Name,Value)` computes error with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A classification bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `NTrained`. `oobLoss` uses only these learners for calculating loss.

Default: `1:NTrained`

`lossfun`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See “Loss Functions” on page 20-1289
- `'classiferror'` — Fraction of misclassified data

- `'exponential'` — See "Loss Functions" on page 20-1289

You can write your own loss function in the syntax described in "Loss Functions" on page 20-1289.

Default: `'classiferror'`

`mode`

String representing the meaning of the output `L`:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`L`

Classification error of the out-of-bag observations, a scalar. `L` can be a vector, or can represent a different quantity, depending on the name-value settings.

Definitions

Out of Bag

Bagging, which stands for "bootstrap aggregation", is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.
- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of `X`.
- `K` is the number of classes in `tree`, represented in `tree.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `tree.ClassNames`.

- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` cost function uses a cost of `0` for correct classification, and `1` for misclassification. In other words, `'classiferror'` uses `COST=ones(K)-eye(K)`.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Find the out-of-bag error for a bagged ensemble from the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'Bag',100,...
    'Tree','type','classification');
L = oobLoss(ens)

L =
    0.0467
```

See Also

`loss` | `oobEdge` | `oobMargin` | `oobPredict`

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Purpose

Out-of-bag regression error

Syntax

```
L = oobLoss(ens)
L = oobLoss(ens,Name,Value)
```

Description

`L = oobLoss(ens)` returns the mean squared error for `ens` computed for out-of-bag data.

`L = oobLoss(ens,Name,Value)` computes error with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A regression bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `NTrained`. `oobLoss` uses only these learners for calculating loss.

Default: `1:NTrained`

`lossfun`

Function handle for loss function, or the string `'mse'`, meaning mean squared error. If you pass a function handle `fun`, `oobLoss` calls it as

```
FUN(Y,Yfit,W)
```

where `Y`, `Yfit`, and `W` are numeric vectors of the same length. `Y` is the observed response, `Yfit` is the predicted response, and `W` is the observation weights.

Default: `'mse'`

`mode`

String representing the meaning of the output `L`:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`L`

Mean squared error of the out-of-bag observations, a scalar. `L` can be a vector, or can represent a different quantity, depending on the name-value settings.

Definitions

Out of Bag

Bagging, which stands for "bootstrap aggregation", is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag"

observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Examples

Compute the out-of-bag error for the `carsmall` data:

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'bag',100,'Tree',...
    'type','regression');
L = oobLoss(ens)

L =
   17.0665
```

See Also

`oobPredict` | `loss`

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ClassificationBaggedEnsemble.oobMargin

Purpose

Out-of-bag classification margins

Syntax

```
margin = oobMargin(ens)
margin = oobMargin(ens,Name,Value)
```

Description

`margin = oobMargin(ens)` returns out-of-bag classification margins.

`margin = oobMargin(ens,Name,Value)` calculates margins with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A classification bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `ens.NTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NTrained`

Output Arguments

`margin`

A numeric column vector of length `size(ens.X,1)`.

Definitions

Out of Bag

Bagging, which stands for "bootstrap aggregation", is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with

replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `ens.X`.

Examples

Find the out-of-bag margin for a bagged ensemble from the Fisher iris data: Find how many elements of margin are equal to `1`.

```
load fisheriris
ens = fitensemble(meas,species,'Bag',100,...
    'Tree','type','classification');
margin = oobMargin(ens);
sum(margin == 1)

ans =
   108
```

See Also

`oobPredict` | `oobLoss` | `oobEdge` | `margin`

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- Chapter 13, “Nonparametric Supervised Learning”

TreeBagger.oobMargin

Purpose

Out-of-bag margins

Syntax

```
mar = oobMargin(B)
mar = oobMargin(B,'param1',val1,'param2',val2,...)
```

Description

`mar = oobMargin(B)` computes an `Nobs`-by-`NTrees` matrix of classification margins for out-of-bag observations in the training data, using the trained bagger `B`.

`mar = oobMargin(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how `oobMargin` computes errors. If set to `'cumulative'` (default), the method computes cumulative margins and `mar` is an `Nobs`-by-`NTrees` matrix, where the first column gives margins from `trees(1)`, second column gives margins from `trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is an `Nobs`-by-`NTrees` matrix, where each column gives margins from each tree in the ensemble. If set to `'ensemble'`, `mar` is a single column of length `Nobs` showing the cumulative margins for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If 'trees' is a numeric vector, the method returns an `Nobs`-by-`NTrees` matrix for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a single column for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first column gives

	margins from `trees(1)`, the second column gives margins from `trees(1:2)` etc.
`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. `oobMargin` uses these weights to combine output from the specified trees by taking a weighted average instead of the simple nonweighted majority vote. You cannot use this argument in the `'individual'` mode.

See Also

`CompactTreeBagger.margin`

TreeBagger.oobMeanMargin

Purpose

Out-of-bag mean margins

Syntax

```
mar = oobMeanMargin(B)
mar = oobMeanMargin(B,'param1',val1,'param2',val2,...)
```

Description

`mar = oobMeanMargin(B)` computes average classification margins for out-of-bag observations in the training data, using the trained bagger `B`. `oobMeanMargin` averages the margins over all out-of-bag observations. `mar` is a row-vector of length `NTrees`, where `NTrees` is the number of trees in the ensemble.

`mar = oobMeanMargin(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how `oobMargin` computes errors. If set to `'cumulative'` (default), is a vector of length NTrees where the first element gives mean margin from `trees(1)`, second column gives mean margins from `trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is a vector of length `NTrees`, where each element is a mean margin from each tree in the ensemble . If set to `'ensemble'`, `mar` is a scalar showing the cumulative mean margin for the entire ensemble .
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element gives mean margin from `trees(1)`, the second element gives mean margin from `trees(1:2)` etc.
`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. `oobMeanMargin` uses these weights to combine output from the specified trees by taking a weighted average instead of the simple nonweighted majority vote. You cannot use this argument in the `'individual'` mode.

See Also

`CompactTreeBagger.meanMargin`

TreeBagger.OOBPermutedVarCountRaiseMargin property

Purpose

Variable importance for raising margin

Description

The `OOBPermutedVarCountRaiseMargin` property is a numeric array of size 1-by-`Nvars` containing a measure of variable importance for each predictor. For any variable, the measure is the difference between the number of raised margins and the number of lowered margins if the values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble. This property is empty for regression trees.

TreeBagger.OOBPermutedVarDeltaError property

Purpose

Variable importance for prediction error

Description

The `OOBPermutedVarDeltaError` property is a numeric array of size 1-by-*Nvars* containing a measure of importance for each predictor variable (feature). For any variable, the measure is the increase in prediction error if the values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble.

TreeBagger.OOBPermutedVarDeltaMeanMargin property

Purpose

Variable importance for classification margin

Description

The `OOBPermutedVarDeltaMeanMargin` property is a numeric array of size 1-by-`Nvars` containing a measure of importance for each predictor variable (feature). For any variable, the measure is the decrease in the classification margin if the values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble. This property is empty for regression trees.

Purpose

Predict out-of-bag response of ensemble

Syntax

```
[label,score] = oobPredict(ens)
[label,score] = oobPredict(ens,Name,Value)
```

Description

`[label,score] = oobPredict(ens)` returns class labels and scores for `ens` for out-of-bag data.

`[label,score] = oobPredict(ens,Name,Value)` computes labels and scores with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A classification bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `ens.NTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NTrained`

Output Arguments

`label`

Classification labels of the same data type as the training data `Y`. There are `N` elements or rows, where `N` is the number of training observations. The label is the class with the highest score. In case of a tie, the label is earliest in `ens.ClassNames`.

`score`

An `N`-by-`K` numeric matrix for `N` observations and `K` classes. A high score indicates that an observation is likely to come from this class. Scores are in the range `0` to `1`.

Definitions

Out of Bag

Bagging, which stands for "bootstrap aggregation", is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Find the out-of-bag predictions and scores for the Fisher iris data. Find the scores in the range `(0.2,0.8)`; these are the scores where there is notable uncertainty in the resulting classifications.

```
load fisheriris
ens = fitensemble(meas,species,'Bag',100,...
    'Tree','type','classification');
[label score] = oobPredict(ens);
unsure = ( (score > .2) & (score < .8));
sum(sum(unsure)) % How many uncertain predictions?

ans =
    16
```

See Also

`oobMargin` | `oobPredict` | `oobLoss` | `oobEdge` | `predict`

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RegressionBaggedEnsemble.oobPredict

Purpose

Predict out-of-bag response of ensemble

Syntax

```
Yfit = oobPredict(ens)
Yfit = oobPredict(ens,Name,Value)
```

Description

`Yfit = oobPredict(ens)` returns the predicted responses for the out-of-bag data in `ens`.

`Yfit = oobPredict(ens,Name,Value)` predicts responses with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A regression bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `NTrained`. `oobLoss` uses only these learners for calculating loss.

Default: `1:NTrained`

Output Arguments

`Yfit`

A vector of predicted responses for out-of-bag data. `Yfit` has `size(ens.X,1)` elements.

You can find the indices of out-of-bag observations for weak learner `L` with the command

```
~ens.UseObsForLearner(:,L)
```

Definitions

Out of Bag

Bagging, which stands for "bootstrap aggregation", is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Examples

Compute out-of-bag predictions for the `carsmall` data. Look at the first three terms of the fit:

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'bag',100,'Tree',...
    'type','regression');
Yfit = oobPredict(ens);
Yfit(1:3) % first three terms

ans =
   15.7964
   14.7162
   14.8062
```

See Also

`oobLoss` | `predict`

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Purpose

Ensemble predictions for out-of-bag observations

Syntax

```
Y = oobPredict(B)
Y = oobPredict(B,'param1',val1,'param2',val2,...)
```

Description

`Y = oobPredict(B)` computes predicted responses using the trained bagger `B` for out-of-bag observations in the training data. The output has one prediction for each observation in the training data. The returned Y is a cell array of strings for classification and a numeric array for regression.

`Y = oobPredict(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'trees'`	Array of tree indices to use for computation of responses. Default is `'all'`.
`'treeweights'`	Array of `NTrees` weights for weighting votes from the specified trees.

See Also

`CompactTreeBagger.predict` | `OOBIndices`

ordinal

Superclasses

categorical

Purpose

Arrays for ordinal categorical data

Description

Ordinal arrays are used to store discrete values that have an ordering but are not numeric. An ordinal array provides efficient storage and convenient manipulation of such data, while also maintaining meaningful labels for the values. Ordinal arrays are often used as grouping variables.

Like a numerical array, an ordinal array can have any size or dimension. You can subscript, concatenate, reshape, sort, etc. ordinal arrays, much like ordinary numeric arrays. You can make comparisons between elements of two ordinal arrays, or between an ordinal array and a single string representing a ordinal value.

Construction

Use the `ordinal` constructor to create an ordinal array from a numeric, logical, or character array, or from a cell array of strings.

ordinal	Construct ordinal categorical array

Methods

Each ordinal array carries along a list of possible values that it can store, known as its levels. The list is created when you create an ordinal array, and you can access it using the `getlevels` method, or modify it using the `addlevels`, `mergelevels`, or `droplevels` methods. Assignment to the array will also add new levels automatically if the values assigned are not already levels of the array. The ordering on values stored in an ordinal array is defined by the order of the list of levels. You can change that order using the `reorderlevels` method.

The following table lists operations available for ordinal arrays.

ismember	Test for membership
mergelevels	Merge levels

sort	Sort elements of ordinal array
sortrows	Sort rows

Inherited Methods

Methods in the following table are inherited from `categorical`.

addlevels	Add levels to categorical array
cat	Concatenate categorical arrays
cellstr	Convert categorical array to cell array of strings
char	Convert categorical array to character array
circshift	Shift categorical array circularly
ctranspose	Transpose categorical matrix
disp	Display categorical array
display	Display categorical array
double	Convert categorical array to double array
droplevels	Drop levels
end	Last index in indexing expression for categorical array
flipdim	Flip categorical array along specified dimension
fliplr	Flip categorical matrix in left/right direction
flipud	Flip categorical matrix in up/down direction
getlabels	Access categorical array labels
getlevels	Get categorical array levels

hist	Plot histogram of categorical data
horzcat	Horizontal concatenation for categorical arrays
int16	Convert categorical array to signed 16-bit integer array
int32	Convert categorical array to signed 32-bit integer array
int64	Convert categorical array to signed 64-bit integer array
int8	Convert categorical array to signed 8-bit integer array
intersect	Set intersection for categorical arrays
ipermute	Inverse permute dimensions of categorical array
isempty	True for empty categorical array
isequal	True if categorical arrays are equal
islevel	Test for levels
ismember	True for elements of categorical array in set
isscalar	True if categorical array is scalar
isundefined	Test for undefined elements
isvector	True if categorical array is vector
length	Length of categorical array
levelcounts	Element counts by level
ndims	Number of dimensions of categorical array

numel	Number of elements in categorical array
permute	Permute dimensions of categorical array
reorderlevels	Reorder levels
repmat	Replicate and tile categorical array
reshape	Resize categorical array
rot90	Rotate categorical matrix 90 degrees
setdiff	Set difference for categorical arrays
setlabels	Label levels
setxor	Set exclusive-or for categorical arrays
shiftdim	Shift dimensions of categorical array
single	Convert categorical array to single array
size	Size of categorical array
squeeze	Squeeze singleton dimensions from categorical array
subsasgn	Subscripted assignment for categorical array
subsindex	Subscript index for categorical array
subsref	Subscripted reference for categorical array

summary	Summary statistics for categorical array
times	Product of categorical arrays
transpose	Transpose categorical matrix
uint16	Convert categorical array to unsigned 16-bit integers
uint32	Convert categorical array to unsigned 32-bit integers
uint64	Convert categorical array to unsigned 64-bit integers
uint8	Convert categorical array to unsigned 8-bit integers
union	Set union for categorical arrays
unique	Unique values in categorical array
vertcat	Vertical concatenation for categorical arrays

Properties

Inherited Properties

Properties in the following table are inherited from `categorical`.

labels	Text labels for levels
undeflabel	Text label for undefined levels

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

Examples

Create an ordinal array from integer data:

```
quality = ordinal([1 2 3; 3 2 1; 2 1 3],{'low' 'medium' 'high'})
```

```
% Find elements meeting a criterion
quality >= 'medium'
ismember(quality,{'low' 'high'})

% Compare two ordinal arrays
quality2 = fliplr(quality)
quality == quality2
```

References

[1] Johnson, N. L., S. Kotz, and A. W. Kemp, Univariate Discrete Distributions, 2nd edition, Wiley, 1992, pp. 124-130.

See Also

`histc` | `nominal`

ordinal

Purpose

Construct ordinal categorical array

Syntax

```
B = ordinal(A)
B = ordinal(A,labels)
B = ordinal(A,labels,levels)
B = ordinal(A,labels,[],edges)
```

Description

`B = ordinal(A)` creates an ordinal array `B` from the array `A`. `A` can be numeric, logical, character, categorical, or a cell array of strings. `ordinal` creates the levels of `B` from the sorted unique values in `A`, and creates default labels for them.

`B = ordinal(A,labels)` labels the levels in `B` using the character array or cell array of strings `labels`. `ordinal` assigns labels to levels in `B` in order according to the sorted unique values in `A`.

`B = ordinal(A,labels,levels)` creates an ordinal array with possible levels defined by `levels`. `levels` is a vector whose values can be compared to those in `A` using the equality operator. `ordinal` assigns labels to each level from the corresponding elements of `labels`. If `A` contains any values not present in `levels`, the levels of the corresponding elements of `B` are undefined. Use `[]` for `labels` to allow `ordinal` to create default labels.

`B = ordinal(A,labels,[],edges)` creates an ordinal array by binning the numeric array `A`, with bin edges given by the numeric vector `edges`. The uppermost bin includes values equal to the right-most edge. `ordinal` assigns labels to each level in `B` from the corresponding elements of `labels`. `edges` must have one more element than `labels`.

By default, an element of `B` is undefined if the corresponding element of `A` is `NaN` (when `A` is numeric), an empty string (when `A` is character), or undefined (when `A` is categorical). `ordinal` treats such elements as "undefined" or "missing" and does not include entries for them among the possible levels for `B`. To create an explicit level for such elements instead of treating them as undefined, you must use the `levels` input, and include `NaN`, the empty string, or an undefined element.

You may include duplicate labels in `labels` in order to merge multiple values in `A` into a single level in `B`.

Examples

Create an ordinal array from integer data, and provide explicit labels:

```
quality1 = ordinal([1 2 3; 3 2 1; 2 1 3],...
   {'low' 'medium' 'high'})
```

Create an ordinal array from integer data, and provide both explicit labels and an explicit order:

```
quality2 = ordinal([1 2 3; 3 2 1; 2 1 3],...
   {'high' 'medium' 'low'},[3 2 1])
```

Create an ordinal array by binning floating point values:

```
size = ordinal(rand(5,2),{'small' 'medium' 'large'},...
   [],[0 1/3 2/3 1])
```

Create an ordinal array from the measurements in Fisher's iris data, ignoring decimal lengths:

```
load fisheriris
m = floor(min(meas(:)));
M = floor(max(meas(:)));
labels = num2str((m:M)');
edges = m:M+1;
cms = ordinal(meas,labels,[],edges)

meas(1:5,:)
ans =
    5.1000    3.5000    1.4000    0.2000
    4.9000    3.0000    1.4000    0.2000
```

```
    4.7000    3.2000    1.3000    0.2000
    4.6000    3.1000    1.5000    0.2000
    5.0000    3.6000    1.4000    0.2000
cms(1:5,:)
ans =
     5     3     1     0
     4     3     1     0
     4     3     1     0
     4     3     1     0
     5     3     1     0
```

Create an age group ordinal array from the data in `hospital.mat`:

```
load hospital
edges = 0:10:100;
labels = strcat(num2str((0:10:90)','%d'),{'s'});
AgeGroup = ordinal(hospital.Age,labels,[],edges);

hospital.Age(1:5)
ans =
    38
    43
    38
    40
    49

AgeGroup(1:5)
ans =
     30s
     40s
     30s
     40s
     40s
```

See Also

`histc` | `nominal`

Purpose

Outlier measure for data

Syntax

```
out = outlierMeasure(B,X)
out = outlierMeasure(B,X,'param1',val1,'param2',val2,...)
```

Description

`out = outlierMeasure(B,X)` computes outlier measures for predictors `X` using trees in the ensemble `B`. The method computes the outlier measure for a given observation by taking an inverse of the average squared proximity between this observation and other observations. `outlierMeasure` then normalizes these outlier measures by subtracting the median of their distribution, taking the absolute value of this difference, and dividing by the median absolute deviation. A high value of the outlier measure indicates that this observation is an outlier.

You can supply the proximity matrix directly by using the `'data'` parameter.

`out = outlierMeasure(B,X,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'data'`	Flag indicating how to treat the `X` input argument. If set to `'predictors'` (default), the method assumes `X` is a matrix of predictors and uses it for computation of the proximity matrix. If set to `'proximity'`, the method treats `X` as a proximity matrix returned by the `proximity` method. If you do not supply the proximity matrix, `outlierMeasure` computes it internally. If you use the `proximity` method to compute a proximity matrix, supplying it as input to `outlierMeasure` reduces computing time.
`'labels'`	Vector of true class labels. True class labels can be either a numeric vector, character matrix, or cell array of strings. When you supply this parameter, the method performs the outlier calculation for any observations using only other observations from the same class. This parameter must specify one label for each observation (row) in `X`.

See Also

`proximity`

Purpose

Measure for determining outliers

Description

The `OutlierMeasure` property is a numeric array of size `Nobs`-by-1, where `Nobs` is the number of observations in the training data, containing outlier measures for each observation.

See Also

`CompactTreeBagger.outlierMeasure`

parallelcoords

Purpose

Parallel coordinates plot

Syntax

```
parallelcoords(X)
parallelcoords(X,...,'Standardize','on')
parallelcoords(X,...,'Standardize','PCA')
parallelcoords(X,...,'Standardize','PCAStd')
parallelcoords(X,...,'Quantile',alpha)
parallelcoords(X,...,'Group',group)
parallelcoords(X,...,'Labels',labels)
parallelcoords(X,...,PropertyName,PropertyValue,...)
h = parallelcoords(X,...)
parallelcoords(axes,...)
```

Description

`parallelcoords(X)` creates a parallel coordinates plot of the multivariate data in the n-by-p matrix `X`. Rows of `X` correspond to observations, columns to variables. A parallel coordinates plot is a tool for visualizing high dimensional data, where each observation is represented by the sequence of its coordinate values plotted against their coordinate indices. `parallelcoords` treats `NaN`s in `X` as missing values and does not plot those coordinate values.

`parallelcoords(X,...,'Standardize','on')` scales each column of `X` to have mean 0 and standard deviation 1 before making the plot.

`parallelcoords(X,...,'Standardize','PCA')` creates a parallel coordinates plot from the principal component scores of `X`, in order of decreasing eigenvalues. `parallelcoords` removes rows of `X` containing missing values (`NaN`s) for principal components analysis (PCA) standardization.

`parallelcoords(X,...,'Standardize','PCAStd')` creates a parallel coordinates plot using the standardized principal component scores.

`parallelcoords(X,...,'Quantile',alpha)` plots only the median and the `alpha` and `1-alpha` quantiles of $f(t)$ at each value of t. This is useful if `X` contains many observations.

`parallelcoords(X,...,'Group',group)` plots the data in different groups with different colors. Groups are defined by `group`, a numeric

array containing a group index for each observation. (See "Grouped Data" on page 2-34.) `group` can also be a categorical variable, character matrix, or cell array of strings, containing a group name for each observation.

`parallelcoords(X,...,'Labels',labels)` labels the coordinate tick marks along the horizontal axis using `labels`, a character array or cell array of strings.

`parallelcoords(X,...,`*`PropertyName`*`,`*`PropertyValue`*`,...)` sets properties to the specified property values for all line graphics objects created by `parallelcoords`.

`h = parallelcoords(X,...)` returns a column vector of handles to the line objects created by parallelcoords, one handle per row of `X`. If you use the `'Quantile'` input argument, `h` contains one handle for each of the three lines objects created. If you use both the `'Quantile'` and the `'Group'` input arguments, `h` contains three handles for each group.

`parallelcoords(axes,...)` plots into the axes with handle `axes`.

Examples

```
% Make a grouped plot of the raw data
load fisheriris
labels = {'Sepal Length','Sepal Width',...
          'Petal Length','Petal Width'};
parallelcoords(meas,'group',species,'labels',labels);

% Plot only the median and quartiles of each group
parallelcoords(meas,'group',species,'labels',labels,...
               'quantile',.25);
```

See Also

`andrewsplot` | `glyphplot`

How To

- "Grouped Data" on page 2-34

ProbDistUnivParam.paramci

Purpose

Return parameter confidence intervals of ProbDistUnivParam object

Syntax

```
CI = paramci(PD)
CI = paramci(PD, Alpha)
```

Description

`CI = paramci(PD)` returns `CI`, a 2-by-`N` array containing 95% confidence intervals for the parameters of the `ProbDistUnivParam` object `PD`. `N` is the number of parameters in the distribution. When you create `PD` by specifying parameters (such as using the `ProbDistUnivParam.ProbDistUnivParam` constructor or using the `fitdist` function and specifying a `'binomial'` or `'generalized pareto'` distribution) rather than by fitting to data, the confidence intervals have a width of `0` because the parameters are viewed as estimates of an unknown parameter.

`CI = paramci(PD, Alpha)` returns `100*(1 - Alpha)`% confidence intervals. Default `Alpha` is `0.05`, which specifies 95% confidence intervals.

Note If you create `PD` with a distribution that does not support confidence intervals, then `CI` contains `NaN` values.

Input Arguments

`PD`	An object of the class `ProbDistUnivParam`.
`Alpha`	A value between `0` and `1` that specifies a confidence interval. Default is `0.05`, which specifies 95% confidence intervals.

Output Arguments

`CI`	A 2-by-`N` array containing `100*(1 - Alpha)`% confidence intervals for the parameters of the `ProbDistUnivParam` object `PD`. `N` is the number of parameters in the distribution.

See Also

`fitdist`

ProbDistParametric.ParamCov property

Purpose

Read-only covariance matrix of parameter estimates of ProbDistParametric object

Description

`ParamCov` is a read-only property of the `ProbDistParametric` class. `ParamCov` is a covariance matrix containing the parameter estimates of a distribution represented by a ProbDistParametric object. `ParamCov` has a size of `NumParams`-by-`NumParams`.

Values

This covariance matrix includes estimates for both the specified parameters and parameters that are fit to the data. For specified parameters, the covariance is `0`, indicating the parameter is known exactly. Use this information to view and compare the descriptions of parameters supplied to create distributions.

ProbDistParametric.ParamDescription property

Purpose

Read-only cell array specifying descriptions of parameters of ProbDistParametric object

Description

`ParamDescription` is a read-only property of the `ProbDistParametric` class. `ParamDescription` is a cell array of strings specifying the descriptions or meanings of the parameters of a distribution represented by a ProbDistParametric object. `ParamDescription` has a length of `NumParams`.

Values

This cell array includes a brief description of the meaning of both the specified parameters and parameters that are fit to the data. The description is the same as the parameter name when no further description information is available. Use this information to view and compare the descriptions of parameters used to create distributions.

ProbDistParametric.ParamIsFixed property

Purpose

Read-only logical array specifying fixed parameters of ProbDistParametric object

Description

`ParamIsFixed` is a read-only property of the `ProbDistParametric` class. `ParamIsFixed` is a logical array specifying the fixed parameters of a distribution represented by a ProbDistParametric object. `ParamIsFixed` has a length of `NumParams`.

Values

This array specifies a `1` (`true`) for fixed parameters, and a `0` (`false`) for parameters that are estimated from the input data. Use this information to view and compare the fixed parameters used to create distributions.

Purpose

Read-only cell array specifying names of parameters of ProbDistParametric object

Description

`ParamNames` is a read-only property of the `ProbDistParametric` class. `ParamNames` is a cell array of strings specifying the names of the parameters of a distribution represented by a ProbDistParametric object. `ParamNames` has a length of `NumParams`.

Values

This cell array includes the names of both the specified parameters and parameters that are fit to the data. Use this information to view and compare the names of parameters used to create distributions.

NaiveBayes.Params property

Purpose

Parameter estimates

Description

The `Params` property is an `NClasses`-by-`NDims` cell array containing the parameter estimates, excluding the class priors. `Params(i,j)` contains the parameter estimates for the `j`th feature in the `i`th class. `Params(i,j)` is an empty cell if the `i`th class is empty.

The entry in `Params(i,j)` depends on the distribution type used for the `j`th feature, as follows:

`'normal'`	A vector of length two. The first element is the mean, and the second element is standard deviation.
`'kernel'`	A `ProbDistUnivKernel` object
`'mvmn'`	A vector containing the probability for each possible value of the `j`th feature in the `i`th class. The order of the probabilities is decided by the sorted order of all the unique values of the `j`th feature.
`'mn'`	A scalar representing the probability the `j`th token appearing in the `i`th class, `Prob(token j | class i)`. It is estimated as `(1 + the number of occurrence of token J in class I)/(NDims + the total number of token occurrence in class I)`.

Purpose

Read-only array specifying values of parameters of ProbDistParametric object

Description

`Params` is a read-only property of the `ProbDistParametric` class. `Params` is an array of values specifying the values of the parameters of a distribution represented by a ProbDistParametric object. `Params` has a length of `NumParams`.

Values

This array includes the values of both the specified parameters and parameters that are fit to the data. Use this information to view and compare the values of parameters used to create distributions.

classregtree.parent

Purpose

Parent node

Syntax

```
p = parent(t)
p = parent(t,nodes)
```

Description

`p = parent(t)` returns an n-element vector `p` containing the number of the parent node for each node in the tree `t`, where n is the number of nodes. The parent of the root node is `0`.

`p = parent(t,nodes)` takes a vector `nodes` of node numbers and returns the parent nodes for the specified nodes.

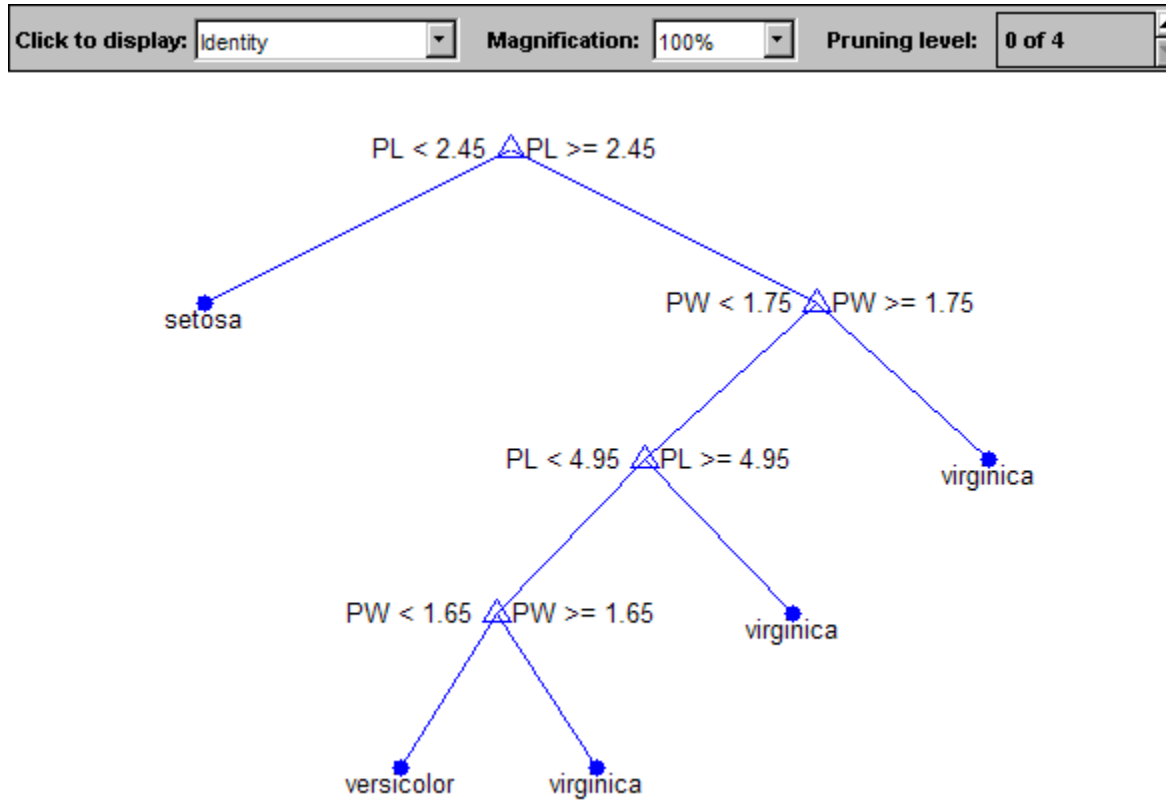
Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 else node 3
2  class = setosa
3  if PW<1.75 then node 4 else node 5
4  if PL<4.95 then node 6 else node 7
5  class = virginica
6  if PW<1.65 then node 8 else node 9
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
p = parent(t)
p =
     0
     1
     1
     3
     3
     4
     4
     6
```

```
6
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `children` | `numnodes`

Purpose

Pareto chart

Syntax

```
pareto(y,names)
[h,ax] = pareto(...)
```

Description

`pareto(y,names)` displays a Pareto chart where the values in the vector y are drawn as bars in descending order. Each bar is labeled with the associated value in the string matrix or cell array, `names`. `pareto(y)` labels each bar with the index of the corresponding element in `y`.

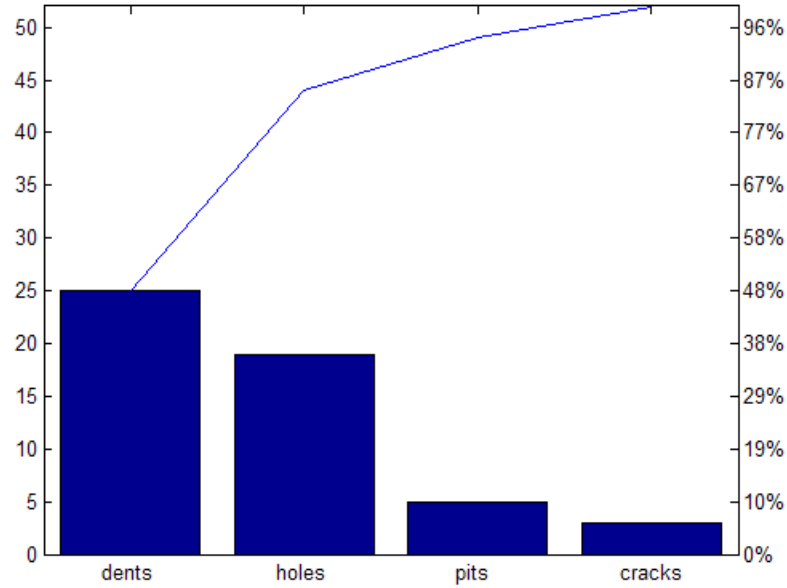
The line above the bars shows the cumulative percentage.

`[h,ax] = pareto(...)` returns a combination of patch and line object handles to the two axes created in `ax`.

Examples

Create a Pareto chart from data measuring the number of manufactured parts rejected for various types of defects.

```
defects = {'pits';'cracks';'holes';'dents'};
quantity = [5 3 19 25];
pareto(quantity,defects)
```



See Also

`bar` | `hist`

Superclasses

piecewisedistribution

Purpose

Empirical distributions with Pareto tails

Construction

paretotails	Construct Pareto tails object

Methods

lowerparams	Lower Pareto tails parameters
upperparams	Upper Pareto tails parameters

Inherited Methods

Methods in the following table are inherited from `piecewisedistribution`.

boundary	Piecewise distribution boundaries
cdf	Cumulative distribution function for piecewise distribution
disp	Display piecewisedistribution object
display	Display piecewisedistribution object
icdf	Inverse cumulative distribution function for piecewise distribution
nsegments	Number of segments
pdf	Probability density function for piecewise distribution
random	Random numbers from piecewise distribution
segment	Segments containing values

Properties

Objects of the `paretotails` class have no properties accessible by dot indexing, `get` methods, or `set` methods. To obtain information about a `paretotails` object, use the appropriate method.

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

How To

- "Generalized Pareto Distribution" on page B-37

Purpose

Construct Pareto tails object

Syntax

```
obj = paretotails(x,pl,pu)
obj = paretotails(x,pl,pu,cdffun)
```

Description

`obj = paretotails(x,pl,pu)` creates an object `obj` defining a distribution consisting of the empirical distribution of `x` in the center and Pareto distributions in the tails. `x` is a real-valued vector of data values whose extreme observations are fit to generalized Pareto distributions (GPDs). `pl` and `pu` identify the lower- and upper-tail cumulative probabilities such that `100*pl` and `100*(1-pu)` percent of the observations in `x` are, respectively, fit to a GPD by maximum likelihood. If `pl` is `0`, or if there are not at least two distinct observations in the lower tail, then no lower Pareto tail is fit. If `pu` is `1`, or if there are not at least two distinct observations in the upper tail, then no upper Pareto tail is fit.

`obj = paretotails(x,pl,pu,cdffun)` uses *`cdffun`* to estimate the cdf of `x` between the lower and upper tail probabilities. *`cdffun`* may be any of the following:

- `'ecdf'` — Uses an interpolated empirical cdf, with data values as the midpoints in the vertical steps in the empirical cdf, and computed by linear interpolation between data values. This is the default.
- `'kernel'` — Uses a kernel-smoothing estimate of the cdf.
- `@fun` — Uses a handle to a function of the form `[p,xi] = fun(x)` that accepts the input data vector `x` and returns a vector `p` of cdf values and a vector `xi` of evaluation points. Values in `xi` must be sorted and distinct but need not equal the values in `x`.

`cdffun` is used to compute the quantiles corresponding to `pl` and `pu` by inverse interpolation, and to define the fitted distribution between these quantiles.

The output object `obj` is a Pareto tails object with methods to evaluate the cdf, inverse cdf, and other functions of the fitted distribution. These methods are well-suited to copula and other Monte Carlo simulations.

The pdf method in the tails is the GPD density, but in the center it is computed as the slope of the interpolated cdf.

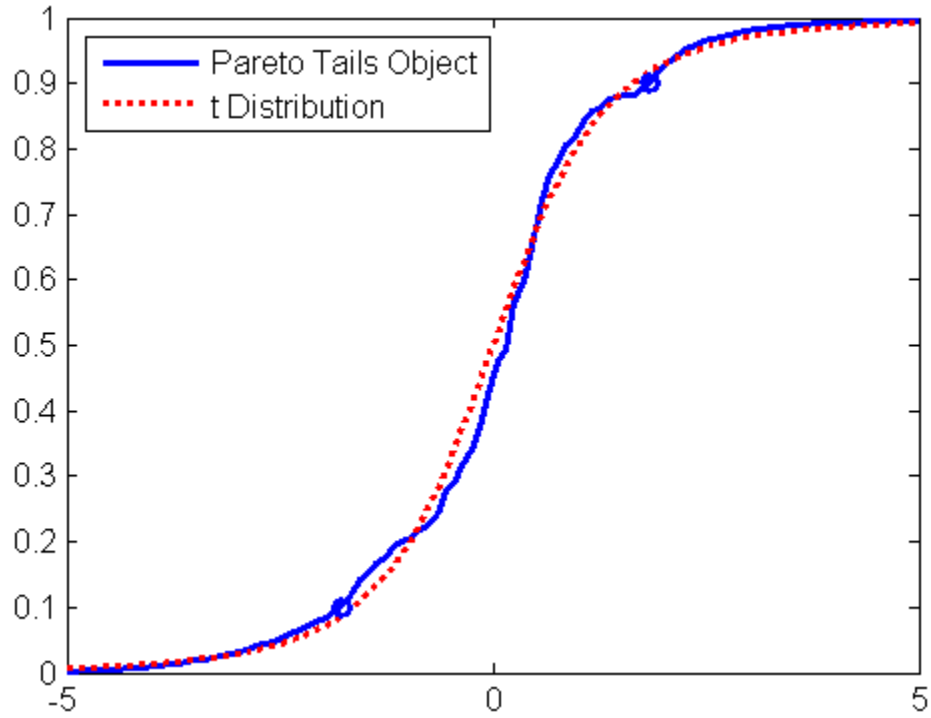
The `paretotails` class is a subclass of the `piecewisedistribution` class, and many of its methods are derived from that class.

Examples

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);
[p,q] = boundary(obj);

x = linspace(-5,5);
plot(x,cdf(obj,x),'b-','LineWidth',2)
hold on
plot(x,tcdf(x,3),'r:','LineWidth',2)
plot(q,p,'bo','LineWidth',2,'MarkerSize',5)
legend('Pareto Tails Object','t Distribution',...
       'Location','NW')
```



See Also

`cdf` | `ecdf` | `gpfit` | `icdf` | `ksdensity`

partialcorr

Purpose

Linear or rank partial correlation coefficients

Syntax

```
RHO = partialcorr(X)
RHO = partialcorr(X,Z)
RHO = partialcorr(X,Y,Z)
[RHO,PVAL] = partialcorr(...)
[...] = partialcorr(...,param1,val1,param2,val2,...)
```

Description

`RHO = partialcorr(X)` returns the sample linear partial correlation coefficients between pairs of variables in `X`, controlling for the remaining variables in `X`. `X` is an n-by-p matrix, with rows corresponding to observations, and columns corresponding to variables. `RHO` is a symmetric p-by-p matrix, where the (i,j)-th entry is the sample linear partial correlation between the i-th and j-th columns in `X`.

`RHO = partialcorr(X,Z)` returns the sample linear partial correlation coefficients between pairs of variables in `X` controlling for the variables in `Z`. `X` is an n-by-p matrix, and `Z` is an n-by-q matrix with rows corresponding to observations, and columns corresponding to variables. The output, `RHO`, is a symmetric p-by-p matrix.

`RHO = partialcorr(X,Y,Z)` returns the sample linear partial correlation coefficients between pairs of variables between `X` and `Y`, controlling for the variables in `Z`. `X` is an n-by-p_1 matrix, `Y` an n-by-p_2 matrix, and `Z` is an n-by-q matrix, with rows corresponding to observations, and columns corresponding to variables. `RHO` is a p_1-by-p_2 matrix, where the (i, j)th entry is the sample linear partial correlation between the ith column in `X` and the jth column in `Y`.

If the covariance matrix of `[X,Z]` is

$$S = \begin{pmatrix} S_{11} & S_{12} \\ {S_{12}}^T & S_{22} \end{pmatrix}$$

then the partial correlation matrix of `X`, controlling for `Z`, can be defined formally as a normalized version of the covariance matrix $S_{xy} = S_{11} - (S_{12}{S_{22}}^{-1}{S_{12}}^T)$

`[RHO,PVAL] = partialcorr(...)` also returns `PVAL`, a matrix of *p*-values for testing the hypothesis of no partial correlation against the alternative that there is a nonzero partial correlation. Each element of `PVAL` is the *p* value for the corresponding element of `RHO`. If `PVAL(I,J)` is small, say less than 0.05, then the partial correlation, `RHO(I,J)`, is significantly different from zero.

`[...] = partialcorr(...,param1,val1,param2,val2,...)` specifies additional parameters and their values. Valid parameter/value pars are listed in the following table.

Parameter	Values
`'type'`	• `'Pearson'` — To compute Pearson (linear) partial correlations. This is the default. • `'Spearman'` — To compute Spearman (rank) partial correlations.
`'rows'`	• `'all'` — To use all rows regardless of missing (`NaN`) values. This is the default. • `'complete'` — To use only rows with no missing values. • `'pairwise'` — To compute `RHO(I,J)` using rows with no missing values in column `I` or `J`.
`'tail'` The alternative hypothesis against which to compute *p*-values for testing the hypothesis of no partial correlation.	• `'both'` (the default) — the correlation is not zero. • `'right'` — the correlation is greater than zero. • `'left'` — the correlation is less than zero.

A 'pairwise' value for the rows parameter can produce a RHO that is not positive definite. A 'complete' value always produces a positive definite RHO, but when data is missing, the estimates will be based on fewer observations, in general.

partialcorr computes *p*-values for linear and rank partial correlations using a Student's *t* distribution for a transformation of the correlation. This is exact for linear partial correlation when X and Z are normal, but is a large-sample approximation otherwise.

See Also

corr | tiedrank | corrcoef

Purpose

Principal component analysis on covariance matrix

Syntax

```
COEFF = pcacov(V)
[COEFF,latent] = pcacov(V)
[COEFF,latent,explained] = pcacov(V)
```

Description

`COEFF = pcacov(V)` performs principal components analysis on the p-by-p covariance matrix `V` and returns the principal component coefficients, also known as loadings. `COEFF` is a p-by-p matrix, with each column containing coefficients for one principal component. The columns are in order of decreasing component variance.

`pcacov` does not standardize `V` to have unit variances. To perform principal components analysis on standardized variables, use the correlation matrix `R = V./(SD*SD')`, where `SD = sqrt(diag(V))`, in place of `V`. To perform principal components analysis directly on the data matrix, use `princomp`.

`[COEFF,latent] = pcacov(V)` returns `latent`, a vector containing the principal component variances, that is, the eigenvalues of `V`.

`[COEFF,latent,explained] = pcacov(V)` returns `explained`, a vector containing the percentage of the total variance explained by each principal component.

Examples

```
load hald
covx = cov(ingredients);
[COEFF,latent,explained] = pcacov(covx)
COEFF =
  0.0678 -0.6460  0.5673 -0.5062
  0.6785 -0.0200 -0.5440 -0.4933
 -0.0290  0.7553  0.4036 -0.5156
 -0.7309 -0.1085 -0.4684 -0.4844

latent =
  517.7969
  67.4964
  12.4054
```

```
    0.2372

explained =
   86.5974
   11.2882
    2.0747
    0.0397
```

References

[1] Jackson, J. E. *A User's Guide to Principal Components*. Hoboken, NJ: John Wiley and Sons, 1991.

[2] Jolliffe, I. T. *Principal Component Analysis*. 2nd ed., New York: Springer-Verlag, 2002.

[3] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

[4] Seber, G. A. F., *Multivariate Observations*, Wiley, 1984.

See Also

`barttest` | `biplot` | `factoran` | `pcares` | `princomp` | `rotatefactors`

Purpose

Residuals from principal component analysis

Syntax

```
residuals = pcares(X,ndim)
[residuals,reconstructed] = pcares(X,ndim)
```

Description

`residuals = pcares(X,ndim)` returns the `residuals` obtained by retaining `ndim` principal components of the n-by-p matrix `X`. Rows of `X` correspond to observations, columns to variables. `ndim` is a scalar and must be less than or equal to p. `residuals` is a matrix of the same size as `X`. Use the data matrix, *not* the covariance matrix, with this function.

`pcares` does not normalize the columns of X. To perform the principal components analysis based on standardized variables, that is, based on correlations, use `pcares(zscore(X), ndim)`. You can perform principal components analysis directly on a covariance or correlation matrix, but without constructing residuals, by using `pcacov`.

`[residuals,reconstructed] = pcares(X,ndim)` returns the reconstructed observations; that is, the approximation to `X` obtained by retaining its first `ndim` principal components.

Examples

This example shows the drop in the residuals from the first row of the Hald data as the number of component dimensions increases from one to three.

```
load hald
r1 = pcares(ingredients,1);
r2 = pcares(ingredients,2);
r3 = pcares(ingredients,3);

r11 = r1(1,:)
r11 =
  2.0350  2.8304  -6.8378  3.0879

r21 = r2(1,:)
r21 =
  -2.4037  2.6930  -1.6482  2.3425
```

```
r31 = r3(1,:)
r31 =
  0.2008  0.1957  0.2045  0.1921
```

References

[1] Jackson, J. E., *A User's Guide to Principal Components*, John Wiley and Sons, 1991.

[2] Jolliffe, I. T., *Principal Component Analysis*, 2nd Edition, Springer, 2002.

[3] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

[4] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

See Also

`factoran` | `pcacov` | `princomp`

Purpose

Input vector of mixing proportions

Description

Optional input vector of mixing proportions `p`, or its default value.

pdf

Purpose

Probability density functions

Syntax

```
Y = pdf(name,X,A)
Y = pdf(name,X,A,B)
Y = pdf(name,X,A,B,C)
```

Description

`Y = pdf(name,X,A)` computes the probability density function for the one-parameter family of distributions specified by `name`. Parameter values for the distribution are given in `A`. Densities are evaluated at the values in `X` and returned in `Y`.

If `X` and `A` are arrays, they must be the same size. If `X` is a scalar, it is expanded to a constant matrix the same size as `A`. If `A` is a scalar, it is expanded to a constant matrix the same size as `X`.

`Y` is the common size of `X` and `A` after any necessary scalar expansion.

`Y = pdf(name,X,A,B)` computes the probability density function for two-parameter families of distributions, where parameter values are given in `A` and `B`.

If `X`, `A`, and `B` are arrays, they must be the same size. If `X` is a scalar, it is expanded to a constant matrix the same size as `A` and `B`. If either `A` or `B` are scalars, they are expanded to constant matrices the same size as `X`.

`Y` is the common size of `X`, `A`, and `B` after any necessary scalar expansion.

`Y = pdf(name,X,A,B,C)` computes the probability density function for three-parameter families of distributions, where parameter values are given in `A`, `B`, and `C`.

If `X`, `A`, `B`, and `C` are arrays, they must be the same size. If `X` is a scalar, it is expanded to a constant matrix the same size as `A`, `B`, and `C`. If any of `A`, `B` or `C` are scalars, they are expanded to constant matrices the same size as `X`.

`Y` is the common size of `X`, `A`, `B` and `C` after any necessary scalar expansion.

Acceptable strings for `name` are:

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'beta' or 'Beta'	"Beta Distribution" on page B-4	a	b	—
'bino' or 'Binomial'	"Binomial Distribution" on page B-7	n: number of trials	p: probability of success for each trial	—
'chi2' or 'Chisquare'	"Chi-Square Distribution" on page B-12	ν: degrees of freedom	—	—
'exp' or 'Exponential'	"Exponential Distribution" on page B-16	μ: mean	—	—
'ev' or 'Extreme Value'	"Extreme Value Distribution" on page B-19	μ: location parameter	σ: scale parameter	—
'f' or 'F'	"F Distribution" on page B-25	$\nu 1$: numerator degrees of freedom	$\nu 2$: denominator degrees of freedom	—
'gam' or 'Gamma'	"Gamma Distribution" on page B-27	a: shape parameter	b: scale parameter	—
'gev' or 'Generalized Extreme Value'	"Generalized Extreme Value Distribution" on page B-32	k: shape parameter	σ: scale parameter	μ: location parameter
'gp' or 'Generalized Pareto'	"Generalized Pareto Distribution" on page B-37	k: tail index (shape) parameter	σ: scale parameter	μ: threshold (location) parameter

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'geo' or 'Geometric'	"Geometric Distribution" on page B-41	p: probability parameter	—	—
'hyge' or 'Hypergeometric'	"Hypergeometric Distribution" on page B-43	M: size of the population	K: number of items with the desired characteristic in the population	n: number of samples drawn
'logn' or 'Lognormal'	"Lognormal Distribution" on page B-51	μ	σ	—
'nbin' or 'Negative Binomial'	"Negative Binomial Distribution" on page B-72	r: number of successes	p: probability of success in a single trial	—
'ncf' or 'Noncentral F'	"Noncentral F Distribution" on page B-78	ν1: numerator degrees of freedom	ν2: denominator degrees of freedom	δ: noncentrality parameter
'nct' or 'Noncentral t'	"Noncentral t Distribution" on page B-80	ν: degrees of freedom	δ: noncentrality parameter	—
'ncx2' or 'Noncentral Chi-square'	"Noncentral Chi-Square Distribution" on page B-76	ν: degrees of freedom	δ: noncentrality parameter	—
'norm' or 'Normal'	"Normal Distribution" on page B-83	μ: mean	σ: standard deviation	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'poiss' or 'Poisson'	"Poisson Distribution" on page B-89	λ: mean	—	—
'rayl' or 'Rayleigh'	"Rayleigh Distribution" on page B-91	b: scale parameter	—	—
't' or 'T'	"Student's t Distribution" on page B-95	ν: degrees of freedom	—	—
'unif' or 'Uniform'	"Uniform Distribution (Continuous)" on page B-99	a: lower endpoint (minimum)	b: upper endpoint (maximum)	—
'unid' or 'Discrete Uniform'	"Uniform Distribution (Discrete)" on page B-101	N: maximum observable value	—	—
'wbl' or 'Weibull'	"Weibull Distribution" on page B-103	a: scale parameter	b: shape parameter	—

Examples

Compute the pdf of the normal distribution with mean 0 and standard deviation 1 at inputs –2, –1, 0, 1, 2:

```
p1 = pdf('Normal',-2:2,0,1)
p1 =
  0.0540   0.2420   0.3989   0.2420   0.0540
```

The order of the parameters is the same as for `normpdf`.

Compute the pdfs of Poisson distributions with rate parameters 0, 1, ..., 4 at inputs 1, 2, ..., 5, respectively:

```
p2 = pdf('Poisson',0:4,1:5)
p2 =
  0.3679  0.2707  0.2240  0.1954  0.1755
```

The order of the parameters is the same as for `poisspdf`.

See Also

`cdf` | `icdf` | `mle` | `random`

Purpose

Probability density function for Gaussian mixture distribution

Syntax

```
y = pdf(obj,X)
```

Description

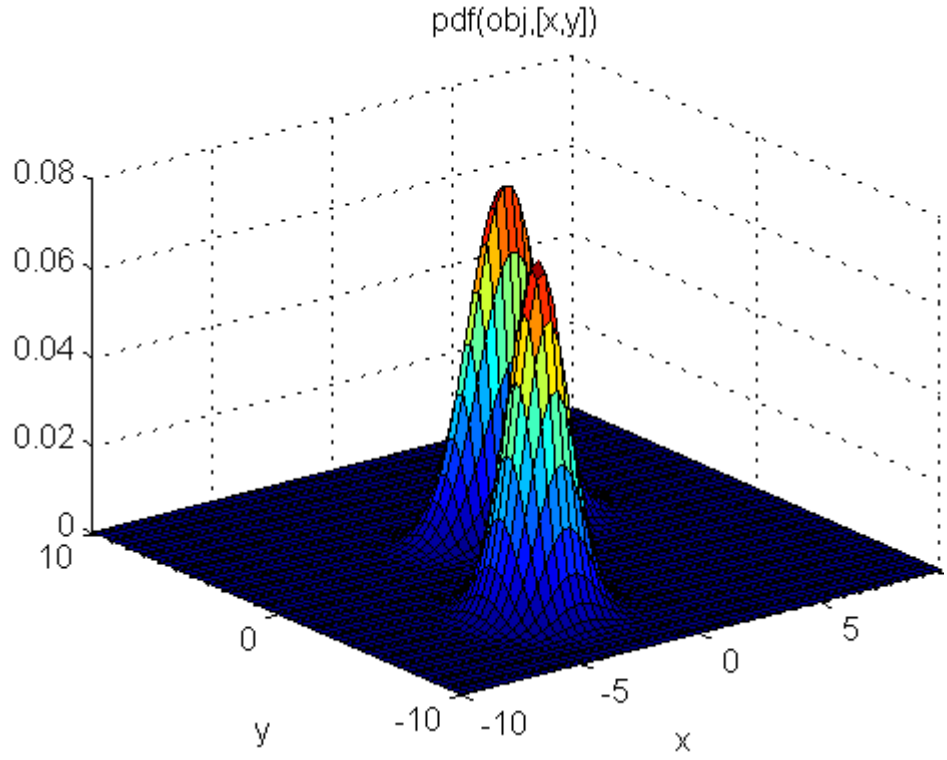
`y = pdf(obj,X)` returns a vector `y` of length n containing the values of the probability density function (pdf) for the `gmdistribution` object `obj`, evaluated at the n-by-d data matrix `X`, where n is the number of observations and d is the dimension of the data. `obj` is an object created by `gmdistribution` or `fit`. `y(I)` is the pdf of observation `I`.

Examples

Create a `gmdistribution` object defining a two-component mixture of bivariate Gaussian distributions:

```
MU = [1 2;-3 -5];
SIGMA = cat(3,[2 0;0 .5],[1 0;0 1]);
p = ones(1,2)/2;
obj = gmdistribution(MU,SIGMA,p);

ezsurf(@(x,y)pdf(obj,[x y]),[-10 10],[-10 10])
```



See Also `gmdistribution | fit | cdf | mvnpdf`

Purpose

Probability density function for piecewise distribution

Syntax

```
P = pdf(obj,X)
```

Description

`P = pdf(obj,X)` returns an array `P` of values of the probability density function for the piecewise distribution object `obj`, evaluated at the values in the array `X`.

Note For a Pareto tails object, the pdf is computed using the generalized Pareto distribution in the tails. In the center, the pdf is computed using the slopes of the cdf, which are interpolated between a set of discrete values. Therefore the pdf in the center is piecewise constant. It is noisy for a *`cdffun`* specified in `paretotails` via the `'ecdf'` option, and somewhat smoother for the `'kernel'` option, but generally not a good estimate of the underlying density of the original data.

Examples

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);
[p,q] = boundary(obj)
p =
    0.1000
    0.9000
q =
   -1.7766
    1.8432

pdf(obj,q)
ans =
    0.2367
    0.1960
```

See Also paretotails | cdf

Purpose

Return probability density function (PDF) for ProbDist object

Syntax

```
Y = pdf(PD, X)
```

Description

`Y = pdf(PD, X)` returns `Y`, an array containing the probability density function (PDF) for the ProbDist object `PD`, evaluated at values in `X`.

Input Arguments

`PD`	An object of the class `ProbDistUnivParam` or `ProbDistUnivKernel`.
`X`	A numeric array of values where you want to evaluate the PDF.

Output Arguments

`Y`	An array containing the probability density function (PDF) for the ProbDist object `PD`.

See Also

`pdf`

Purpose

Pairwise distance between pairs of objects

Syntax

```
D = pdist(X)
D = pdist(X,distance)
```

Description

`D = pdist(X)` computes the Euclidean distance between pairs of objects in m-by-n data matrix `X`. Rows of `X` correspond to observations, and columns correspond to variables. `D` is a row vector of length $m(m-1)/2$, corresponding to pairs of observations in `X`. The distances are arranged in the order (2,1), (3,1), ..., (m,1), (3,2), ..., (m,2), ..., (m,m–1)). `D` is commonly used as a dissimilarity matrix in clustering or multidimensional scaling.

To save space and computation time, `D` is formatted as a vector. However, you can convert this vector into a square matrix using the `squareform` function so that element i, j in the matrix, where $i < j$, corresponds to the distance between objects i and j in the original data set.

`D = pdist(X,distance)` computes the distance between objects in the data matrix, `X`, using the method specified by *`distance`*, which can be any of the following character strings.

Metric	Description
`'euclidean'`	Euclidean distance (default).
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between rows in X is scaled by dividing by the corresponding element of the standard deviation `S=nanstd(X)`. To specify another value for `S`, use `D=pdist(X,'seuclidean',S)`.
`'cityblock'`	City block metric.
`'minkowski'`	Minkowski distance. The default exponent is 2. To specify a different exponent, use `D = pdist(X,'minkowski',P)`, where `P` is a scalar positive value of the exponent.

Metric	Description
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'mahalanobis'`	Mahalanobis distance, using the sample covariance of `X` as computed by `nancov`. To compute the distance with a different covariance, use `D = pdist(X,'mahalanobis',C)`, where the matrix `C` is symmetric and positive definite.
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors).
`'correlation'`	One minus the sample correlation between points (treated as sequences of values).
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).
`'hamming'`	Hamming distance, which is the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.

custom distance function	A distance function specified using @:
	`D = pdist(X,@distfun)`
	A distance function must be of form
	`d2 = distfun(XI,XJ)`
	taking as arguments a 1-by-n vector `XI`, corresponding to a single row of `X`, and an m2-by-n matrix `XJ`, corresponding to multiple rows of `X`. `distfun` must accept a matrix `XJ` with an arbitrary number of rows. `distfun` must return an m2-by-1 vector of distances `d2`, whose kth element is the distance between `XI` and `XJ(k,:)`.

The output `D` is arranged in the order of ((2,1),(3,1),..., (m,1),(3,2),...(m,2),.....(m,m–1)), i.e. the lower left triangle of the full m-by-m distance matrix in column order. To get the distance between the ith and jth observations ($i < j$), either use the formula $D((i–1)*(m–i/2)+j–i)$, or use the helper function `Z = squareform(D)`, which returns an m-by-m square symmetric matrix, with the (i,j) entry equal to distance between observation i and observation j.

Metrics

Given an m-by-n data matrix `X`, which is treated as m (1-by-n) row vectors $\mathtt{x}_1$, $\mathtt{x}_2$, ..., $\mathtt{x}_m$, the various distances between the vector $\mathtt{x}_s$ and $\mathtt{x}_t$ are defined as follows:

- Euclidean distance

  $$d_{st}^2 = (x_s - x_t)(x_s - x_t)'$$

  Notice that the Euclidean distance is a special case of the Minkowski metric, where `p = 2`.

- Standardized Euclidean distance

  $$d_{st}^2 = (x_s - x_t)V^{-1}(x_s - x_t)'$$

  where `V` is the n-by-n diagonal matrix whose jth diagonal element is $\mathtt{S}(j)^2$, where `S` is the vector of standard deviations.

- Mahalanobis distance

  $$d_{st}^2 = (x_s - x_t)C^{-1}(x_s - x_t)'$$

  where `C` is the covariance matrix.

- City block metric

  $$d_{st} = \sum_{j=1}^{n} \left| x_{sj} - x_{tj} \right|$$

Notice that the city block distance is a special case of the Minkowski metric, where p=1.

- Minkowski metric

$$d_{st} = \sqrt[p]{\sum_{j=1}^{n} \left| x_{sj} - x_{tj} \right|^p}$$

Notice that for the special case of p = 1, the Minkowski metric gives the city block metric, for the special case of p = 2, the Minkowski metric gives the Euclidean distance, and for the special case of p = ∞, the Minkowski metric gives the Chebychev distance.

- Chebychev distance

$$d_{st} = \max_j \left\{ \left| x_{sj} - x_{tj} \right| \right\}$$

Notice that the Chebychev distance is a special case of the Minkowski metric, where p = ∞.

- Cosine distance

$$d_{st} = 1 - \frac{x_s x_t'}{\sqrt{(x_s x_s')(x_t x_t')}}$$

- Correlation distance

$$d_{st} = 1 - \frac{(x_s - \bar{x}_s)(x_t - \bar{x}_t)'}{\sqrt{(x_s - \bar{x}_s)(x_s - \bar{x}_s)'}\sqrt{(x_t - \bar{x}_t)(x_t - \bar{x}_t)'}}$$

where

$$\bar{x}_s = \frac{1}{n}\sum_j x_{sj} \quad \text{and} \quad \bar{x}_t = \frac{1}{n}\sum_j x_{tj}$$

- Hamming distance

$$d_{st} = (\#(x_{sj} \neq x_{tj}) / n)$$

- Jaccard distance

$$d_{st} = \frac{\#\left[\left(x_{sj} \neq x_{tj}\right) \cap \left(\left(x_{sj} \neq 0\right) \cup \left(x_{tj} \neq 0\right)\right)\right]}{\#\left[\left(x_{sj} \neq 0\right) \cup \left(x_{tj} \neq 0\right)\right]}$$

- Spearman distance

$$d_{st} = 1 - \frac{(r_s - \bar{r}_s)(r_t - \bar{r}_t)'}{\sqrt{(r_s - \bar{r}_s)(r_s - \bar{r}_s)'}\sqrt{(r_t - \bar{r}_t)(r_t - \bar{r}_t)'}}$$

  where

  - r_{sj} is the rank of x_{sj} taken over x_{1j}, x_{2j}, ...x_{mj}, as computed by `tiedrank`
  - r_s and r_t are the coordinate-wise rank vectors of x_s and x_t, i.e., $r_s = (r_{s1}, r_{s2}, \ldots\ r_{sn})$
  - $\bar{r}_s = \frac{1}{n}\sum_j r_{sj} = \frac{(n+1)}{2}$
  - $\bar{r}_t = \frac{1}{n}\sum_j r_{tj} = \frac{(n+1)}{2}$

Examples

Generate random data and find the unweighted Euclidean distance and then find the weighted distance using two different methods:

```
% Compute the ordinary Euclidean distance.
X = randn(100, 5);
D = pdist(X,'euclidean');  % euclidean distance
```

```
% Compute the Euclidean distance with each coordinate
% difference scaled by the standard deviation.
Dstd = pdist(X,'seuclidean');

% Use a function handle to compute a distance that weights
% each coordinate contribution differently.
Wgts = [.1 .3 .3 .2 .1];     % coordinate weights
weuc = @(XI,XJ,W)(sqrt(bsxfun(@minus,XI,XJ).^2 * W'));
Dwgt = pdist(X, @(Xi,Xj) weuc(Xi,Xj,Wgts));
```

See Also

cluster | clusterdata | cmdscale | cophenet | dendrogram | inconsistent | linkage | pdist2 | silhouette | squareform

Purpose

Pairwise distance between two sets of observations

Syntax

```
D = pdist2(X,Y)
D = pdist2(X,Y,distance)
D = pdist2(X,Y,'minkowski',P)
D = pdist2(X,Y,'mahalanobis',C)
D = pdist2(X,Y,distance,'Smallest',K)
D = pdist2(X,Y,distance,'Largest',K)
[D,I] = pdist2(X,Y,distance,'Smallest',K)
[D,I] = pdist2(X,Y,distance,'Largest',K)
```

Description

`D = pdist2(X,Y)` returns a matrix `D` containing the Euclidean distances between each pair of observations in the *mx*-by-*n* data matrix `X` and *my*-by-*n* data matrix `Y`. Rows of `X` and `Y` correspond to observations, columns correspond to variables. `D` is an *mx*-by-*my* matrix, with the (*i*,*j*) entry equal to distance between observation *i* in `X` and observation *j* in `Y`. The (*i*,*j*) entry will be `NaN` if observation *i* in `X` or observation *j* in `Y` contain `NaN`s.

`D = pdist2(X,Y,distance)` computes `D` using `distance`. Choices are:

Metric	Description
`'euclidean'`	Euclidean distance (default).
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between rows in `X` and `Y` is scaled by dividing by the corresponding element of the standard deviation computed from `X`, `S=nanstd(X)`. To specify another value for `S`, use `D = PDIST2(X,Y,'seuclidean',S)`.
`'cityblock'`	City block metric.
`'minkowski'`	Minkowski distance. The default exponent is 2. To compute the distance with a different exponent, use `D = pdist2(X,Y,'minkowski',P)`, where the exponent `P` is a scalar positive value.

Metric	Description
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'mahalanobis'`	Mahalanobis distance, using the sample covariance of `X` as computed by `nancov`. To compute the distance with a different covariance, use `D = pdist2(X,Y,'mahalanobis',C)` where the matrix `C` is symmetric and positive definite.
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors).
`'correlation'`	One minus the sample correlation between points (treated as sequences of values).
`'spearman'`	One minus the sample Spearman's rank correlation between observations, treated as sequences of values.
`'hamming'`	Hamming distance, the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.
function	A distance function specified using @: `D = pdist2(X,Y,@distfun)`. A distance function must be of the form `function D2 = distfun(ZI, ZJ)` taking as arguments a 1-by-*n* vector `ZI` containing a single observation from `X` or `Y`, an *m2*-by-*n* matrix `ZJ` containing multiple observations from `X` or `Y`, and returning an *m2*-by-1 vector of distances `D2`, whose `J`th element is the distance between the observations `ZI` and `ZJ(J,:)`.

Metric	Description
	If your data is not sparse, generally it is faster to use a built-in `distance` than to use a function handle.

`D = pdist2(X,Y,distance,'Smallest',K)` returns a `K`-by-*my* matrix `D` containing the `K` smallest pairwise distances to observations in `X` for each observation in `Y`. `pdist2` sorts the distances in each column of `D` in ascending order. `D = pdist2(X,Y,distance,'Largest',K)` returns the `K` largest pairwise distances sorted in descending order. If `K` is greater than *mx*, `pdist2` returns an *mx*-by-*my* distance matrix. For each observation in `Y`, `pdist2` finds the `K` smallest or largest distances by computing and comparing the distance values to all the observations in `X`.

`[D,I] = pdist2(X,Y,distance,'Smallest',K)` returns a `K`-by-*my* matrix `I` containing indices of the observations in `X` corresponding to the `K` smallest pairwise distances in `D`. `[D,I] = pdist2(X,Y,distance,'Largest',K)` returns indices corresponding to the `K` largest pairwise distances.

Metrics

Given an *mx*-by-*n* data matrix `X`, which is treated as *mx* (1-by-*n*) row vectors x_1, x_2, ..., x_{mx}, and *my*-by-*n* data matrix `Y`, which is treated as *my* (1-by-*n*) row vectors y_1, y_2, ...,y_{my}, the various distances between the vector x_s and y_t are defined as follows:

- Euclidean distance

  $$d_{st}^2 = (x_s - y_t)(x_s - y_t)'$$

  Notice that the Euclidean distance is a special case of the Minkowski metric, where `p=2`.

- Standardized Euclidean distance

  $$d_{st}^2 = (x_s - y_t)V^{-1}(x_s - y_t)'$$

where V is the n-by-n diagonal matrix whose jth diagonal element is $S(j)^2$, where S is the vector of standard deviations.

- Mahalanobis distance

$$d_{st}^2 = (x_s - y_t)C^{-1}(x_s - y_t)'$$

where C is the covariance matrix.

- City block metric

$$d_{st} = \sum_{j=1}^{n} \left| x_{sj} - y_{tj} \right|$$

Notice that the city block distance is a special case of the Minkowski metric, where p=1.

- Minkowski metric

$$d_{st} = \sqrt[p]{\sum_{j=1}^{n} \left| x_{sj} - y_{tj} \right|^p}$$

Notice that for the special case of p = 1, the Minkowski metric gives the City Block metric, for the special case of p = 2, the Minkowski metric gives the Euclidean distance, and for the special case of p=∞, the Minkowski metric gives the Chebychev distance.

- Chebychev distance

$$d_{st} = \max_j \left\{ \left| x_{sj} - y_{tj} \right| \right\}$$

Notice that the Chebychev distance is a special case of the Minkowski metric, where p=∞.

- Cosine distance

$$d_{st} = \left(1 - \frac{x_s y_t'}{\sqrt{(x_s x_s')(y_t y_t')}}\right)$$

- Correlation distance

$$d_{st} = 1 - \frac{(x_s - \bar{x}_s)(y_t - \bar{y}_t)'}{\sqrt{(x_s - \bar{x}_s)(x_s - \bar{x}_s)'}\sqrt{(y_t - \bar{y}_t)(y_t - \bar{y}_t)'}}$$

  where

$$\bar{x}_s = \frac{1}{n}\sum_j x_{sj} \text{ and}$$
$$\bar{y}_t = \frac{1}{n}\sum_j y_{tj}$$

- Hamming distance

$$d_{st} = (\#(x_{sj} \neq y_{tj}) / n)$$

- Jaccard distance

$$d_{st} = \frac{\#\left[\left(x_{sj} \neq y_{tj}\right) \cap \left(\left(x_{sj} \neq 0\right) \cup \left(y_{tj} \neq 0\right)\right)\right]}{\#\left[\left(x_{sj} \neq 0\right) \cup \left(y_{tj} \neq 0\right)\right]}$$

- Spearman distance

$$d_{st} = 1 - \frac{(r_s - \bar{r}_s)(r_t - \bar{r}_t)'}{\sqrt{(r_s - \bar{r}_s)(r_s - \bar{r}_s)'}\sqrt{(r_t - \bar{r}_t)(r_t - \bar{r}_t)'}}$$

  where

- r_{sj} is the rank of x_{sj} taken over x_{1j}, x_{2j}, ...$x_{mx,j}$, as computed by `tiedrank`
- r_{tj} is the rank of y_{tj} taken over y_{1j}, y_{2j}, ...$y_{my,j}$, as computed by `tiedrank`
- r_s and r_t are the coordinate-wise rank vectors of x_s and y_t, i.e. $r_s = (r_{s1}, r_{s2}, \ldots\ r_{sn})$ and $r_t = (r_{t1}, r_{t2}, \ldots\ r_{tn})$

- $\bar{r}_s = \frac{1}{n}\sum_j r_{sj} = \frac{(n+1)}{2}$
- $\bar{r}_t = \frac{1}{n}\sum_j r_{tj} = \frac{(n+1)}{2}$

Examples

Generate random data and find the unweighted Euclidean distance, then find the weighted distance using two different methods:

```
% Compute the ordinary Euclidean distance
X = randn(100, 5);
Y = randn(25, 5);
D = pdist2(X,Y,'euclidean'); % euclidean distance

% Compute the Euclidean distance with each coordinate
% difference scaled by the standard deviation
Dstd = pdist2(X,Y,'seuclidean');

% Use a function handle to compute a distance that weights
% each coordinate contribution differently.
Wgts = [.1 .3 .3 .2 .1];
weuc = @(XI,XJ,W)(sqrt(bsxfun(@minus,XI,XJ).^2 * W'));
Dwgt = pdist2(X,Y, @(Xi,Xj) weuc(Xi,Xj,Wgts));
```

See Also

`pdist` | `createns` | `knnsearch` | `KDTreeSearcher` | `ExhaustiveSearcher`

pearsrnd

Purpose

Pearson system random numbers

Syntax

```
r = pearsrnd(mu,sigma,skew,kurt,m,n)
r = pearsrnd(mu,sigma,skew,kurt)
r = pearsrnd(mu,sigma,skew,kurt,m,n,...)
r = pearsrnd(mu,sigma,skew,kurt,[m,n,...])
[r,type] = pearsrnd(...)
[r,type,coefs] = pearsrnd(...)
```

Description

`r = pearsrnd(mu,sigma,skew,kurt,m,n)` returns an `m`-by-`n` matrix of random numbers drawn from the distribution in the Pearson system with mean `mu`, standard deviation `sigma`, skewness `skew`, and kurtosis `kurt`. The parameters `mu`, `sigma`, `skew`, and `kurt` must be scalars.

Note Because `r` is a random sample, its sample moments, especially the skewness and kurtosis, typically differ somewhat from the specified distribution moments.

`pearsrnd` uses the definition of kurtosis for which a normal distribution has a kurtosis of 3. Some definitions of kurtosis subtract 3, so that a normal distribution has a kurtosis of 0. The `pearsrnd` function does not use this convention.

Some combinations of moments are not valid; in particular, the kurtosis must be greater than the square of the skewness plus 1. The kurtosis of the normal distribution is defined to be 3.

`r = pearsrnd(mu,sigma,skew,kurt)` returns a scalar value.

`r = pearsrnd(mu,sigma,skew,kurt,m,n,...)` or `r = pearsrnd(mu,sigma,skew,kurt,[m,n,...])` returns an `m`-by-`n`-by-... array.

`[r,type] = pearsrnd(...)` returns the type of the specified distribution within the Pearson system. `type` is a scalar integer from `0`

to 7. Set m and n to 0 to identify the distribution type without generating any random values.

The seven distribution types in the Pearson system correspond to the following distributions:

- 0 — Normal distribution
- 1 — Four-parameter beta distribution
- 2 — Symmetric four-parameter beta distribution
- 3 — Three-parameter gamma distribution
- 4 — Not related to any standard distribution. The density is proportional to:

  $$(1 + ((x - a)/b)^2)^{-c} \exp(-d \arctan((x - a)/b)).$$

- 5 — Inverse gamma location-scale distribution
- 6 — F location-scale distribution
- 7 — Student's t location-scale distribution

`[r,type,coefs] = pearsrnd(...)` returns the coefficients `coefs` of the quadratic polynomial that defines the distribution via the differential equation

$$\frac{d}{dx}\log(p(x)) = \frac{-(a + x)}{c(0) + c(1)x + c(2)x^2}.$$

Examples

Generate random values from the standard normal distribution:

```
r = pearsrnd(0,1,0,3,100,1);  % Equivalent to randn(100,1)
```

Determine the distribution type:

```
[r,type] = pearsrnd(0,1,1,4,0,0);
r =
```

```
     []
type =
     1
```

References

[1] Johnson, N.L., S. Kotz, and N. Balakrishnan (1994) Continuous Univariate Distributions, Volume 1, Wiley-Interscience, Pg 15, Eqn 12.33.

See Also

`random | johnsrnd`

Purpose

Compute Receiver Operating Characteristic (ROC) curve or other performance curve for classifier output

Syntax

```
[X,Y] = perfcurve(labels,scores,posclass)
[X,Y] = perfcurve(labels,scores,posclass,'Name',value)
[X,Y,T,AUC,OPTROCPT,SUBY,SUBYNAMES] = perfcurve(labels,scores,
   posclass)
[X,Y,T,AUC] = perfcurve(labels,scores,posclass)
```

Description

`[X,Y] = perfcurve(labels,scores,posclass)` computes a ROC curve for a vector of classifier predictions `scores` given true class labels, `labels`. `labels` can be a numeric vector, logical vector, character matrix, cell array of strings or categorical vector. `scores` is a numeric vector of scores returned by a classifier for some data. `posclass` is the positive class label (scalar), either numeric (for numeric `labels`), logical (for logical `labels`), or char. The returned values `X` and `Y` are coordinates for the performance curve and can be visualized with `plot(X,Y)`. For more information on `labels`, `scores`, and `posclass`, see "Input Arguments" on page 20-1377 . For more information on `X` and `Y`, see "Output Arguments" on page 20-1381.

`[X,Y] = perfcurve(labels,scores,posclass,'Name',value)` specifies one or more optional parameter name/value pairs, with *`Name`* in single quotes. See "Input Arguments" on page 20-1377 for a list of inputs, parameter name/value pairs, and respective explanations.

See "Grouped Data" on page 2-34 for more information on grouping variables.

`[X,Y,T,AUC,OPTROCPT,SUBY,SUBYNAMES] = perfcurve(labels,scores,posclass)` returns:

- An array of thresholds on classifier scores for the computed values of `X` and `Y` (`T`).
- The area under curve (`AUC`) for the computed values of `X` and `Y`.
- The optimal operating point of the ROC curve (`OPTROCPT`).
- An array of `Y` values for negative subclasses (`SUBY`).

- A cell array of negative class names (SUBYNAMES).

For more information on each output, see "Output Arguments" on page 20-1381.

`[X,Y,T,AUC] = perfcurve(labels,scores,posclass)` also returns pointwise confidence bounds for the computed values `X`, `Y`, `T`, and `AUC` if you supply cell arrays for `labels` and `scores` or set `NBoot` (see "Input Arguments" on page 20-1377) to a positive integer. To compute the confidence bounds, `perfcurve` uses either vertical averaging (VA) or threshold averaging (TA). The returned values `Y` are an *m*-by-3 array in which the 1st element in every row gives the mean value, the 2nd element gives the lower bound and the 3rd element gives the upper bound. The returned `AUC` is a row-vector with 3 elements following the same convention. For VA, the returned values `T` are an *m*-by-3 array and `X` is a column-vector. For TA, the returned values `X` are an *m*-by-3 matrix and `T` is a column-vector.

`perfcurve` computes confidence bounds using either cross-validation or bootstrap. If you supply cell arrays for `labels` and `scores`, `perfcurve` uses cross-validation and treats elements in the cell arrays as cross-validation folds. `labels` can be a cell array of numeric vectors, logical vectors, character matrices, cell arrays of strings or categorical vectors. All elements in `labels` must have the same type. `scores` is a cell array of numeric vectors. The cell arrays for `labels` and `scores` must have the same number of elements, and the number of labels in cell *k* must be equal to the number of scores in cell *k* for any *k* in the range from 1 to the number of elements in `scores`.

If you set `NBoot` to a positive integer, `perfcurve` generates `nboot` bootstrap replicas to compute pointwise confidence bounds. You cannot supply cell arrays for `labels` and `scores` and set `NBoot` to a positive integer at the same time.

`perfcurve` returns pointwise confidence bounds. It does not return a simultaneous confidence band for the entire curve.

If you use `'XCrit'` or `'YCrit'` options described below to set the criterion for `X` or `Y` to an anonymous function, `perfcurve` can only compute confidence bounds by bootstrap.

Input Arguments

`labels`	`labels` can be a numeric vector, logical vector, character matrix, cell array of strings or categorical vector.
`scores`	`scores` is a numeric vector of scores returned by a classifier for some data. This vector must have as many elements as `labels` does.
`posclass`	`posclass` is the positive class label (scalar), either numeric (for numeric `labels`) or char. The specified positive class must be in the array of input labels.

Name-Value Pair Arguments

Name	Value and Description
`negClass`	List of negative classes. Can be either a numeric array or an array of chars or a cell array of strings. By default, `negClass` is set to `'all'` and all classes found in the input array of labels that are not the positive class are considered negative. If `negClass` is a subset of the classes found in the input array of labels, instances with labels that do not belong to either positive or negative classes are discarded.
`xCrit`	Criterion to compute for X. This criterion must be a monotone function of the positive class score. `perfcurve` supports the following criteria: • `TP` — Number of true positive instances. • `FN` — Number of false negative instances. • `FP` — Number of false positive instances.

Name	Value and Description

- `TN` — Number of true negative instances.
- `TP+FP` — Sum of `TP` and `FP`.
- `RPP` — Rate of positive predictions. `RPP=(TP+FP)/(TP+FN+FP+TN)`
- `RNP` — Rate of negative predictions. `RNP=(TN+FN)/(TP+FN+FP+TN)`
- `accu` — Accuracy. `accu = (TP+TN)/(TP+FN+FP+TN)`
- `TPR`, `sens`, `reca` — True positive rate, sensitivity, recall. `TPR, sens, reca = TP/(TP+FN)`
- `FNR`, `miss` — False negative rate, miss. `FNR,miss=FN/(TP+FN)`
- `FPR`, `fall` — False positive rate, fallout. `FPR,fall=FP/(TN+FP)`
- `TNR`, `spec` — True negative rate, specificity. `TNR,spec=TN/(TN+FP)`
- `PPV`, `prec` — Positive predictive value, precision. `PPV,prec=TP/(TP+FP)`
- `NPV` — Negative predictive value. `NPV=TN/(TN+FN)`
- `ecost` — Expected cost. `ecost=(TP*COST(P|P)+FN*COST(N|P)+FP*COST(P|N)+TN*COST(N|N))/(TP+FN+FP+TN)`

In addition, you can define an arbitrary criterion by supplying an anonymous function of three arguments, `(C,scale,cost)`, where `C` is a 2-by-2 confusion matrix, `scale` is a 2-by-1 array of class scales, and `cost` is a 2-by-2 misclassification cost matrix.

Caution Some of these criteria return `NaN` values at one of the two special thresholds, `'reject all'` and `'accept all'`.

Name	Value and Description
`yCrit`	Criterion to compute for `Y`. `perfcurve` supports the same criteria as for `X`. This criterion does not have to be a monotone function of the positive class score.
`XVals`	Values for the `X` criterion. The default value for `xVals` is `'all'` and `perfcurve` computes `X` and `Y` values for all scores. If the value for `xVals` is not `'all'`, it must be a numeric array. In this case, `perfcurve` computes `X` and `Y` only for the specified `xVals`.
`TVals`	Thresholds for the positive class score. By default, `TVals` is unset and `perfcurve` computes `X`, `Y`, and `T` values for all scores. You can set `TVals` to either `'all'` or a numeric array. If `TVals` is set to `'all'` or unset and `XVals` is unset, `perfcurve` returns `X`, `Y`, and `T` values for all scores and computes pointwise confidence bounds for `Y` and `X` using threshold averaging. If `TVals` is set to a numeric array, `perfcurve` returns `X`, `Y`, and `T` values for the specified thresholds and computes pointwise confidence bounds for `Y` and `X` at these thresholds using threshold averaging. You cannot set `XVals` and `TVals` at the same time.
`UseNearest`	`'on'` to use nearest values found in the data instead of the specified numeric `XVals` or `TVals` and `'off'` otherwise. If you specify numeric `XVals` and set `UseNearest` to 'on', `perfcurve` returns nearest unique values `X` found in the data, as well as corresponding values of `Y` and `T`. If you specify numeric `XVals` and set `UseNearest` to `'off'`, `perfcurve` returns these `XVals` sorted. By default this parameter is set to `'on'`. If you compute confidence bounds by cross-validation or bootstrap, this parameter is always `'off'`.

Name	Value and Description
`ProcessNaN`	Specifies how `perfcurve` processes `NaN` scores. The default value is `'ignore'` and `perfcurve` removes observations with `NaN` scores from the data. If you set the parameter to `'addtofalse'`, `perfcurve` adds instances with `NaN` scores to false classification counts in the respective class. That is, `perfcurve` always counts instances from the positive class as false negative (FN), and always counts instances from the negative class as false positive (FP).
`Prior`	Either string or array with two elements. It represents prior probabilities for the positive and negative class, respectively. Default is `'empirical'`, that is, `perfcurve` derives prior probabilities from class frequencies. If set to `'uniform'`, `perfcurve` sets all prior probabilities equal.
`Cost`	A 2-by-2 matrix of misclassification costs `[C(P|P) C(N|P); C(P|N) C(N|N)]` where `C(I|J)` is the cost of misclassifying class `J` as class `I`. By default set to `[0 0.5; 0.5 0]`.
`Alpha`	A numeric value between 0 and 1. `perfcurve` returns 100*(1-*Alpha*) percent pointwise confidence bounds for `X`, `Y`, `T` and `AUC`. By default set to 0.05 for 95% confidence interval.
`Weights`	A numeric vector of non-negative observation weights. This vector must have as many elements as `scores` or `labels` do. If you supply cell arrays for `scores` and `labels` and you need to supply `weights`, you must supply them as a cell array too. In this case, every element in `weights` must be a numeric vector with as many elements as the corresponding element in `scores`: `numel(weights{1})==numel(scores{1})` etc. To compute `X`, `Y` and `T` or to compute confidence bounds by cross-validation, `perfcurve` uses these observation weights instead of observation counts. To compute confidence bounds by bootstrap, `perfcurve` samples *N* out of *N* with replacement using these weights as multinomial sampling probabilities.

Name	Value and Description
`NBoot`	Number of bootstrap replicas for computation of confidence bounds. Must be a positive integer. By default this parameter is set to zero, and bootstrap confidence bounds are not computed. If you supply cell arrays for `labels` and `scores`, this parameter must be set to zero because `perfcurve` cannot use both cross-validation and bootstrap to compute confidence bounds.
`BootType`	Confidence interval type `bootci` uses to compute confidence bounds. You can specify any type supported by `bootci`. By default set to `'bca'`.
`BootArg`	Optional input arguments for `bootci` used to compute confidence bounds. You can specify all arguments `bootci` supports. Empty by default.

Output Arguments

`X` — *x*-coordinates for the performance curve. By default, `X` is false positive rate, FPR, (equivalently, fallout, or 1–specificity). To change this output, use the `'xCrit'` name/value input. For accepted criterion, see `'xCrit'` in "Input Arguments" on page 20-1377 for more information.

`Y` — *y*-coordinates for the performance curve. By default, `Y` is true positive rate, TPR, (equivalently, recall, or sensitivity). To change this output, use the `'yCrit'` input. For accepted criterion, see `'xCrit'` in "Input Arguments" on page 20-1377 for more information.

`T` — An array of thresholds on classifier scores for the computed values of `X` and `Y`. It has the same number of rows as `X` and `Y`. For each threshold, `TP` is the count of true positive observations with scores greater or equal to this threshold, and `FP` is the count of false positive observations with scores greater or equal to this threshold. `perfcurve` defines negative counts, `TN` and `FN`, in a similar way then sorts the thresholds in the descending order which corresponds to the ascending order of positive counts.

For the `M` distinct thresholds found in the array of scores, `perfcurve` returns the `X`, `Y` and `T` arrays with `M+1` rows. `perfcurve` sets elements `T(2:M+1)` to the distinct thresholds, and `T(1)` replicates `T(2)`. By convention, `T(1)` represents the highest `'reject all'` threshold and `perfcurve` computes the corresponding values of `X` and `Y` for `TP=0` and `FP=0`. `T(end)` is the lowest `'accept all'` threshold for which `TN=0` and `FN=0`.

`AUC` — The area under curve (`AUC`) for the computed values of `X` and `Y`. If you set `xVals` to `'all'` (the default), `perfcurve` computes `AUC` using the returned `X` and `Y` values. If `xVals` is a numeric array, `perfcurve` computes `AUC` using `X` and `Y` values found from all distinct scores in the interval specified by the smallest and largest elements of `xVals`. More precisely, `perfcurve` finds `X` values for all distinct thresholds as if `xVals` were set to `'all'`, then uses a subset of these (with corresponding `Y` values) between `min(xVals)` and `max(xVals)` to compute `AUC`. The function uses trapezoidal approximation to estimate the area. If the first or last value of `X` or `Y` are `NaN`s, `perfcurve` removes them to allow calculation of `AUC`. This takes care of criteria that produce `NaN`s for the special `'reject all'` or `'accept all'` thresholds, for example, positive predictive value (PPV) or negative predictive value (NPV).

`OPTROCPT` The optimal operating point of the ROC curve as an array of size 1-by-2 with FPR and TPR values for the optimal ROC operating point. `perfcurve` computes `optrocpt` only for the standard ROC curve and sets to `NaN`s otherwise. To obtain the optimal operating point for the ROC curve, `perfcurve` first finds the slope, `S`, using

$$S = \frac{\cos t(P \mid N) - \cos t(N \mid N)}{\cos t(N \mid P) - \cos t(P \mid P)} * \frac{N}{P}$$

where `cost(I|J)` is the cost of assigning an instance of class `J` to class `I`, and `P=TP+FN` and `N=TN+FP` are the total instance counts in the positive and negative class, respectively. `perfcurve` then finds the optimal operating point by moving the straight line with slope `S` from the upper left corner of the ROC plot (`FPR=0`, `TPR=1`) down and to the right until it intersects the ROC curve.

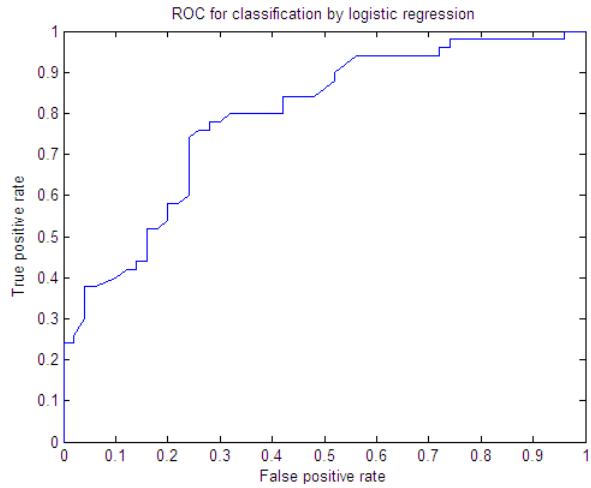
`SUBY` An array of `Y` values for negative subclasses. If you only specify one negative class, `SUBY` is identical to `Y`. Otherwise `SUBY` is a matrix of size `M`-by-`K`, where `M` is the number of returned values for `X` and `Y`, and `K` is the number of negative classes. `perfcurve` computes `Y` values by summing counts over all negative classes. `SUBY` gives values of the `Y` criterion for each negative class separately. For each negative class, `perfcurve` places a new column in `SUBY` and fills it with `Y` values for TN and FP counted just for this class.

`SUBYNAMES` A cell array of negative class names. If you provide an input array, `negClass`, of negative class names, `perfcurve` copies it into `SUBYNAMES`. If you do not provide `negClass`, `perfcurve` extracts `SUBYNAMES` from input labels. The order of `SUBYNAMES` is the same as the order of columns in `SUBY`, that is, `SUBY(:,1)` is for negative class `SUBYNAMES{1}` etc.

Examples

Plot the ROC curve for classification by logistic regression:

```
load fisheriris
x = meas(51:end,1:2);
% iris data, 2 classes and 2 features
y = (1:100)'>50;
% versicolor=0, virginica=1
b = glmfit(x,y,'binomial');
% logistic regression
p = glmval(b,x,'logit');
% fit probabilities for scores
[X,Y,T,AUC] = perfcurve(species(51:end,:),p,'virginica');
plot(X,Y)
xlabel('False positive rate'); ylabel('True positive rate')
title('ROC for classification by logistic regression')
```



Obtain errors on TPR by vertical averaging

```
[X,Y] = perfcurve(species(51:end,:),p,'virginica',...
   'nboot',1000,'xvals','all');
% plot errors
```

```
errorbar(X,Y(:,1),Y(:,2)-Y(:,1),Y(:,3)-Y(:,1));
```

References

[1] T. Fawcett, ROC Graphs: Notes and Practical Considerations for Researchers, 2004.

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[3] J. Davis and M. Goadrich, The relationship between precision-recall and ROC curves, in Proceedings of ICML '06, 233-240, 2006.

[4] C. Moskowitz and M. Pepe, Quantifying and comparing the predictive accuracy of continuous prognostic factors for binary outcomes, Biostatistics 5, 113-127, 2004.

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[6] W. Briggs and R. Zaretzki, The Skill Plot: A Graphical Technique for Evaluating Continuous Diagnostic Tests, Biometrics 63, 250-261, 2008.

[7] http://www2.cs.uregina.ca/~hamilton/courses/831/notes/lift_chart/lift_chart.htm http://www.dmreview.com/news/5329-1.html.

[8] R. Bettinger, Cost-Sensitive Classifier Selection Using the ROC Convex Hull Method, SAS Institute.

[9] http://www.stata.com/statalist/archive/2003-02/msg00060.html

See Also

`bootci` | `glmfit` | `mnrfit` | `classify` | `NaiveBayes` | `classregtree`

How To

- "Grouped Data" on page 2-34
- "Performance Curves" on page 12-32
- "Plotting a Classification Performance Curve" on page 13-115

perms

Purpose

Enumeration of permutations

Syntax

```
P = perms(v)
```

Description

`P = perms(v)`, where `v` is a row vector of length `n`, creates a matrix whose rows consist of all possible permutations of the `n` elements of `v`. The matrix `P` contains `n!` rows and `n` columns.

`perms` is only practical when `n` is less than about 11 (for `n = 11`, the output takes over 3 gigabytes).

Examples

```
perms([2 4 6])

ans =

   6   4   2
   6   2   4
   4   6   2
   4   2   6
   2   4   6
   2   6   4
```

See Also

`combnk`

Purpose

Permute dimensions of categorical array

Syntax

```
B = permute(A,order)
```

Description

`B = permute(A,order)` rearranges the dimensions of the categorical array A so that they are in the order specified by the vector `order`. The array produced has the same values as `A` but the order of the subscripts needed to access any particular element are rearranged as specified by `order`. The elements of `order` must be a rearrangement of the numbers from 1 to `n`.

See Also

`circshift` | `ipermute`

piecewisedistribution

Purpose

Piecewise-defined distributions

Construction

`piecewisedistribution` is an abstract class. To construct a `piecewisedistribution` object, use the subclass constructor, `paretotails`.

Methods

boundary	Piecewise distribution boundaries
cdf	Cumulative distribution function for piecewise distribution
disp	Display piecewisedistribution object
display	Display piecewisedistribution object
icdf	Inverse cumulative distribution function for piecewise distribution
nsegments	Number of segments
pdf	Probability density function for piecewise distribution
random	Random numbers from piecewise distribution
segment	Segments containing values

Properties

Objects of the `piecewisedistribution` class have no properties accessible by dot indexing, `get` methods, or `set` methods. To obtain information about a `piecewisedistribution` object, use the appropriate method.

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

Purpose

Create piecewise distribution object

Description

`piecewisedistribution` is an abstract class, and you cannot create instances of it directly. You can create `paretotails` objects that are derived from this class.

See Also

`paretotails`

plsregress

Purpose

Partial least-squares regression

Syntax

```
[XL,YL] = plsregress(X,Y,ncomp)
[XL,YL,XS] = plsregress(X,Y,ncomp)
[XL,YL,XS,YS] = plsregress(X,Y,ncomp)
[XL,YL,XS,YS,BETA] = PLSREGRESS(X,Y,ncomp,...)
[XL,YL,XS,YS,BETA,PCTVAR] = plsregress(X,Y,ncomp)
[XL,YL,XS,YS,BETA,PCTVAR,MSE] = plsregress(X,Y,ncomp)
[XL,YL,XS,YS,BETA,PCTVAR,MSE] = plsregress(...,param1,val1,
   param2,val2,...)
[XL,YL,XS,YS,BETA,PCTVAR,MSE,stats] = PLSREGRESS(X,Y,ncomp,
   ...)
```

Description

`[XL,YL] = plsregress(X,Y,ncomp)` computes a partial least-squares (PLS) regression of `Y` on `X`, using `ncomp` PLS components, and returns the predictor and response loadings in `XL` and `YL`, respectively. `X` is an n-by-p matrix of predictor variables, with rows corresponding to observations and columns to variables. `Y` is an n-by-m response matrix. `XL` is a p-by-`ncomp` matrix of predictor loadings, where each row contains coefficients that define a linear combination of PLS components that approximate the original predictor variables. `YL` is an m-by-`ncomp` matrix of response loadings, where each row contains coefficients that define a linear combination of PLS components that approximate the original response variables.

`[XL,YL,XS] = plsregress(X,Y,ncomp)` returns the predictor scores `XS`, that is, the PLS components that are linear combinations of the variables in `X`. `XS` is an n-by-`ncomp` orthonormal matrix with rows corresponding to observations and columns to components.

`[XL,YL,XS,YS] = plsregress(X,Y,ncomp)` returns the response scores `YS`, that is, the linear combinations of the responses with which the PLS components `XS` have maximum covariance. `YS` is an n-by-`ncomp` matrix with rows corresponding to observations and columns to components. `YS` is neither orthogonal nor normalized.

`plsregress` uses the SIMPLS algorithm, first centering `X` and `Y` by subtracting off column means to get centered variables `X0` and `Y0`.

However, it does not rescale the columns. To perform PLS with standardized variables, use `zscore` to normalize `X` and `Y`.

If `ncomp` is omitted, its default value is `min(size(X,1)-1,size(X,2))`.

The relationships between the scores, loadings, and centered variables `X0` and `Y0` are:

`XL = (XS\X0)' = X0'*XS`,

`YL = (XS\Y0)' = Y0'*XS`,

`XL` and `YL` are the coefficients from regressing `X0` and `Y0` on `XS`, and `XS*XL'` and `XS*YL'` are the PLS approximations to `X0` and `Y0`.

`plsregress` initially computes `YS` as:

`YS = Y0*YL = Y0*Y0'*XS`,

By convention, however, `plsregress` then orthogonalizes each column of `YS` with respect to preceding columns of `XS`, so that `XS'*YS` is lower triangular.

`[XL,YL,XS,YS,BETA] = PLSREGRESS(X,Y,ncomp,...)` returns the PLS regression coefficients `BETA`. `BETA` is a (p+1)-by-m matrix, containing intercept terms in the first row:

`Y = [ones(n,1),X]*BETA + RESIDUALS`,

`Y0 = X0*BETA(2:end,:)  + RESIDUALS`.

`[XL,YL,XS,YS,BETA,PCTVAR] = plsregress(X,Y,ncomp)` returns a 2-by-`ncomp` matrix `PCTVAR` containing the percentage of variance explained by the model. The first row of `PCTVAR` contains the percentage of variance explained in `X` by each PLS component, and the second row contains the percentage of variance explained in `Y`.

`[XL,YL,XS,YS,BETA,PCTVAR,MSE] = plsregress(X,Y,ncomp)` returns a 2-by-(`ncomp`+1) matrix `MSE` containing estimated mean-squared errors for PLS models with `0:ncomp` components. The first row of `MSE` contains mean-squared errors for the predictor variables in `X`, and the second row contains mean-squared errors for the response variable(s) in `Y`.

`[XL,YL,XS,YS,BETA,PCTVAR,MSE] = plsregress(...,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs from the following table to control the calculation of `MSE`.

Parameter	Value
`'cv'`	The method used to compute `MSE`. • When the value is a positive integer `k`, `plsregress` uses `k`-fold cross-validation. • When the value is an object of the `cvpartition` class, other forms of cross-validation can be specified. • When the value is `'resubstitution'`, `plsregress` uses `X` and `Y` both to fit the model and to estimate the mean-squared errors, without cross-validation. The default is `'resubstitution'`.
`'mcreps'`	A positive integer indicating the number of Monte-Carlo repetitions for cross-validation. The default value is `1`. The value must be `1` if the value of `'cv'` is `'resubstitution'`.
`options`	A structure that specifies whether to run in parallel, and specifies the random stream or streams. Create the `options` structure with `statset`. Option fields: • `UseParallel` — Set to `'always'` to compute in parallel. Default is `'never'`. • `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. Default is `'never'`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. • `Streams` — A `RandStream` object or cell array consisting of one such object. If you do not specify `Streams`, `plsregress` uses the default stream.

Parameter	Value
	For more information on using parallel computing, see Chapter 17, "Parallel Statistics".

`[XL,YL,XS,YS,BETA,PCTVAR,MSE,stats] = PLSREGRESS(X,Y,ncomp,...)` returns a structure `stats` with the following fields:

- `W` — A p-by-`ncomp` matrix of PLS weights so that `XS = XO*W`.
- `T2` — The T^2 statistic for each point in `XS`.
- `Xresiduals` — The predictor residuals, that is, `XO-XS*XL'`.
- `Yresiduals` — The response residuals, that is, `YO-XS*YL'`.

Examples

Load data on near infrared (NIR) spectral intensities of 60 samples of gasoline at 401 wavelengths, and their octane ratings:

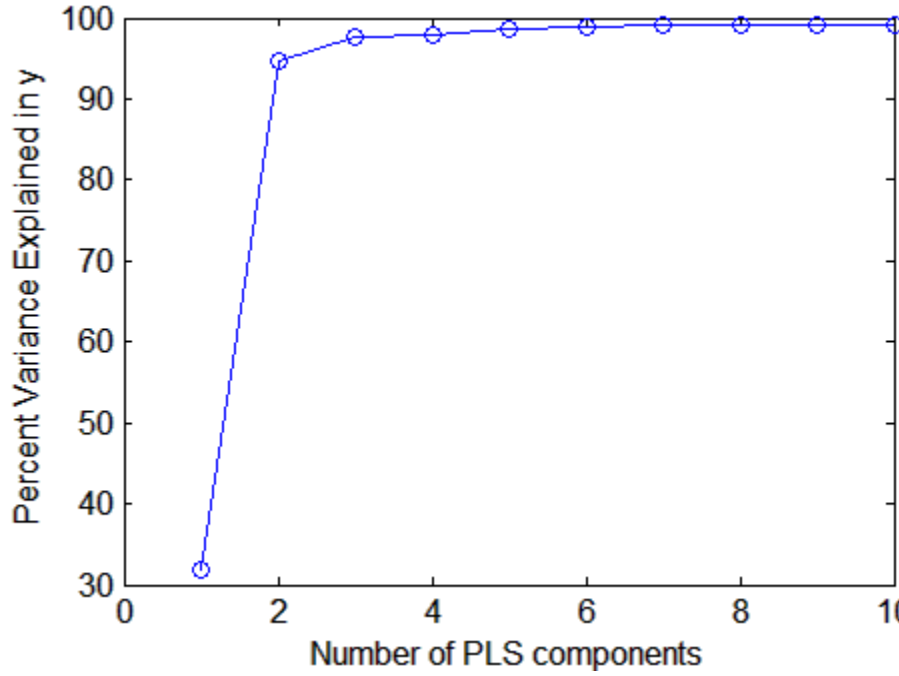
```
load spectra
X = NIR;
y = octane;
```

Perform PLS regression with ten components:

```
[XL,yl,XS,YS,beta,PCTVAR] = plsregress(X,y,10);
```

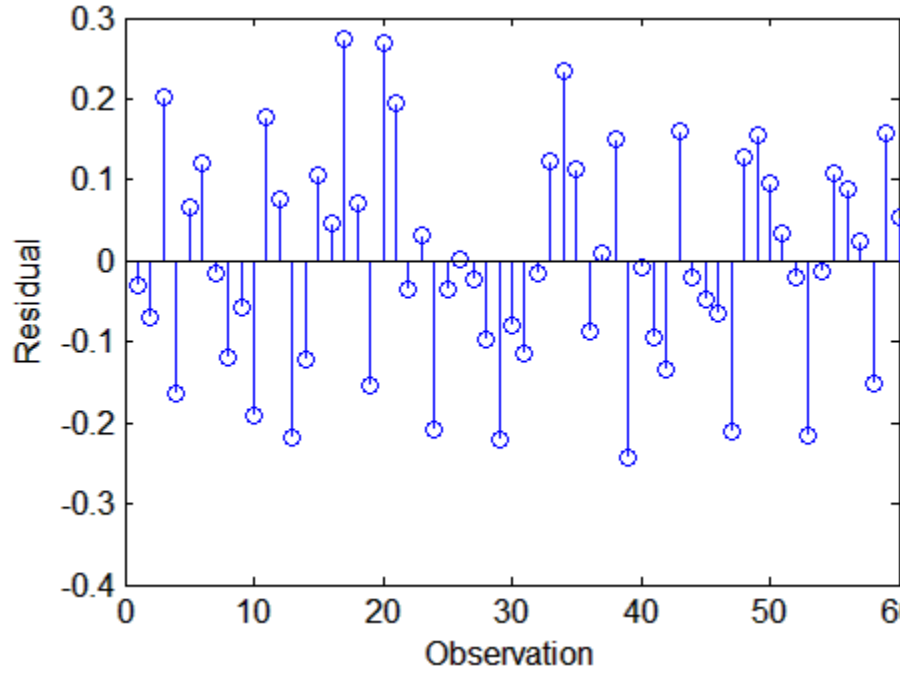
Plot the percent of variance explained in the response variable as a function of the number of components:

```
plot(1:10,cumsum(100*PCTVAR(2,:)),'-bo');
xlabel('Number of PLS components');
ylabel('Percent Variance Explained in y');
```



Compute the fitted response and display the residuals:

```
yfit = [ones(size(X,1),1) X]*beta;
residuals = y-yfit;

stem(residuals)
xlabel('Observation');
ylabel('Residual');
```



References

[1] de Jong, S. "SIMPLS: An Alternative Approach to Partial Least Squares Regression." *Chemometrics and Intelligent Laboratory Systems*. Vol. 18, 1993, pp. 251–263.

[2] Rosipal, R., and N. Kramer. "Overview and Recent Advances in Partial Least Squares." *Subspace, Latent Structure and Feature Selection: Statistical and Optimization Perspectives Workshop (SLSFS 2005), Revised Selected Papers (Lecture Notes in Computer Science 3940)*. Berlin, Germany: Springer-Verlag, 2006, pp. 34–51.

See Also

`regress` | `sequentialfs`

sobolset.PointOrder property

Purpose

Point generation method

Description

The `PointOrder` property contains a string that specifies the order in which the Sobol sequence points are produced. The property value must be one of `'standard'` or `'graycode'`. When set to `'standard'` the points produced match the original Sobol sequence implementation. When set to `'graycode'`, the sequence is generated using an implementation that uses the Gray code of the index instead of the index itself.

Purpose

Point set from which stream is drawn

Description

The `PointSet` property contains a copy of the point set from which the stream is providing points. The point set is specified during construction of a quasi-random stream and cannot subsequently be altered.

Examples

```
Q = qrandstream('sobol', 5, 'Skip', 8);
% Create a new stream based on the same sequence as that in Q
Q2 = qrandstream(Q.PointSet);
u1 = qrand(Q, 10)
u2 = qrand(Q2, 10) % contains exactly the same values as u1
```

poisscdf

Purpose

Poisson cumulative distribution function

Syntax

```
P = poisscdf(X,lambda)
```

Description

`P = poisscdf(X,lambda)` computes the Poisson cdf at each of the values in `X` using the corresponding mean parameters in `lambda`. `X` and `lambda` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `lambda` must be positive.

The Poisson cdf is

$$p = F(x \mid \lambda) = e^{-\lambda} \sum_{i=0}^{floor(x)} \frac{\lambda^i}{i!}$$

Examples

For example, consider a Quality Assurance department that performs random tests of individual hard disks. Their policy is to shut down the manufacturing process if an inspector finds more than four bad sectors on a disk. What is the probability of shutting down the process if the mean number of bad sectors (λ) is two?

```
probability = 1-poisscdf(4,2)
probability =
  0.0527
```

About 5% of the time, a normally functioning manufacturing process produces more than four flaws on a hard disk.

Suppose the average number of flaws (λ) increases to four. What is the probability of finding fewer than five flaws on a hard drive?

```
probability = poisscdf(4,4)
probability =
  0.6288
```

This means that this faulty manufacturing process continues to operate after this first inspection almost 63% of the time.

See Also

`cdf` | `poisspdf` | `poissinv` | `poisstat` | `poissfit` | `poissrnd`

How To

- “Poisson Distribution” on page B-89

poissfit

Purpose

Poisson parameter estimates

Syntax

```
lambdahat = poissfit(data)
[lambdahat,lambdaci] = poissfit(data)
[lambdahat,lambdaci] = poissfit(data,alpha)
```

Description

`lambdahat = poissfit(data)` returns the maximum likelihood estimate (MLE) of the parameter of the Poisson distribution, λ, given the data `data`.

`[lambdahat,lambdaci] = poissfit(data)` also gives 95% confidence intervals in `lamdaci`.

`[lambdahat,lambdaci] = poissfit(data,alpha)` gives `100(1 - alpha)`% confidence intervals. For example `alpha = 0.001` yields 99.9% confidence intervals.

The sample mean is the MLE of λ.

$$\hat{\lambda} = \frac{1}{n}\sum_{i=1}^{n} x_i$$

Examples

```
r = poissrnd(5,10,2);
[l,lci] = poissfit(r)
l =
    7.4000    6.3000
lci =
    5.8000    4.8000
    9.1000    7.9000
```

See Also

`mle` | `poisspdf` | `poisscdf` | `poissinv` | `poisstat` | `poissrnd`

How To

- "Poisson Distribution" on page B-89

Purpose

Poisson inverse cumulative distribution function

Syntax

```
X = poissinv(P,lambda)
```

Description

`X = poissinv(P,lambda)` returns the smallest value `X` such that the Poisson cdf evaluated at `X` equals or exceeds `P`, using mean parameters in `lambda`. `P` and `lambda` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input.

Examples

If the average number of defects (λ) is two, what is the 95th percentile of the number of defects?

```
poissinv(0.95,2)
ans =
   5
```

What is the median number of defects?

```
median_defects = poissinv(0.50,2)
median_defects =
   2
```

See Also

`icdf` | `poisscdf` | `poisspdf` | `poisstat` | `poissfit` | `poissrnd`

How To

- “Poisson Distribution” on page B-89

poisspdf

Purpose

Poisson probability density function

Syntax

```
Y = poisspdf(X,lambda)
```

Description

`Y = poisspdf(X,lambda)` computes the Poisson pdf at each of the values in `X` using mean parameters in `lambda`. `X` and `lambda` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `lambda` must all be positive.

The Poisson pdf is

$$y = f(x \mid \lambda) = \frac{\lambda^x}{x!} e^{-\lambda} I_{(0,1,\ldots)}(x)$$

where x can be any nonnegative integer. The density function is zero unless x is an integer.

Examples

A computer hard disk manufacturer has observed that flaws occur randomly in the manufacturing process at the average rate of two flaws in a 4 GB hard disk and has found this rate to be acceptable. What is the probability that a disk will be manufactured with no defects?

In this problem, $\lambda = 2$ and $x = 0$.

```
p = poisspdf(0,2)
p =
  0.1353
```

See Also

`pdf` | `poisscdf` | `poissinv` | `poisstat` | `poissfit` | `poissrnd`

How To

- "Poisson Distribution" on page B-89

Purpose

Poisson random numbers

Syntax

```
R = poissrnd(lambda)
R = poissrnd(lambda,m,n,...)
R = poissrnd(lambda,[m,n,...])
```

Description

`R = poissrnd(lambda)` generates random numbers from the Poisson distribution with mean parameter `lambda`. `lambda` can be a vector, a matrix, or a multidimensional array. The size of `R` is the size of `lambda`.

`R = poissrnd(lambda,m,n,...)` or `R = poissrnd(lambda,[m,n,...])` generates an `m`-by-`n`-by-... array. The `lambda` parameter can be a scalar or an array of the same size as `R`.

Examples

Generate a random sample of 10 pseudo-observations from a Poisson distribution with $\lambda = 2$.

```
lambda = 2;

random_sample1 = poissrnd(lambda,1,10)
random_sample1 =
   1   0   1   2   1   3   4   2   0   0

random_sample2 = poissrnd(lambda,[1 10])
random_sample2 =
   1   1   1   5   0   3   2   2   3   4

random_sample3 = poissrnd(lambda(ones(1,10)))
random_sample3 =
   3   2   1   1   0   0   4   0   2   0
```

See Also

`random` | `poisspdf` | `poisscdf` | `poissinv` | `poisstat` | `poissfit`

How To

- "Poisson Distribution" on page B-89

poisstat

Purpose

Poisson mean and variance

Syntax

```
M = poisstat(lambda)
[M,V] = poisstat(lambda)
```

Description

`M = poisstat(lambda)` returns the mean of the Poisson distribution using mean parameters in `lambda`. The size of `M` is the size of `lambda`.

`[M,V] = poisstat(lambda)` also returns the variance `V` of the Poisson distribution.

For the Poisson distribution with parameter λ, both the mean and variance are equal to λ.

Examples

Find the mean and variance for the Poisson distribution with λ = 2.

```
[m,v] = poisstat([1 2; 3 4])
m =
   1   2
   3   4
v =
   1   2
   3   4
```

See Also

`poisspdf` | `poisscdf` | `poissinv` | `poissfit` | `poissrnd`

How To

- “Poisson Distribution” on page B-89

Purpose

Polynomial confidence intervals

Syntax

```
Y = polyconf(p,X)
[Y,DELTA] = polyconf(p,X,S)
[Y,DELTA] = polyconf(p,X,S,param1,val1,param2,val2,...)
```

Description

`Y = polyconf(p,X)` evaluates the polynomial `p` at the values in `X`. `p` is a vector of coefficients in descending powers.

`[Y,DELTA] = polyconf(p,X,S)` takes outputs `p` and `S` from `polyfit` and generates 95% prediction intervals `Y − DELTA` for new observations at the values in `X`.

`[Y,DELTA] = polyconf(p,X,S,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs chosen from the following list.

Parameter	Value
`'alpha'`	A value between 0 and 1 specifying a confidence level of `100*(1-alpha)`%. The default is `0.05`.
`'mu'`	A two-element vector containing centering and scaling parameters. With this option, `polyconf` uses `(X-mu(1))/mu(2)` in place of `X`.
`'predopt'`	Either `'observation'` (the default) to compute prediction intervals for new observations at the values in `X`, or `'curve'` to compute confidence intervals for the fit evaluated at the values in `X`. See below.
`'simopt'`	Either `'off'` (the default) for nonsimultaneous bounds, or `'on'` for simultaneous bounds. See below.

The `'predopt'` and `'simopt'` parameters can be understood in terms of the following functions:

- $p(x)$ — the unknown mean function estimated by the fit

- $l(x)$ — the lower confidence bound
- $u(x)$ — the upper confidence bound

Suppose you make a new observation y_{n+1} at x_{n+1}, so that

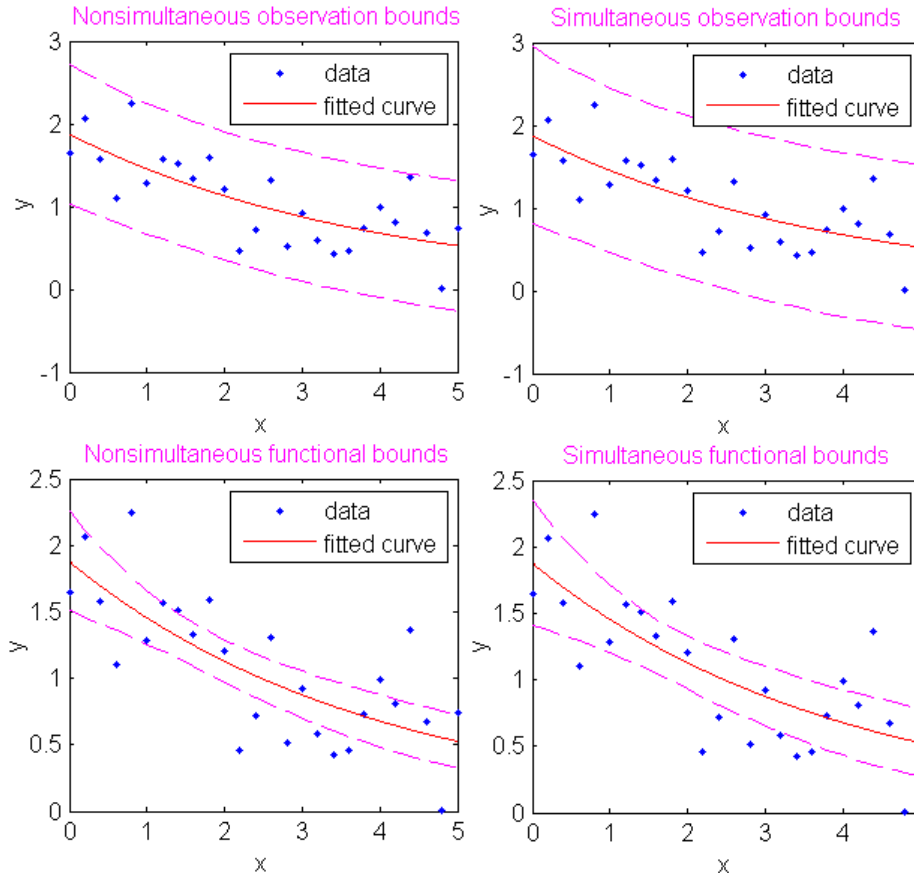
$$y_{n+1}(x_{n+1}) = p(x_{n+1}) + \varepsilon_{n+1}$$

By default, the interval $[l_{n+1}(x_{n+1}), u_{n+1}(x_{n+1})]$ is a 95% confidence bound on $y_{n+1}(x_{n+1})$.

The following combinations of the `'predopt'` and `'simopt'` parameters allow you to specify other bounds.

`'simopt'`	`'predopt'`	**Bounded Quantity**
`'off'`	`'observation'`	$y_{n+1}(x_{n+1})$ (default)
`'off'`	`'curve'`	$p(x_{n+1})$
`'on'`	`'observation'`	$y_{n+1}(x)$, for all x
`'on'`	`'curve'`	$p(x)$, for all x

In general, `'observation'` intervals are wider than `'curve'` intervals, because of the additional uncertainty of predicting a new response value (the curve plus random errors). Likewise, simultaneous intervals are wider than nonsimultaneous intervals, because of the additional uncertainty of bounding values for all predictors x.



Examples

This example uses code from the documentation example function `polydemo`, and calls the documentation example function `polystr` to convert the coefficient vector `p` into a string for the polynomial expression displayed in the figure title. It combines the functions `polyfit`, `polyval`, `roots`, and `polyconf` to produce a formatted display of data with a polynomial fit.

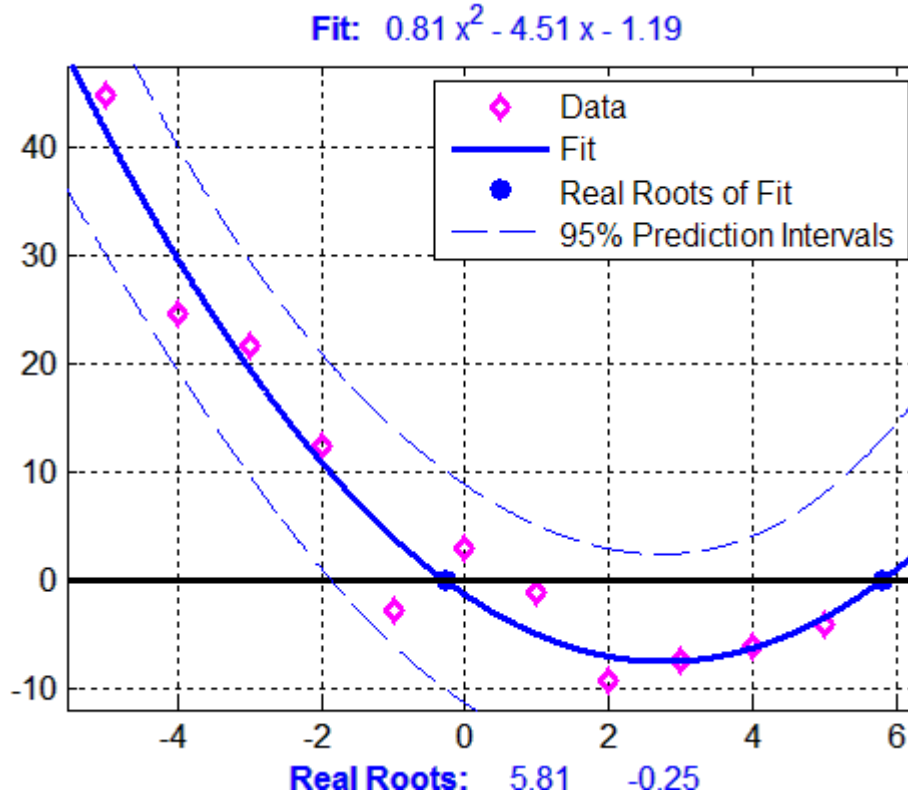
Note Statistics Toolbox documentation example files are located in the `\help\toolbox\stats\examples` subdirectory of your MATLAB root folder (`matlabroot`). This subdirectory is not on the MATLAB path at installation. To use the files in this subdirectory, either add the subdirectory to the MATLAB path (`addpath`) or make the subdirectory your current working folder (`cd`).

Display simulated data with a quadratic trend, a fitted quadratic polynomial, and 95% prediction intervals for new observations:

```
xdata = -5:5;
ydata = x.^2 - 5*x - 3 + 5*randn(size(x));

degree = 2;  % Degree of the fit
alpha = 0.05; % Significance level

% Compute the fit and return the structure used by
% POLYCONF.
[p,S] = polyfit(xdata,ydata,degree);

% Compute the real roots and determine the extent of the
% data.
r = roots(p)';        % Roots as a row vector.
real_r = r(imag(r) == 0);  % Real roots.

% Assure that the data are row vectors.
xdata = reshape(xdata,1,length(xdata));
ydata = reshape(ydata,1,length(ydata));

% Extent of the data.
mx = min([real_r,xdata]);
Mx = max([real_r,xdata]);
my = min([ydata,0]);
My = max([ydata,0]);
```

```
% Scale factors for plotting.
sx = 0.05*(Mx-mx);
sy = 0.05*(My-my);

% Plot the data, the fit, and the roots.
hdata = plot(xdata,ydata,'md','MarkerSize',5,...
  'LineWidth',2);
hold on
xfit = mx-sx:0.01:Mx+sx;
yfit = polyval(p,xfit);
hfit = plot(xfit,yfit,'b-','LineWidth',2);
hroots = plot(real_r,zeros(size(real_r)),...
              'bo','MarkerSize',5,...
              'LineWidth',2,...
              'MarkerFaceColor','b');
grid on
plot(xfit,zeros(size(xfit)),'k-','LineWidth',2)
axis([mx-sx Mx+sx my-sy My+sy])

% Add prediction intervals to the plot.
[Y,DELTA] = polyconf(p,xfit,S,'alpha',alpha);
hconf = plot(xfit,Y+DELTA,'b--');
plot(xfit,Y-DELTA,'b--')

% Display the polynomial fit and the real roots.
approx_p = round(100*p)/100; % Round for display.
htitle = title(['{\bf Fit:   }',...
  texlabel(polystr(approx_p))]);
set(htitle,'Color','b')
approx_real_r = round(100*real_r)/100; % Round for display.
hxlabel = xlabel(['{\bf Real Roots:     }',...
    num2str(approx_real_r)]);
set(hxlabel,'Color','b')

% Add a legend.
legend([hdata,hfit,hroots,hconf],...
        'Data','Fit','Real Roots of Fit',...
```

```
'95% Prediction Intervals')
```



See Also

`polyfit` | `polyval` | `polytool`

Purpose

Interactive polynomial fitting

Syntax

```
polytool
polytool(x,y)
polytool(x,y,n)
polytool(x,y,n,alpha)
polytool(x,y,n,alpha,xname,yname)
h = polytool(...)
```

Description

`polytool`

`polytool(x,y)` fits a line to the vectors `x` and `y` and displays an interactive plot of the result in a graphical interface. You can use the interface to explore the effects of changing the parameters of the fit and to export fit results to the workspace.

`polytool(x,y,n)` initially fits a polynomial of degree `n`. The default is `1`, which produces a linear fit.

`polytool(x,y,n,alpha)` initially plots `100(1 - alpha)`% confidence intervals on the predicted values. The default is `0.05` which results in 95% confidence intervals.

`polytool(x,y,n,alpha,xname,yname)` labels the `x` and `y` values on the graphical interface using the strings `xname` and `yname`. Specify `n` and `alpha` as `[]` to use their default values.

`h = polytool(...)` outputs a vector of handles, `h`, to the line objects in the plot. The handles are returned in the degree: data, fit, lower bounds, upper bounds.

See Also

`polyfit` | `polyval` | `polyconf` | `invpred`

gmdistribution.posterior

Purpose

Posterior probabilities of components

Syntax

```
P = posterior(obj,X)
[P,nlogl] = posterior(obj,X)
```

Description

`P = posterior(obj,X)` returns the posterior probabilities of each of the k components in the Gaussian mixture distribution defined by `obj` for each observation in the data matrix `X`. `X` is n-by-d, where n is the number of observations and d is the dimension of the data. `obj` is an object created by `gmdistribution` or `fit`. `P` is n-by-k, with `P(I,J)` the probability of component `J` given observation `I`.

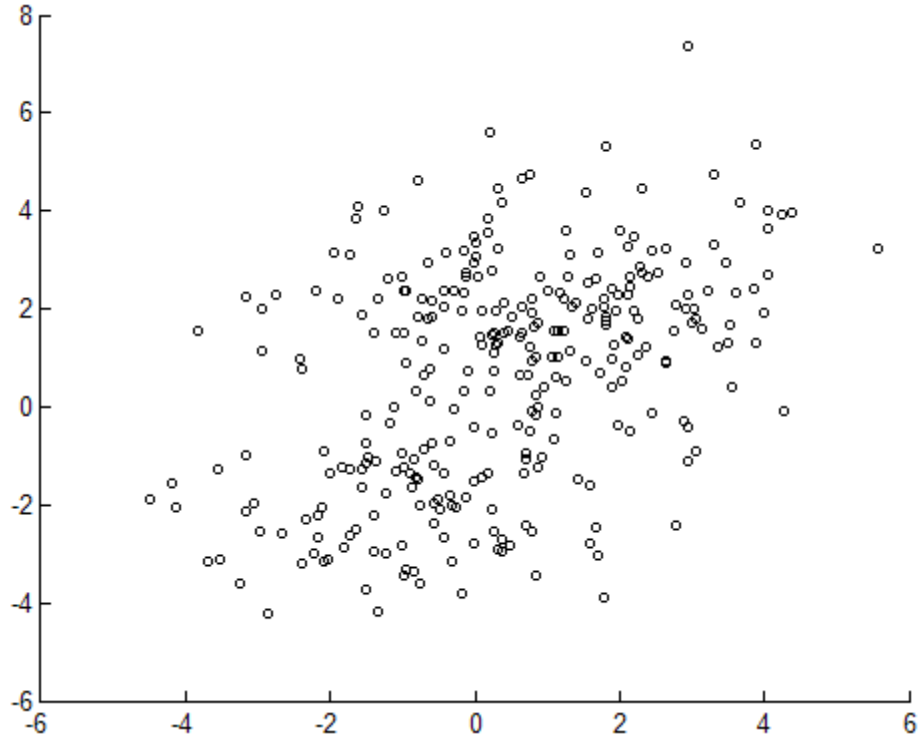
`posterior` treats `NaN` values as missing data. Rows of `X` with `NaN` values are excluded from the computation.

`[P,nlogl] = posterior(obj,X)` also returns `nlogl`, the negative log-likelihood of the data.

Examples

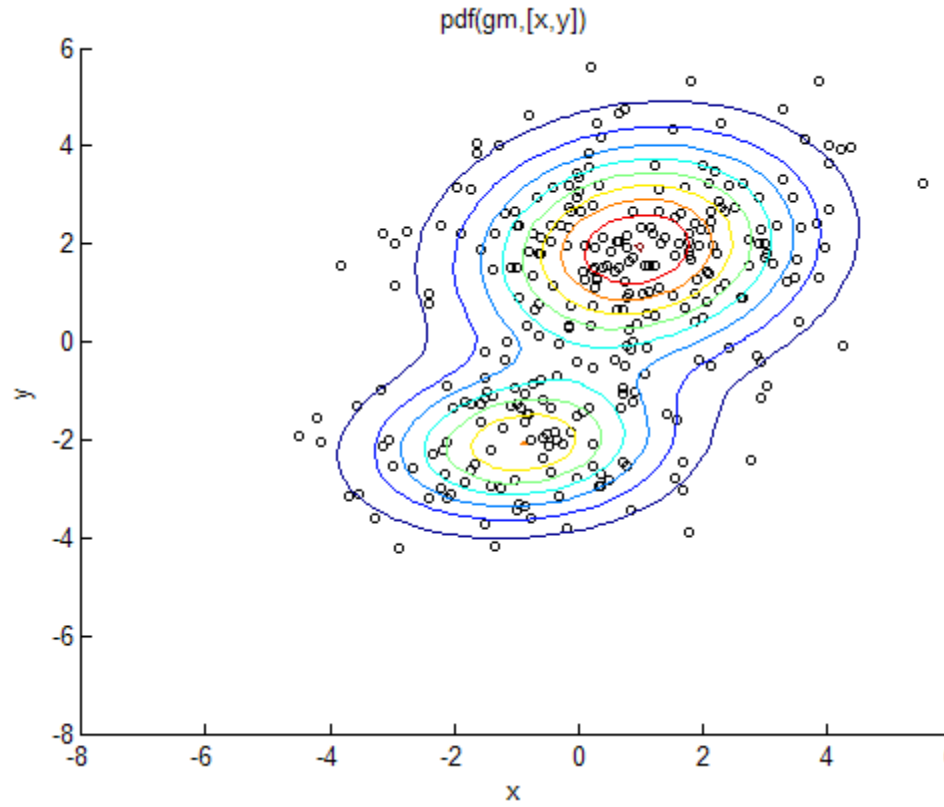
Generate data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function:

```
MU1 = [1 2];
SIGMA1 = [2 0; 0 .5];
MU2 = [-3 -5];
SIGMA2 = [1 0; 0 1];
X = [mvnrnd(MU1,SIGMA1,1000);mvnrnd(MU2,SIGMA2,1000)];

scatter(X(:,1),X(:,2),10,'.')
hold on
```



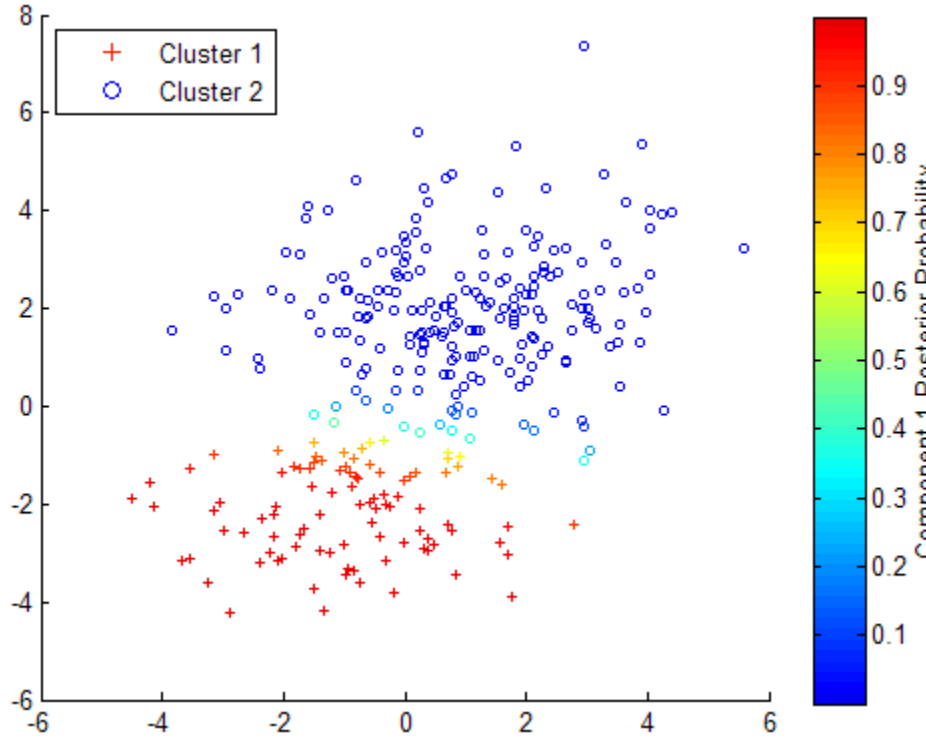
Fit a two-component Gaussian mixture model:

```
obj = gmdistribution.fit(X,2);
h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
```



Compute posterior probabilities of the components:

```
P = posterior(obj,X);

delete(h)
scatter(X(:,1),X(:,2),10,P(:,1),'.')
hb = colorbar;
ylabel(hb,'Component 1 Probability')
```



See Also

`gmdistribution` | `fit` | `cluster` | `mahal`

NaiveBayes.posterior

Purpose

Compute posterior probability of each class for test data

Syntax

```
post = posterior(nb,test)
[post,cpre] = posterior(nb,test)
[post,cpre,logp] = posterior(nb,test)
[...] = posterior(..., 'HandleMissing',val)
```

Description

`post = posterior(nb,test)` returns the posterior probability of the observations in `test` according to the `NaiveBayes` object `nb`. `test` is a `N`-by-`nb.ndims` matrix, where `N` is the number of observations in the test data. Rows of `test` correspond to points, columns of `test` correspond to features. `post` is a `N`-by-`nb.nclasses` matrix containing the posterior probability of each observation for each class. `post(i,j)` is the posterior probability of point I belonging to class `j`. Classes are ordered the same as `nb.clevels`, i.e., column `j` of `post` corresponds to the `j`th class in `nb.clevels`. The posterior probabilities corresponding to any empty classes are `NaN`.

`[post,cpre] = posterior(nb,test)` returns `cpre`, an `N`-by-1 vector, containing the class to which each row of `test` has been assigned. `cpre` has the same type as `nb.CLevels`.

`[post,cpre,logp] = posterior(nb,test)` returns `logp`, an `N`-by-1 vector containing estimates of the log of the probability density function (PDF). `logp(i)` is the log of the PDF of point `i`. The PDF value of point `i` is the sum of `Prob(point I | class J) * Pr{class J}` taken over all classes.

`[...] = posterior(..., 'HandleMissing',val)` specifies how `posterior` treats NaN (missing values). `val` can be one of the following:

`'off'` (default)	Observations with `NaN` in any of the columns are not classified into any class. The corresponding rows in `post` and `logp` are `NaN`. The corresponding rows in `cpre` are `NaN` (if `obj.clevels` is numeric or logical), empty strings (if `obj.clevels` is char or cell array of strings) or (if `obj.clevels` is categorical).
`'on'`	For observations having `NaN` in some (but not all) columns, `post` and `cpre` are computed using the columns with non-`NaN` values. Corresponding `logp` values are `NaN`.

See Also

`NaiveBayes | fit | predict`

prctile

Purpose

Calculate percentile values

Syntax

```
Y = prctile(X,p)
Y = prctile(X,p,dim)
```

Description

`Y = prctile(X,p)` returns percentiles of the values in `X`. `p` is a scalar or a vector of percent values. When `X` is a vector, `Y` is the same size as `p` and `Y(i)` contains the `p(i)`th percentile. When `X` is a matrix, the `i`th row of `Y` contains the `p(i)`th percentiles of each column of `X`. For N-dimensional arrays, `prctile` operates along the first nonsingleton dimension of `X`.

`Y = prctile(X,p,dim)` calculates percentiles along dimension `dim`. The `dim`'th dimension of `Y` has length `length(p)`.

Percentiles are specified using percentages, from 0 to 100. For an n-element vector `X`, `prctile` computes percentiles as follows:

1. The sorted values in `X` are taken to be the 100(0.5/n), 100(1.5/n), ..., 100([n-0.5]/n) percentiles.
2. Linear interpolation is used to compute percentiles for percent values between 100(0.5/n) and 100([n-0.5]/n).
3. The minimum or maximum values in `X` are assigned to percentiles for percent values outside that range.

`prctile` treats `NaN`s as missing values and removes them.

Examples

```
x = (1:5)'*(1:5)
x =
   1   2   3   4   5
   2   4   6   8  10
   3   6   9  12  15
   4   8  12  16  20
   5  10  15  20  25

y = prctile(x,[25 50 75])
```

```
y =
   1.7500   3.5000   5.2500   7.0000   8.7500
   3.0000   6.0000   9.0000  12.0000  15.0000
   4.2500   8.5000  12.7500  17.0000  21.2500
```

CompactClassificationDiscriminant.predict

Purpose

Predict classification

Syntax

```
label = predict(obj,X)
[label,score] = predict(obj,X)
[label,score,cost] = predict(obj,X)
```

Description

`label = predict(obj,X)` returns a vector of predicted class labels for a matrix `X`, based on `obj`, a trained full or compact classifier.

`[label,score] = predict(obj,X)` returns a matrix of scores (posterior probabilities).

`[label,score,cost] = predict(obj,X)` returns a matrix of costs; `label` is the vector or minimal costs for each row of `cost`.

Input Arguments

`obj`

Discriminant analysis classifier of class `ClassificationDiscriminant` or `CompactClassificationDiscriminant`, typically constructed with `ClassificationDiscriminant.fit`.

`X`

Matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `obj`.

Output Arguments

`label`

Vector of class labels of the same type as the response data used in training `obj`. Each entry of `labels` corresponds to a predicted class label for the corresponding row of `X`; see "Predicted Class Label" on page 20-1422.

`score`

Numeric matrix of size `N`-by-`K`, where `N` is the number of observations (rows) in `X`, and `K` is the number of classes (in

`obj.ClassNames`). `score(i,j)` is the posterior probability that row `i` of `X` is of class `j`; see "Posterior Probability" on page 20-1421.

`cost`

Matrix of expected costs of size `N`-by-`K`. `cost(i,j)` is the cost of classifying row `i` of `X` as class `j`. See "Cost" on page 20-1422.

Definitions

Posterior Probability

The posterior probability that a point z belongs to class j is the product of the prior probability and the multivariate normal density. The density function of the multivariate normal with mean μ_j and covariance Σ_j at a point z is

$$P(x \mid k) = \frac{1}{\left(2\pi|\Sigma_k|\right)^{1/2}} \exp\left(-\frac{1}{2}(x-\mu_k)^T \Sigma_k^{-1}(x-\mu_k)\right),$$

where $|\Sigma_k|$ is the determinant of Σ_k, and Σ_k^{-1} is the inverse matrix.

Let $P(k)$ represent the prior probability of class k. Then the posterior probability that an observation x is of class k is

$$\hat{P}(k \mid x) = \frac{P(x \mid k)P(k)}{P(x)},$$

where $P(x)$ is a normalization constant, the sum over k of $P(x \mid k)P(k)$.

Prior Probability

The prior probability is one of three choices:

- `'uniform'` — The prior probability of class `k` is one over the total number of classes.
- `'empirical'` — The prior probability of class `k` is the number of training samples of class `k` divided by the total number of training samples.

- Custom — The prior probability of class `k` is the `k`th element of the `prior` vector. See `ClassificationDiscriminant.fit`.

After creating a classifier `obj`, you can set the prior by dot addressing:

```
obj.Prior = v;
```

where `v` is a vector of positive elements representing the frequency with which each element occurs. You do not need to retrain the classifier when you set a new prior.

Cost

The matrix of expected costs per observation is defined in "Cost" on page 12-8.

Predicted Class Label

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \arg\min_{y=1,\ldots,K} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

Examples

Examine predictions for a few rows in the Fisher iris data:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species);
X = meas(99:102,:); % take four rows
```

```
[label score cost] = predict(obj,X)

label =
    'versicolor'
    'versicolor'
    'virginica'
    'virginica'

score =
    0.0000    1.0000    0.0000
    0.0000    0.9999    0.0001
    0.0000    0.0000    1.0000
    0.0000    0.0011    0.9989

cost =
    1.0000    0.0000    1.0000
    1.0000    0.0001    0.9999
    1.0000    1.0000    0.0000
    1.0000    0.9989    0.0011
```

See Also

`ClassificationDiscriminant` | `ClassificationDiscriminant.fit` | `edge` | `loss` | `margin`

How To

- “Discriminant Analysis” on page 12-3

CompactClassificationEnsemble.predict

Purpose

Predict classification

Syntax

```
labels = predict(ens,X)
[labels,score] = predict(ens,X)
[labels,...] = predict(ens,X,Name,Value)
```

Description

`labels = predict(ens,X)` returns a vector of predicted class labels for a matrix `X`, based on `ens`, a trained full or compact classification ensemble.

`[labels,score] = predict(ens,X)` also returns scores for all classes.

`[labels,...] = predict(ens,X,Name,Value)` predicts classifications with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A classification ensemble created by `fitensemble`, or a compact classification ensemble created by `compact`.

`X`

A matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `ens`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners `predict` uses for computation of responses, a numeric vector.

Default: `1:T`, where `T` is the number of weak learners in `ens`

`UseObsForLearner`

A logical matrix of size `N`-by-`T`, where:

- `N` is the number of rows of `X`.
- `T` is the number of weak learners in `ens`.

When `UseObsForLearner(i,j)` is `true`, learner `j` is used in predicting the class of row `i` of `X`.

Default: `true(N,T)`

Output Arguments

`labels`

Vector of classification labels. `labels` has the same data type as the labels used in training `ens`.

`score`

A matrix with one row per observation and one column per class. For each observation and each class, the score generated by each tree is the probability of this observation originating from this class computed as the fraction of observations of this class in a tree leaf. `predict` averages these scores over all trees in the ensemble.

Definitions

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Train a boosting ensemble for the `ionosphere` data, and predict the classification of the mean of the data:

```
load ionosphere;
ada = fitensemble(X,Y,'AdaBoostM1',100,'tree');
Xbar = mean(X);
[ypredict score] = predict(ada,Xbar)

ypredict =
    'g'

score =
   -2.9460    2.9460
```

See Also

`margin` | `edge` | `loss`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Predict classification

Syntax

```
label = predict(tree,X)
[label,score] = predict(tree,X)
[label,score,node] = predict(tree,X)
[label,score,node,cnum] = predict(tree,X)
[label,...] = predict(tree,X,Name,Value)
```

Description

`label = predict(tree,X)` returns a vector of predicted class labels for a matrix `X`, based on `tree`, a trained full or compact classification tree.

`[label,score] = predict(tree,X)` returns a matrix of scores, indicating the likelihood that a label comes from a particular class.

`[label,score,node] = predict(tree,X)` returns a vector of predicted node numbers for the classification, based on `tree`.

`[label,score,node,cnum] = predict(tree,X)` returns a vector of predicted class number for the classification, based on `tree`.

`[label,...] = predict(tree,X,Name,Value)` returns labels with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`tree`

A classification tree created by `ClassificationTree.fit`, or a compact classification tree created by `compact`.

`X`

A matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `tree`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`subtrees`

Numeric vector of pruning levels, with `0` representing the full, unpruned tree. To use the `subtrees` name-value pair, `tree` must include a pruning sequence as created by the `ClassificationTree.fit` or `prune` methods. If `subtrees` has `T` elements, and `X` has `N` rows, then `labels` is an `N`-by-`T` matrix. The `i`th column of `labels` contains the fitted values produced by the `subtrees(I)` subtree. Similarly, `score` is an `N`-by-`K`-by-`T` array, and `node` and `cnum` are `N`-by-`T` matrices. `subtrees` must be sorted in ascending order. (To compute fitted values for a tree that is not part of the optimal pruning sequence, first use `prune` to prune the tree.)

Default: `0`

Output Arguments

`label`

Vector of class labels of the same type as the response data used in training `tree`. Each entry of `labels` corresponds to a predicted class label for the corresponding row of `X`.

`score`

Numeric matrix of size `N`-by-`K`, where `N` is the number of observations (rows) in `X`, and `K` is the number of classes (in `tree.ClassNames`). `score(i,j)` is the posterior probability that row `i` of `X` is of class `j`.

`node`

Numeric vector of node numbers for the predicted classes. Each entry corresponds to the predicted node in `tree` for the corresponding row of `X`.

`cnum`

Numeric vector of class numbers corresponding to the predicted `labels`. Each entry of `cnum` corresponds to a predicted class number for the corresponding row of `X`.

Definitions

Predictive Measure of Association

The predictive measure of association between the optimal split on variable i and a surrogate split on variable j is:

$$\lambda_{i,j} = \frac{\min(P_L, P_R) - \left(1 - P_{L_i L_j} - P_{R_i R_j}\right)}{\min(P_L, P_R)}.$$

Here

- P_L and P_R are the node probabilities for the optimal split of node i into Left and Right nodes respectively.
- $P_{L_i L_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Left.
- $P_{R_i R_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Right.

Clearly, $\lambda_{i,j}$ lies from $-\infty$ to 1. Variable j is a worthwhile surrogate split for variable i if $\lambda_{i,j} > 0$.

Examples

Examine predictions for a few rows in the Fisher iris data:

```
load fisheriris
tree = ClassificationTree.fit(meas,species);
X = meas(99:102,:); % take four rows
[label score node cnum] = predict(tree,X)

label =
    'versicolor'
    'versicolor'
    'virginica'
    'virginica'

score =
```

```
         0    1.0000         0
         0    1.0000         0
         0    0.0217    0.9783
         0    0.0217    0.9783

node =
     8
     8
     5
     5

cnum =
     2
     2
     3
     3
```

Examine predictions from pruned trees for the Fisher iris model:

```
load fisheriris
tree = ClassificationTree.fit(meas,species);
X = meas(99:102,:); % taking four rows
[label score node cnum] = predict(tree,X,'subtrees',[2 3 4])

label =
    'versicolor'    'versicolor'    'setosa'
    'versicolor'    'versicolor'    'setosa'
    'virginica'     'versicolor'    'setosa'
    'virginica'     'versicolor'    'setosa'

score(:,:,1) =
         0    0.9074    0.0926
         0    0.9074    0.0926
         0    0.0217    0.9783
         0    0.0217    0.9783
```

```
score(:,:,2) =
         0    0.5000    0.5000
         0    0.5000    0.5000
         0    0.5000    0.5000
         0    0.5000    0.5000

score(:,:,3) =
    0.3333    0.3333    0.3333
    0.3333    0.3333    0.3333
    0.3333    0.3333    0.3333
    0.3333    0.3333    0.3333

node =
     4     3     1
     4     3     1
     5     3     1
     5     3     1

cnum =
     2     2     1
     2     2     1
     3     2     1
     3     2     1
```

Algorithms

`predict` generates predictions by following the branches of `tree` until it reaches a leaf node or a missing value. If `predict` reaches a leaf node, it returns the classification of that node.

If `predict` reaches a node with a missing value for a predictor, its behavior depends on the setting of the `Surrogate` name-value pair when `ClassificationTree.fit` constructs `tree`.

- **`Surrogate = 'off'`** (default) — `predict` returns the label with the largest number of training samples that reach the node.
- **`Surrogate = 'on'`** — `predict` uses the best surrogate split at the node. If all surrogate split variables with positive *predictive measure of association* are missing, `predict` returns the label with the largest

number of training samples that reach the node. For a definition, see "Predictive Measure of Association" on page 20-1429.

See Also

`ClassificationTree.fit` | `compact` | `prune` | `loss` | `edge` | `margin`

How To

- Chapter 13, "Nonparametric Supervised Learning"

Purpose

Predict response of ensemble

Syntax

```
Yfit = predict(ens,Xdata)
Yfit = predict(ens,Xdata,Name,Value)
```

Description

`Yfit = predict(ens,Xdata)` returns predicted responses to the data in `Xdata`, based on the `ens` regression ensemble model.

`Yfit = predict(ens,Xdata,Name,Value)` predicts with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

Regression ensemble created by `fitensemble`, or by the `compact` method.

`Xdata`

Numeric array with the same number of columns as the array used for creating `ens`. Each row of `Xdata` corresponds to one data point, and each column corresponds to one predictor.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `ens.NTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NTrained`

`UseObsForLearner`

A logical matrix of size `N`-by-`NTrained`, where `N` is the number of observations in `ens.X`, and `NTrained` is the number of weak learners. When `UseObsForLearner(I,J)` is `true`, `predict` uses learner `J` in predicting observation `I`.

Default: `true(N,NTrained)`

Output Arguments

`Yfit`

A numeric column vector with the same number of rows as `Xdata`. Each row of `Yfit` gives the predicted response to the corresponding row of `Xdata`, based on the `ens` regression model.

Examples

Find the predicted mileage for a four-cylinder car, with 200 cubic inch engine displacement, 150 horsepower, weighing 3000 lbs, based on the `carsmall` data:

```
load carsmall
X = [Cylinders Displacement Horsepower Weight];
rens = fitensemble(X,MPG,'LSBoost',100,'Tree');
Mileage = predict(rens,[4 200 150 3000])

Mileage =
   20.4982
```

See Also

`loss` | `fitensemble`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Predict response of regression tree

Syntax

```
Yfit = predict(tree,Xdata)
[Yfit,node] = predict(tree,Xdata)
[Yfit,node] = predict(tree,Xdata,Name,Value)
```

Description

`Yfit = predict(tree,Xdata)` returns predicted responses to the data in `Xdata`, based on the `tree` regression tree.

`[Yfit,node] = predict(tree,Xdata)` returns the predicted node numbers of `tree` in response to `Xdata`.

`[Yfit,node] = predict(tree,Xdata,Name,Value)` predicts response with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`tree`

Regression tree created by `RegressionTree.fit`, or by the `compact` method.

`Xdata`

Numeric array with the same number of columns as the array used for creating `tree`. Each row of `Xdata` corresponds to one data point, and each column corresponds to one predictor.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`subtrees`

Numeric vector of pruning levels, with 0 representing the full, unpruned tree. To use the `subtrees` name-value pair, `tree` must include a pruning sequence as created by the `RegressionTree.fit` or `prune` methods. If `subtrees` has `T`

elements, and X has N rows, then Yfit is an N-by-T matrix. The ith column of Yfit contains the fitted values produced by the subtrees(I) subtree. Similarly, node is an N-by-T matrix. subtrees must be sorted in ascending order. (To compute fitted values for a tree that is not part of the optimal pruning sequence, first use prune to prune the tree.)

Default: 0

Output Arguments

Yfit

A numeric column vector with the same number of rows as Xdata. Each row of Yfit gives the predicted response to the corresponding row of Xdata, based on the tree regression model.

node

Numeric vector of node numbers for the predictions. Each entry corresponds to the predicted leaf node in tree for the corresponding row of Xdata.

Examples

Find the predicted mileage for a car with 200 cubic inch engine displacement, 150 horsepower, weighing 3000 lbs, based on the carsmall data:

```
load carsmall
X = [Displacement Horsepower Weight];
tree = RegressionTree.fit(X,MPG);
Mileage = predict(tree,[200 150 3000])

Mileage =
   21.9375
```

See Also

RegressionTree.fit | compact | loss

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Predict response

Syntax

```
YFIT = predict(B,X)
[YFIT,stdevs] = predict(B,X)
[YFIT,scores] = predict(B,X)
[YFIT,scores,stdevs] = predict(B,X)
Y = predict(B,X,'param1',val1,'param2',val2,...)
```

Description

`YFIT = predict(B,X)` computes the predicted response of the trained ensemble `B` for predictors `X`. By default, `predict` takes a democratic (nonweighted) average vote from all trees in the ensemble. In `X`, rows represent observations and columns represent variables. `YFIT` is a cell array of strings for classification and a numeric array for regression.

For regression, `[YFIT,stdevs] = predict(B,X)` also returns standard deviations of the computed responses over the ensemble of the grown trees.

For classification, `[YFIT,scores] = predict(B,X)` returns scores for all classes. `scores` is a matrix with one row per observation and one column per class. For each observation and each class, the score generated by each tree is the probability of this observation originating from this class computed as the fraction of observations of this class in a tree leaf. `predict` averages these scores over all trees in the ensemble.

`[YFIT,scores,stdevs] = predict(B,X)` also returns standard deviations of the computed scores for classification. `stdevs` is a matrix with one row per observation and one column per class, with standard deviations taken over the ensemble of the grown trees.

`Y = predict(B,X,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'trees'`	Array of tree indices to use for computation of responses. Default is `'all'`.
`'treeweights'`	Array of `NTrees` weights for weighting votes from the specified trees.
`'useifort'`	Logical matrix of size `Nobs`-by-`NTrees` indicating which trees to use to make predictions for each observation. By default all trees are used for all observations.

See Also

`classregtree.eval` | `TreeBagger.predict`

Purpose

Predict class label for test data

Syntax

```
cpre = predict(nb,test)
cpre = predict(...,'HandleMissing',val)
```

Description

`cpre = predict(nb,test)` classifies each row of data in `test` into one of the classes according to the `NaiveBayes` classifier `nb`, and returns the predicted class level `cpre`. `test` is an `N`-by-`nb.ndims` matrix, where `N` is the number of observations in the test data. Rows of `test` correspond to points, columns of `test` correspond to features. `cpre` is an `N`-by-1 vector of the same type as `nb.CLevels`, and it indicates the class to which each row of `test` has been assigned.

`cpre = predict(...,'HandleMissing',val)` specifies how `predict` treats `NaN` (missing values). `val` can be one of the following:

`'off'` (default)	Observations with `NaN` in any of the columns are not classified into any class. The corresponding rows in `post` and `logp` are `NaN`. The corresponding rows in `cpre` are `NaN` (if `obj.clevels` is numeric or logical), empty strings (if `obj.clevels` is char or cell array of strings) or `<undefined>` (if `obj.clevels` is categorical).
`'on'`	For observations having `NaN` in some (but not all) columns, `post` and `predict` computes `cpre` using the columns with non-`NaN` values. Corresponding `logp` values are `NaN`.

See Also

`NaiveBayes` | `fit` | `posterior`

TreeBagger.predict

Purpose

Predict response

Syntax

```
Y = predict(B,X)
[Y,stdevs] = predict(B,X)
[Y,scores] = predict(B,X)
[Y,scores,stdevs] = predict(B,X)
Y = predict(B,X,'param1',val1,'param2',val2,...)
```

Description

`Y = predict(B,X)` computes predicted response of the trained ensemble `B` for data `X`. The output has one prediction for each row of `X`. The returned `Y` is a cell array of strings for classification and a numeric array for regression.

For regression, `[Y,stdevs] = predict(B,X)` also returns standard deviations of the computed responses over the ensemble of the grown trees.

For classification, `[Y,scores] = predict(B,X)` returns scores for all classes. `scores` is a matrix with one row per observation and one column per class. For each observation and each class, the score generated by each tree is the probability of this observation originating from this class computed as the fraction of observations of this class in a tree leaf. `predict` averages these scores over all trees in the ensemble.

`[Y,scores,stdevs] = predict(B,X)` also returns standard deviations of the computed scores for classification. `stdevs` is a matrix with one row per observation and one column per class, with standard deviations taken over the ensemble of the grown trees.

`Y = predict(B,X,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'trees'`	Array of tree indices to use for computation of responses. Default is `'all'`.
`'treeweights'`	Array of `NTrees` weights for weighting votes from the specified trees.
`'useifort'`	Logical matrix of size `Nobs`-by-`NTrees` indicating which trees to use to make predictions for each observation. By default all trees are used for all observations.

See Also

`CompactTreeBagger.predict`

CompactClassificationEnsemble.predictorImportance

Purpose

Estimates of predictor importance

Syntax

```
imp = predictorImportance(ens)
[imp,ma] = predictorImportance(ens)
```

Description

`imp = predictorImportance(ens)` computes estimates of predictor importance for `ens` by summing these estimates over all weak learners in the ensemble. `imp` has one element for each input predictor in the data used to train this ensemble. A high value indicates that this predictor is important for `ens`.

`[imp,ma] = predictorImportance(ens)` returns a `P`-by-`P` matrix with predictive measures of association for `P` predictors, when the learners in `ens` contain surrogate splits. See "Definitions" on page 20-1443.

Input Arguments

`ens`

A classification ensemble created by `fitensemble`, or by the `compact` method.

Output Arguments

`imp`

A row vector with the same number of elements as the number of predictors (columns) in `ens.X`. The entries are the estimates of predictor importance, with `0` representing the smallest possible importance.

`ma`

A `P`-by-`P` matrix of predictive measures of association for `P` predictors. Element `ma(I,J)` is the predictive measure of association averaged over surrogate splits on predictor `J` for which predictor `I` is the optimal split predictor. `predictorImportance` averages this predictive measure of association over all trees in the ensemble.

Definitions

Predictor Importance

`predictorImportance` computes estimates of predictor importance for `ens` by summing changes in the *risk* due to splits on every predictor and dividing the sum by the number of tree nodes. If `ens` is grown without surrogate splits, this sum is taken over best splits found at each branch node. If `ens` is grown with surrogate splits, this sum is taken over all splits at each branch node including surrogate splits. `imp` has one element for each input predictor in the data used to train `ens`. Predictor importance associated with this split is computed as the difference between the risk for the parent node and the total risk for the two children.

Impurity and Node Error

`ClassificationTree` splits nodes based on either *impurity* or *node error*. Impurity means one of several things, depending on your choice of the `SplitCriterion` name-value pair:

- Gini's Diversity Index (`gdi`) — The Gini index of a node is

  $$1 - \sum_i p^2(i),$$

  where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index `0`; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.

- Deviance (`'deviance'`) — With $p(i)$ defined as for the Gini index, the deviance of a node is

  $$-\sum_i p(i) \log p(i).$$

  A pure node has deviance `0`; otherwise, the deviance is positive.

- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a

split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

$$P(L)P(R)\left(\sum_i |L(i) - R(i)|\right)^2,$$

where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.

- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with largest number of training samples at a node, the node error is

  $1 - p(j)$.

Predictive Measure of Association

The predictive measure of association between the optimal split on variable i and a surrogate split on variable j is:

$$\lambda_{i,j} = \frac{\min(P_L, P_R) - \left(1 - P_{L_i L_j} - P_{R_i R_j}\right)}{\min(P_L, P_R)}.$$

Here

- P_L and P_R are the node probabilities for the optimal split of node i into Left and Right nodes respectively.
- $P_{L_i L_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Left.
- $P_{R_i R_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Right.

Clearly, $\lambda_{i,j}$ lies from $-\infty$ to 1. Variable j is a worthwhile surrogate split for variable i if $\lambda_{i,j} > 0$.

Element `ma(i,j)` is the predictive measure of association averaged over surrogate splits on predictor `j` for which predictor `i` is the optimal split predictor. This average is computed by summing positive values of the predictive measure of association over optimal splits on predictor `i` and surrogate splits on predictor `j` and dividing by the total number of optimal splits on predictor `i`, including splits for which the predictive measure of association between predictors `i` and `j` is negative.

Examples

Estimate the predictor importance for all variables in the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
imp = predictorImportance(ens)

imp =
    0.0001    0.0005    0.0384    0.0146
```

The first two predictors are not very important in `ens`.

Estimate the predictor importance for all variables in the Fisher iris data for an ensemble where the trees contain surrogate splits:

```
load fisheriris
surrtree = ClassificationTree.template('Surrogate','on');
ens2 = fitensemble(meas,species,'AdaBoostM2',100,surrtree);
[imp2,ma] = predictorImportance(ens2)

imp2 =
    0.0224    0.0142    0.0525    0.0508

ma =
    1.0000         0    0.0001    0.0001
    0.0115    1.0000    0.0023    0.0054
```

```
    0.2810    0.1747    1.0000    0.5372
    0.0789    0.0463    0.2339    1.0000
```

The first two predictors show much more importance than in the previous example.

See Also

`predictorImportance`

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Purpose

Estimates of predictor importance

Syntax

```
imp = predictorImportance(tree)
```

Description

`imp = predictorImportance(tree)` computes estimates of predictor importance for `tree` by summing changes in the risk due to splits on every predictor and dividing the sum by the number of tree nodes.

Input Arguments

`tree`

A classification tree created by `ClassificationTree.fit`, or by the `compact` method.

Output Arguments

`imp`

A row vector with the same number of elements as the number of predictors (columns) in `tree.X`. The entries are the estimates of predictor importance, with `0` representing the smallest possible importance.

Definitions

Predictor Importance

`predictorImportance` computes estimates of predictor importance for `tree` by summing changes in the *risk* due to splits on every predictor and dividing the sum by the number of tree nodes. If `tree` is grown without surrogate splits, this sum is taken over best splits found at each branch node. If `tree` is grown with surrogate splits, this sum is taken over all splits at each branch node including surrogate splits. `imp` has one element for each input predictor in the data used to train `tree`. Predictor importance associated with this split is computed as the difference between the risk for the parent node and the total risk for the two children.

Estimates of predictor importance do not depend on the order of predictors if you use surrogate splits, but do depend on the order if you do not use surrogate splits.

If you use surrogate splits, `predictorImportance` computes estimates before the tree is reduced by pruning or merging leaves. If you do not

use surrogate splits, `predictorImportance` computes estimates after the tree is reduced by pruning or merging leaves. Therefore, reducing the tree by pruning affects the predictor importance for a tree grown without surrogate splits, and does not affect the predictor importance for a tree grown with surrogate splits.

Impurity and Node Error

`ClassificationTree` splits nodes based on either *impurity* or *node error*. Impurity means one of several things, depending on your choice of the `SplitCriterion` name-value pair:

- Gini's Diversity Index (`gdi`) — The Gini index of a node is

  $$1 - \sum_i p^2(i),$$

  where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index `0`; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.

- Deviance (`'deviance'`) — With $p(i)$ defined as for the Gini index, the deviance of a node is

  $$-\sum_i p(i) \log p(i).$$

  A pure node has deviance `0`; otherwise, the deviance is positive.

- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

  $$P(L)P(R)\left(\sum_i |L(i) - R(i)|\right)^2,$$

where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.

- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with largest number of training samples at a node, the node error is

  $1 - p(j)$.

Examples

Estimate the predictor importance for all variables in the Fisher iris data:

```
load fisheriris
tree = ClassificationTree.fit(meas,species);
imp = predictorImportance(tree)

imp =
         0         0    0.0403    0.0303
```

The first two elements of `imp` are zero. Therefore, the first two predictors do not enter into `tree` calculations for classifying irises.

Estimate the predictor importance for all variables in the Fisher iris data for a tree grown with surrogate splits:

```
tree2 = ClassificationTree.fit(meas,species,...
    'Surrogate','on');
imp2 = predictorImportance(tree2)

imp2 =
    0.0287    0.0136    0.0560    0.0556
```

In this case, all predictors have some importance. As you expect by comparing to the first example, the first two predictors are less important than the final two.

Estimates of predictor importance do not depend on the order of predictors if you use surrogate splits, but do depend on the order if you do not use surrogate splits. For example, permute the order of the data columns in the previous example:

```
load fisheriris
meas3 = meas(:,[4 1 3 2]);
tree3 = ClassificationTree.fit(meas3,species);
imp3 = predictorImportance(tree2)

imp3 =
    0.0674         0    0.0033         0
```

The estimates of predictor importance are not a permutation of `imp` from the first example.

Estimate the predictor importance using surrogate splits.

```
tree4 = ClassificationTree.fit(meas3,species,...
    'Surrogate','on');
imp4 = predictorImportance(tree4)

imp4 =
    0.0556    0.0287    0.0560    0.0136
```

`imp4` is a permutation of `imp2`, demonstrating that estimates of predictor importance do not depend on the order of predictors with surrogate splits.

See Also

`predictorImportance`

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Purpose

Estimates of predictor importance

Syntax

```
imp = predictorImportance(ens)
[imp,ma] = predictorImportance(ens)
```

Description

`imp = predictorImportance(ens)` computes estimates of predictor importance for `ens` by summing these estimates over all weak learners in the ensemble. `imp` has one element for each input predictor in the data used to train this ensemble. A high value indicates that this predictor is important for `ens`.

`[imp,ma] = predictorImportance(ens)` returns a `P`-by-`P` matrix with predictive measures of association for `P` predictors.

Input Arguments

`ens`

A regression ensemble created by `fitensemble`, or by the `compact` method.

Output Arguments

`imp`

A row vector with the same number of elements as the number of predictors (columns) in `ens.X`. The entries are the estimates of predictor importance, with `0` representing the smallest possible importance.

`ma`

A `P`-by-`P` matrix of predictive measures of association for `P` predictors. Element `ma(I,J)` is the predictive measure of association averaged over surrogate splits on predictor `J` for which predictor `I` is the optimal split predictor. `predictorImportance` averages this predictive measure of association over all trees in the ensemble.

Definitions

Predictor Importance

`predictorImportance` computes estimates of predictor importance for `tree` by summing changes in the mean squared error (MSE) due to

splits on every predictor and dividing the sum by the number of tree nodes. If the tree is grown without surrogate splits, this sum is taken over best splits found at each branch node. If the tree is grown with surrogate splits, this sum is taken over all splits at each branch node including surrogate splits. `imp` has one element for each input predictor in the data used to train this tree. At each node, MSE is estimated as node error weighted by the node probability. Variable importance associated with this split is computed as the difference between MSE for the parent node and the total MSE for the two children.

Predictive Measure of Association

The predictive measure of association between the optimal split on variable i and a surrogate split on variable j is:

$$\lambda_{i,j} = \frac{\min(P_L, P_R) - \left(1 - P_{L_i L_j} - P_{R_i R_j}\right)}{\min(P_L, P_R)}.$$

Here

- P_L and P_R are the node probabilities for the optimal split of node i into Left and Right nodes respectively.
- $P_{L_i L_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Left.
- $P_{R_i R_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Right.

Clearly, $\lambda_{i,j}$ lies from $-\infty$ to 1. Variable j is a worthwhile surrogate split for variable i if $\lambda_{i,j} > 0$.

Element `ma(i,j)` is the predictive measure of association averaged over surrogate splits on predictor `j` for which predictor `i` is the optimal split predictor. This average is computed by summing positive values of the predictive measure of association over optimal splits on predictor `i` and surrogate splits on predictor `j` and dividing by the total number of

optimal splits on predictor `i`, including splits for which the predictive measure of association between predictors `i` and `j` is negative.

Examples

Estimate the predictor importance for all numeric variables in the `carsmall` data:

```
load carsmall
X = [Acceleration Cylinders Displacement ...
    Horsepower Model_Year Weight];
ens = fitensemble(X,MPG,'LSBoost',100,'Tree');
imp = predictorImportance(ens)

imp =
    0.0082         0    0.0049    0.0133    0.0142    0.1737
```

The weight (last predictor) has the most impact on mileage (MPG). The second predictor has importance 0; this means the number of cylinders has no impact on predictions made with `ens`.

Estimate the predictor importance for all variables in the `carsmall` data for an ensemble where the trees contain surrogate splits:

```
load carsmall
surrtree = RegressionTree.template('Surrogate','on');
X = [Acceleration Cylinders Displacement ...
    Horsepower Model_Year Weight];
ens2 = fitensemble(X,MPG,'LSBoost',100,surrtree);
[imp2,ma] = predictorImportance(ens2)

imp2 =
    0.0725    0.1342    0.1425    0.1397    0.1380    0.1855

ma =
    1.0000    0.0414    0.0607    0.0782    0.0102    0.0322
         0    1.0000         0         0         0         0
    0.0441    0.0704    1.0000    0.0883    0.0175    0.0913
    0.0944    0.1166    0.1400    1.0000    0.0390    0.1308
```

```
    0.0121    0.0139    0.0127    0.0127    1.0000    0.0113
    0.0818    0.1317    0.2072    0.1878    0.0340    1.0000
```

While weight (last predictor) still has the most impact on mileage (MPG), this estimate has the second predictor (number of cylinders) is essentially tied for third most important predictor.

See Also

`predictorImportance`

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Purpose

Estimates of predictor importance

Syntax

```
imp = predictorImportance(tree)
```

Description

`imp = predictorImportance(tree)` computes estimates of predictor importance for `tree` by summing changes in the mean squared error due to splits on every predictor and dividing the sum by the number of tree nodes.

Input Arguments

`tree`

A regression tree created by `RegressionTree.fit`, or by the `compact` method.

Output Arguments

`imp`

A row vector with the same number of elements as the number of predictors (columns) in `tree.X`. The entries are the estimates of predictor importance, with `0` representing the smallest possible importance.

Definitions

Predictor Importance

`predictorImportance` computes estimates of predictor importance for `tree` by summing changes in the mean squared error (MSE) due to splits on every predictor and dividing the sum by the number of tree nodes. If the tree is grown without surrogate splits, this sum is taken over best splits found at each branch node. If the tree is grown with surrogate splits, this sum is taken over all splits at each branch node including surrogate splits. `imp` has one element for each input predictor in the data used to train this tree. At each node, MSE is estimated as node error weighted by the node probability. Variable importance associated with this split is computed as the difference between MSE for the parent node and the total MSE for the two children.

Estimates of predictor importance do not depend on the order of predictors if you use surrogate splits, but do depend on the order if you do not use surrogate splits.

If you use surrogate splits, `predictorImportance` computes estimates before the tree is reduced by pruning or merging leaves. If you do not use surrogate splits, `predictorImportance` computes estimates after the tree is reduced by pruning or merging leaves. Therefore, reducing the tree by pruning affects the predictor importance for a tree grown without surrogate splits, and does not affect the predictor importance for a tree grown with surrogate splits.

Examples

Find predictor importance for the `carsmall` data. Use just the numeric predictors:

```
load carsmall
X = [Acceleration Cylinders Displacement ...
    Horsepower Model_Year Weight];
tree = RegressionTree.fit(X,MPG);
imp = predictorImportance(tree)

imp =
    0.0315         0    0.1082    0.0686    0.1629    1.2924
```

The weight (last predictor) has the most impact on mileage (MPG). The second predictor has importance 0; this means the number of cylinders has no impact on predictions made with `tree`.

Estimate the predictor importance for all variables in the `carsmall` data for a tree grown with surrogate splits:

```
load carsmall
X = [Acceleration Cylinders Displacement ...
    Horsepower Model_Year Weight];
tree2 = RegressionTree.fit(X,MPG,...
    'Surrogate','on');
imp2 = predictorImportance(tree2)

imp2 =
    0.5287    1.1977    1.2400    0.7059    1.0677    1.4106
```

While weight (last predictor) still has the most impact on mileage (MPG), this estimate has the second predictor (number of cylinders) as the third most important predictor.

See Also

`predictorImportance`

How To

- Chapter 13, “Nonparametric Supervised Learning”

princomp

Purpose

Principal component analysis (PCA) on data

Syntax

```
[COEFF,SCORE] = princomp(X)
[COEFF,SCORE,latent] = princomp(X)
[COEFF,SCORE,latent,tsquare] = princomp(X)
[...] = princomp(X,'econ')
```

Description

`COEFF = princomp(X)` performs principal components analysis (PCA) on the *n*-by-*p* data matrix `X`, and returns the principal component coefficients, also known as loadings. Rows of `X` correspond to observations, columns to variables. `COEFF` is a *p*-by-*p* matrix, each column containing coefficients for one principal component. The columns are in order of decreasing component variance.

`princomp` centers `X` by subtracting off column means, but does not rescale the columns of `X`. To perform principal components analysis with standardized variables, that is, based on correlations, use `princomp(zscore(X))`. To perform principal components analysis directly on a covariance or correlation matrix, use `pcacov`.

`[COEFF,SCORE] = princomp(X)` returns `SCORE`, the principal component scores; that is, the representation of `X` in the principal component space. Rows of `SCORE` correspond to observations, columns to components.

`[COEFF,SCORE,latent] = princomp(X)` returns `latent`, a vector containing the eigenvalues of the covariance matrix of `X`.

`[COEFF,SCORE,latent,tsquare] = princomp(X)` returns `tsquare`, which contains Hotelling's T^2 statistic for each data point.

The scores are the data formed by transforming the original data into the space of the principal components. The values of the vector `latent` are the variance of the columns of `SCORE`. Hotelling's T^2 is a measure of the multivariate distance of each observation from the center of the data set.

When `n <= p`, `SCORE(:,n:p)` and `latent(n:p)` are necessarily zero, and the columns of `COEFF(:,n:p)` define directions that are orthogonal to `X`.

`[...] = princomp(X,'econ')` returns only the elements of `latent` that are not necessarily zero, and the corresponding columns of `COEFF` and `SCORE`, that is, when `n <= p`, only the first `n-1`. This can be significantly faster when `p` is much larger than `n`.

Examples

Compute principal components for the `ingredients` data in the Hald data set, and the variance accounted for by each component.

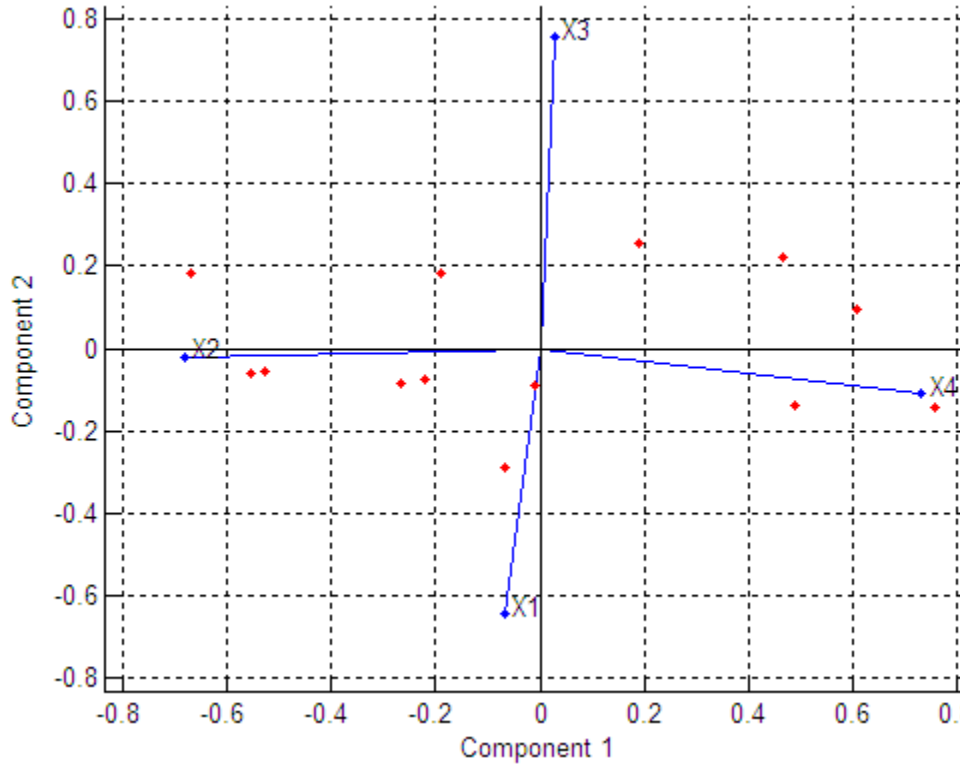
```
load hald;
[pc,score,latent,tsquare] = princomp(ingredients);
pc,latent

pc =
  0.0678 -0.6460  0.5673 -0.5062
  0.6785 -0.0200 -0.5440 -0.4933
 -0.0290  0.7553  0.4036 -0.5156
 -0.7309 -0.1085 -0.4684 -0.4844

latent =
 517.7969
  67.4964
  12.4054
   0.2372
```

The following command and plot show that two components account for 98% of the variance:

```
cumsum(latent)./sum(latent)
ans =
      0.86597
      0.97886
       0.9996
            1
biplot(pc(:,1:2),'Scores',score(:,1:2),'VarLabels',...
  {'X1' 'X2' 'X3' 'X4'})
```



For a more detailed example and explanation of this analysis method, see “Principal Component Analysis (PCA)” on page 10-31.

References

[1] Jackson, J. E., *A User’s Guide to Principal Components*, John Wiley and Sons, 1991, p. 592.

[2] Jolliffe, I. T., *Principal Component Analysis*, 2nd edition, Springer, 2002.

[3] Krzanowski, W. J. *Principles of Multivariate Analysis: A User’s Perspective*. New York: Oxford University Press, 1988.

[4] Seber, G. A. F., *Multivariate Observations*, Wiley, 1984.

See Also

`barttest` | `biplot` | `canoncorr` | `factoran` | `pcacov` | `pcares` | `rotatefactors`

How To

- "Principal Component Analysis (PCA)" on page 10-31

TreeBagger.Prior property

Purpose

Prior class probabilities

Description

The `Prior` property is a vector with prior probabilities for classes. This property is empty for ensembles of regression trees.

See Also

`classregtree`

Purpose

Object representing probability distribution

Description

ProbDist is an abstract class representing a probability distribution.

Construction

ProbDist is an abstract class. You cannot create instances of this class directly. You can construct an object in a subclass, such as `ProbDistUnivParam` or `ProbDistUnivKernel`, either by calling the subclass constructors (`ProbDistUnivParam.ProbDistUnivParam` or `ProbDistUnivKernel.ProbDistUnivKernel`) or by using the `fitdist` function.

Methods

cdf	Return cumulative distribution function (CDF) for ProbDist object
pdf	Return probability density function (PDF) for ProbDist object
random	Generate random number drawn from ProbDist object

Properties

DistName	Read-only string containing probability distribution name of ProbDist object
InputData	Read-only structure containing information about input data to ProbDist object
Support	Read-only structure containing information about support of ProbDist object

Copy Semantics

Value. To learn how this affects your use of the class, see Copying Objects in the MATLAB Programming Fundamentals documentation.

See Also

`fitdist` | `ProbDistParametric` | `ProbDistKernel` | `ProbDistUnivParam` | `ProbDistUnivKernel` | `ProbDistUnivParam.ProbDistUnivParam` | `ProbDistUnivKernel.ProbDistUnivKernel`

Superclasses

ProbDist

Purpose

Object representing nonparametric probability distribution defined by kernel smoothing

Description

ProbDistKernel is an abstract class defining the properties and methods of a nonparametric distribution defined by a kernel smoothing function.

Construction

ProbDistKernel is an abstract class. You cannot create instances of this class directly. You can construct an object in a subclass, `ProbDistUnivKernel`, either by calling the subclass constructor, `ProbDistUnivKernel.ProbDistUnivKernel`, or by using the `fitdist` function.

Methods

cdf	Return cumulative distribution function (CDF) for ProbDist object
pdf	Return probability density function (PDF) for ProbDist object
random	Generate random number drawn from ProbDist object

Note The above methods are inherited from the `ProbDist` class.

Properties

BandWidth	Read-only value specifying bandwidth of kernel smoothing function for ProbDistKernel object
DistName	Read-only string containing probability distribution name of ProbDist object

InputData	Read-only structure containing information about input data to ProbDist object
Kernel	Read-only string specifying name of kernel smoothing function for ProbDistKernel object
Support	Read-only structure containing information about support of ProbDist object

Note Some of the above properties are inherited from the `ProbDist` class.

Copy Semantics

Value. To learn how this affects your use of the class, see Copying Objects in the MATLAB Programming Fundamentals documentation.

See Also

`fitdist | ProbDist | ProbDistUnivKernel | ProbDistUnivKernel.ProbDistUnivKernel`

Superclasses

ProbDist

Purpose

Object representing parametric probability distribution

Description

ProbDistParametric is an abstract class defining the properties and methods of a parametric probability distribution.

Construction

ProbDistParametric is an abstract class. You cannot create instances of this class directly. You can construct an object in its subclass, `ProbDistUnivParam`, either by calling the subclass constructor, `ProbDistUnivParam.ProbDistUnivParam`, or by using the `fitdist` function.

Methods

cdf	Return cumulative distribution function (CDF) for ProbDist object
pdf	Return probability density function (PDF) for ProbDist object
random	Generate random number drawn from ProbDist object

Note The above methods are inherited from the `ProbDist` class.

Properties

DistName	Read-only string containing probability distribution name of ProbDist object
InputData	Read-only structure containing information about input data to ProbDist object

NLogL	Read-only value specifying negative log likelihood for input data to ProbDistParametric object
NumParams	Read-only value specifying number of parameters of ProbDistParametric object
ParamCov	Read-only covariance matrix of parameter estimates of ProbDistParametric object
ParamDescription	Read-only cell array specifying descriptions of parameters of ProbDistParametric object
ParamIsFixed	Read-only logical array specifying fixed parameters of ProbDistParametric object
ParamNames	Read-only cell array specifying names of parameters of ProbDistParametric object
Params	Read-only array specifying values of parameters of ProbDistParametric object
Support	Read-only structure containing information about support of ProbDist object

Note Some of the above properties are inherited from the `ProbDist` class.

Copy Semantics

Value. To learn how this affects your use of the class, see Copying Objects in the MATLAB Programming Fundamentals documentation.

See Also

`fitdist` | `ProbDist` | `ProbDistUnivParam` | `ProbDistUnivParam.ProbDistUnivParam`

ProbDistUnivKernel

Superclasses

ProbDistKernel

Purpose

Object representing univariate kernel probability distribution

Description

A ProbDistUnivKernel object represents a univariate nonparametric probability distribution defined by kernel smoothing. You create this object using the `fitdist` function to fit the distribution to data.

Construction

fitdist	Fit probability distribution to data

Methods

cdf	Return cumulative distribution function (CDF) for ProbDist object
icdf	Return inverse cumulative distribution function (ICDF) for ProbDistUnivKernel object
iqr	Return interquartile range (IQR) for ProbDistUnivKernel object
median	Return median of ProbDistUnivKernel object
pdf	Return probability density function (PDF) for ProbDist object
random	Generate random number drawn from ProbDist object

Note Some of the above methods are inherited from the `ProbDistKernel` class.

Properties

BandWidth	Read-only value specifying bandwidth of kernel smoothing function for ProbDistKernel object
DistName	Read-only string containing probability distribution name of ProbDist object
InputData	Read-only structure containing information about input data to ProbDist object
Kernel	Read-only string specifying name of kernel smoothing function for ProbDistKernel object
NLogL	Read-only value specifying negative log likelihood for input data to ProbDistUnivKernel object
Support	Read-only structure containing information about support of ProbDist object

Note Some of the above properties are inherited from the `ProbDistKernel` class.

Copy Semantics

Value. To learn how this affects your use of the class, see Copying Objects in the MATLAB Programming Fundamentals documentation.

References

[1] Bowman, A. W., and A. Azzalini. *Applied Smoothing Techniques for Data Analysis.* New York: Oxford University Press, 1997.

See Also `fitdist` | `ksdensity` | `ProbDist` | `ProbDistKernel` | `ProbDistUnivKernel.ProbDistUnivKernel`

Purpose

Construct ProbDistUnivKernel object

Syntax

```
PD = ProbDistUnivKernel(X)
PD = ProbDistUnivKernel(X, param1, val1, param2, val2, ...)
```

Description

Tip Although you can use this constructor function to create a ProbDistUnivKernel object, using the `fitdist` function is an easier way to create the ProbDistUnivKernel object.

`PD = ProbDistUnivKernel(X)` creates *PD*, a ProbDistUnivKernel object, which represents a nonparametric probability distribution, based on a normal kernel smoothing function.

`PD = ProbDistUnivKernel(X, param1, val1, param2, val2, ...)` specifies optional parameter name/value pairs, as described in the Parameter/Values table. Parameter and value names are case insensitive.

Input Arguments

X	A column vector of data.

Note Any NaN values in *X* are ignored by the fitting calculations.

Parameter	Values
`'censoring'`	A Boolean vector the same size as `X`, containing `1`s when the corresponding elements in `X` are right-censored observations and `0`s when the corresponding elements are exact observations. Default is a vector of `0`s. **Note** Any NaN values in this censoring vector are ignored by the fitting calculations.
`'frequency'`	A vector the same size as `X`, containing nonnegative integers specifying the frequencies for the corresponding elements in `X`. Default is a vector of `1`s. **Note** Any NaN values in this frequency vector are ignored by the fitting calculations.
`'kernel'`	A string specifying the type of kernel smoother to use. Choices are: • `'normal'` (default) • `'box'` • `'triangle'` • `'epanechnikov'`

Parameter	Values
`'support'`	Any of the following to specify the support: • `'unbounded'` — Default. If the density can extend over the whole real line. • `'positive'` — To restrict it to positive values. • A two-element vector giving finite lower and upper limits for the support of the density.
`'width'`	A value specifying the bandwidth of the kernel smoothing window. The default is optimal for estimating normal densities, but you may want to choose a smaller value to reveal features such as multiple modes.

Output Arguments

PD	An object in the `ProbDistUnivKernel` class, which is derived from the `ProbDist` class. It represents a nonparametric probability distribution.

References

[1] Bowman, A. W., and A. Azzalini. *Applied Smoothing Techniques for Data Analysis*. New York: Oxford University Press, 1997.

See Also

`fitdist | ksdensity`

ProbDistUnivParam

Superclasses

ProbDistParametric

Purpose

Object representing univariate parametric probability distribution

Description

A ProbDistUnivParam object represents a univariate parametric probability distribution. You create this object by using the constructor (`ProbDistUnivParam.ProbDistUnivParam`) and supplying parameter values, or by using the `fitdist` function to fit the distribution to data.

Construction

fitdist	Fit probability distribution to data
ProbDistUnivParam	Construct ProbDistUnivParam object

Methods

cdf	Return cumulative distribution function (CDF) for ProbDist object
icdf	Return inverse cumulative distribution function (ICDF) for ProbDistUnivParam object
iqr	Return interquartile range (IQR) for ProbDistUnivParam object
mean	Return mean of ProbDistUnivParam object
median	Return median of ProbDistUnivParam object
paramci	Return parameter confidence intervals of ProbDistUnivParam object
pdf	Return probability density function (PDF) for ProbDist object

random	Generate random number drawn from ProbDist object
std	Return standard deviation of ProbDistUnivParam object
var	Return variance of ProbDistUnivParam object

Note Some of the above methods are inherited from the `ProbDistParametric` class.

Properties

DistName	Read-only string containing probability distribution name of ProbDist object
InputData	Read-only structure containing information about input data to ProbDist object
NLogL	Read-only value specifying negative log likelihood for input data to ProbDistParametric object
NumParams	Read-only value specifying number of parameters of ProbDistParametric object
ParamCov	Read-only covariance matrix of parameter estimates of ProbDistParametric object
ParamDescription	Read-only cell array specifying descriptions of parameters of ProbDistParametric object

ParamIsFixed	Read-only logical array specifying fixed parameters of ProbDistParametric object
ParamNames	Read-only cell array specifying names of parameters of ProbDistParametric object
Params	Read-only array specifying values of parameters of ProbDistParametric object
Support	Read-only structure containing information about support of ProbDist object

Note The above properties are inherited from the `ProbDistParametric` class.

Note Parameter values are also properties. For example, if you create `PD`, a univariate parametric probability distribution object that represents a normal distribution, then `PD.mu` and `PD.sigma` are properties that give the values of the mu and sigma parameters.

Copy Semantics

Value. To learn how this affects your use of the class, see Copying Objects in the MATLAB Programming Fundamentals documentation.

References

[1] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 1, Hoboken, NJ: Wiley-Interscience, 1993.

[2] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 2, Hoboken, NJ: Wiley-Interscience, 1994.

See Also

`fitdist` | `ProbDist` | `ProbDistParametric` | `ProbDistUnivParam.ProbDistUnivParam`

How To

- Appendix B, "Distribution Reference"

ProbDistUnivParam

Purpose

Construct ProbDistUnivParam object

Syntax

```
PD = ProbDistUnivParam(DistName, Params)
```

Description

`PD = ProbDistUnivParam(DistName, Params)` creates *PD*, a ProbDistUnivParam object, which represents a probability distribution. This distribution is defined by the parametric distribution specified by *DistName*, with parameters specified by the numeric vector *Params*.

Input Arguments

DistName

A string specifying a distribution. Choices are:

- `'beta'`
- `'binomial'`
- `'birnbaumsaunders'`
- `'exponential'`
- `'extreme value'` or `ev'`
- `'gamma'`
- `'generalized extreme value'` or `'gev'`
- `'generalized pareto'` or `'gp'`
- `'inversegaussian'`
- `'logistic'`
- `'loglogistic'`
- `'lognormal'`
- `'nakagami'`
- `'negative binomial'` or `'nbin'`
- `'normal'`
- `'poisson'`

- `'rayleigh'`
- `'rician'`
- `'tlocationscale'`
- `'weibull'` or `'wbl'`

For more information on these parametric distributions, see Appendix B, "Distribution Reference".

`Params` — Numeric vector of distribution parameters. The number and type of parameters depends on the distribution you specify with *`DistName`*. For information on parameters for each distribution type, see Appendix B, "Distribution Reference".

Output Arguments

`PD` — An object in the `ProbDistUnivParam` class, which is derived from the `ProbDist` class. It represents a parametric probability distribution.

Examples

1 Create an object representing a normal distribution with a mean of 100 and a standard deviation of 10.

```
pd = ProbDistUnivParam('normal',[100 10])

pd =

normal distribution

    mu = 100
    sigma = 10
```

2 Generate a 4-by-5 matrix of random values from this distribution.

```
random(pd,4,5)

ans =

  105.3767  103.1877  135.7840  107.2540   98.7586
  118.3389   86.9231  127.6944   99.3695  114.8970
   77.4115   95.6641   86.5011  107.1474  114.0903
  108.6217  103.4262  130.3492   97.9503  114.1719
```

References

[1] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 1, Hoboken, NJ: Wiley-Interscience, 1993.

[2] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 2, Hoboken, NJ: Wiley-Interscience, 1994.

See Also

`fitdist`

How To

- Appendix B, “Distribution Reference”

Purpose

Probability plots

Syntax

```
probplot(Y)
probplot(distribution,Y)
probplot(Y,cens,freq)
probplot(ax,Y)
probplot(...,'noref')
probplot(ax,PD)
probplot(ax,fun,params)
h = probplot(...)
```

Description

`probplot(Y)` produces a normal probability plot comparing the distribution of the data `Y` to the normal distribution. `Y` can be a single vector, or a matrix with a separate sample in each column. The plot includes a reference line useful for judging whether the data follow a normal distribution.

`probplot` uses midpoint probability plotting positions. The i^{th} sorted value from a sample of size N is plotted against the midpoint in the jump of the empirical CDF on the y axis. With uncensored data, that midpoint is $(i–0.5)/N$. With censored data (see below), the y value is more complicated to compute.

`probplot(distribution,Y)` creates a probability plot for the distribution specified by *`distribution`*. Acceptable strings for *`distribution`* are:

- `'exponential'` — Exponential probability plot (nonnegative values)
- `'extreme value'` — Extreme value probability plot (all values)
- `'lognormal'` — Lognormal probability plot (positive values)
- `'normal'` — Normal probability plot (all values)
- `'rayleigh'` — Rayleigh probability plot (positive values)
- `'weibull'` — Weibull probability plot (positive values)

The *y* axis scale is based on the selected distribution. The *x* axis has a log scale for the Weibull and lognormal distributions, and a linear scale for the others.

Not all distributions are appropriate for all data sets, and `probplot` will error when asked to create a plot with a data set that is inappropriate for a specified distribution. Appropriate data ranges for each distribution are given parenthetically in the list above.

`probplot(Y,cens,freq)` or `probplot(distname,Y,cens,freq)` requires a vector `Y`. `cens` is a vector of the same size as `Y` and contains `1` for observations that are right-censored and `0` for observations that are observed exactly. `freq` is a vector of the same size as Y, containing integer frequencies for the corresponding elements in `Y`.

`probplot(ax,Y)` takes a handle `ax` to an existing probability plot, and adds additional lines for the samples in `Y`. `ax` is a handle for a set of axes.

`probplot(...,'noref')` omits the reference line.

`probplot(ax,PD)` takes a probability distribution object, `PD`, and adds a fitted line to the axes specified by `ax` to represent the probability distribution specified by `PD`. `PD` is a ProbDist object of the `ProbDistUnivParam` class or `ProbDistUnivKernel` class.

`probplot(ax,fun,params)` takes a function `fun` and a set of parameters, `params`, and adds fitted lines to the axes of an existing probability plot specified by `ax`. `fun` is a function handle to a cdf function, specified with `@` (for example, `@wblcdf`). `params` is the set of parameters required to evaluate `fun`, and is specified as a cell array or vector. The function must accept a vector of `X` values as its first argument, then the optional parameters, and must return a vector of cdf values evaluated at `X`.

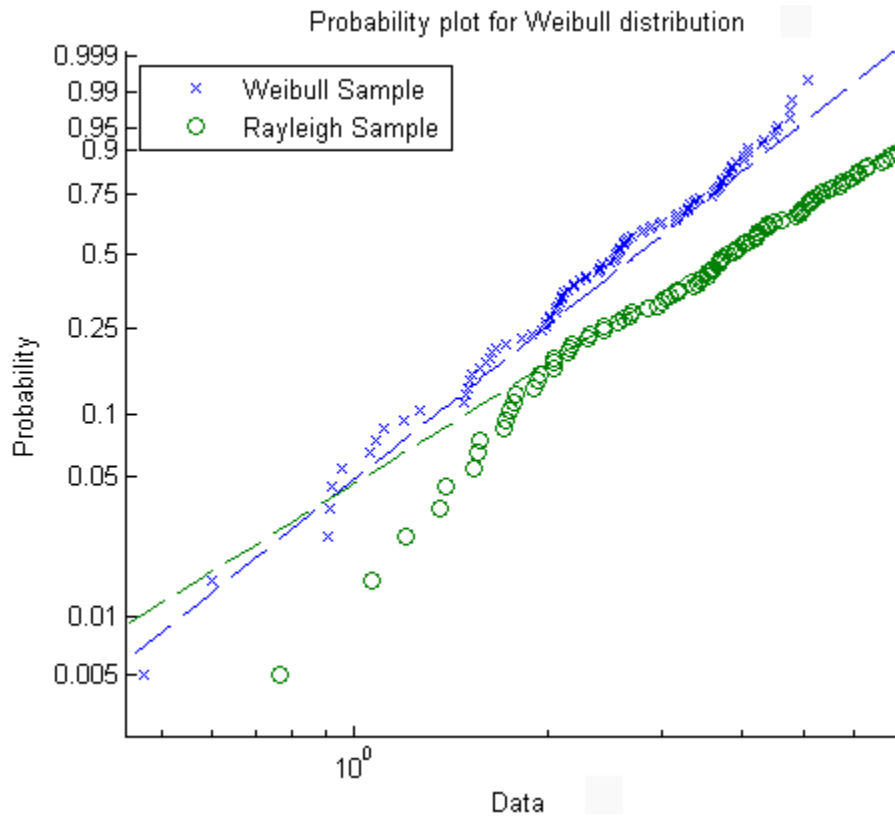
`h = probplot(...)` returns handles to the plotted lines.

Examples

Example 1

The following plot assesses two samples, one from a Weibull distribution and one from a Rayleigh distribution, to see if they may have come from a Weibull population.

```
x1 = wblrnd(3,3,100,1);
x2 = raylrnd(3,100,1);
probplot('weibull',[x1 x2])
legend('Weibull Sample','Rayleigh Sample','Location','NW')
```



Example 2

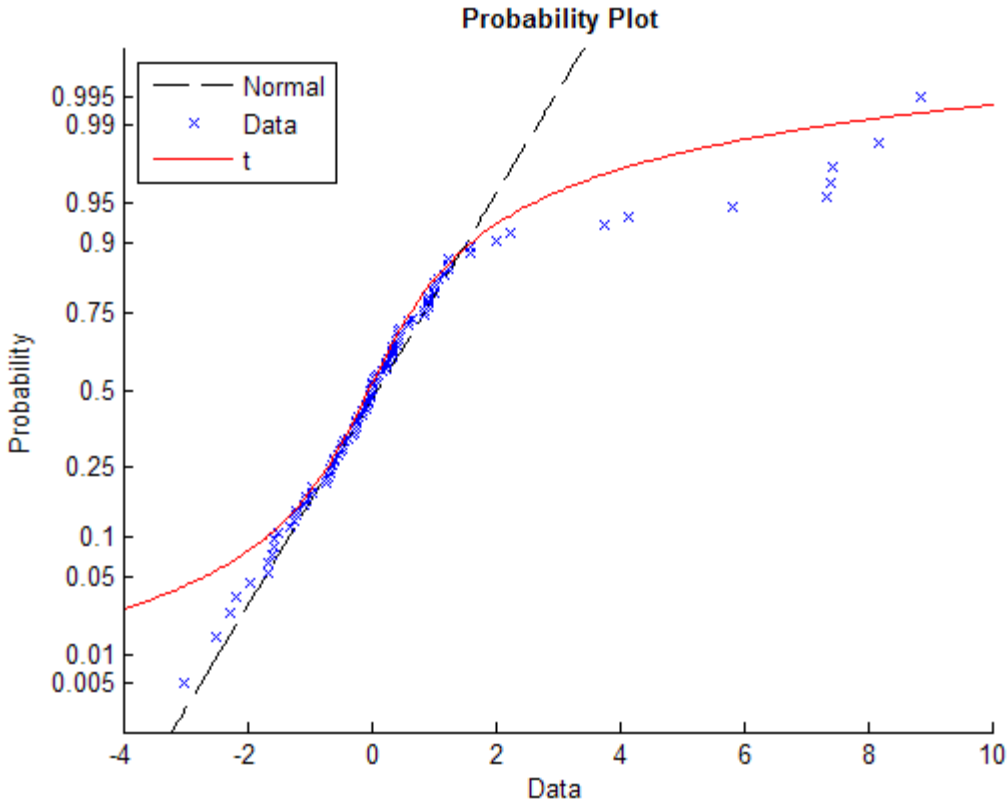
Consider the following data, with about 20% outliers:

```
left_tail = -exprnd(1,10,1);
right_tail = exprnd(5,10,1);
center = randn(80,1);
```

```
data = [left_tail;center;right_tail];
```

Neither a normal distribution nor a *t* distribution fits the tails very well:

```
probplot(data);
p = mle(data,'dist','tlo');
t = @(data,mu,sig,df)cdf('tlocationscale',data,mu,sig,df);
h = probplot(gca,t,p);
set(h,'color','r','linestyle','-')
title('{\bf Probability Plot}')
legend('Data','Normal','t','Location','NW')
```



See Also

normplot | ecdf | wblplot

procrustes

Purpose

Procrustes analysis

Syntax

```
d = procrustes(X,Y)
[d,Z] = procrustes(X,Y)
[d,Z,transform] = procrustes(X,Y)
[...] = procrustes(...,'scaling',flag)
[...] = procrustes(...,'reflection',flag)
```

Description

`d = procrustes(X,Y)` determines a linear transformation (translation, reflection, orthogonal rotation, and scaling) of the points in matrix `Y` to best conform them to the points in matrix `X`. The goodness-of-fit criterion is the sum of squared errors. `procrustes` returns the minimized value of this dissimilarity measure in `d`. `d` is standardized by a measure of the scale of `X`, given by:

```
sum(sum((X-repmat(mean(X,1),size(X,1),1)).^2,1))
```

That is, the sum of squared elements of a centered version of `X`. However, if `X` comprises repetitions of the same point, the sum of squared errors is not standardized.

`X` and `Y` must have the same number of points (rows), and `procrustes` matches `Y(i)` to `X(i)`. Points in `Y` can have smaller dimension (number of columns) than those in `X`. In this case, `procrustes` adds columns of zeros to `Y` as necessary.

`[d,Z] = procrustes(X,Y)` also returns the transformed `Y` values.

`[d,Z,transform] = procrustes(X,Y)` also returns the transformation that maps `Y` to `Z`. `transform` is a structure array with fields:

- `c` — Translation component
- `T` — Orthogonal rotation and reflection component
- `b` — Scale component

That is:

```
c = transform.c;
```

```
T = transform.T;
b = transform.b;

Z = b*Y*T + c;
```

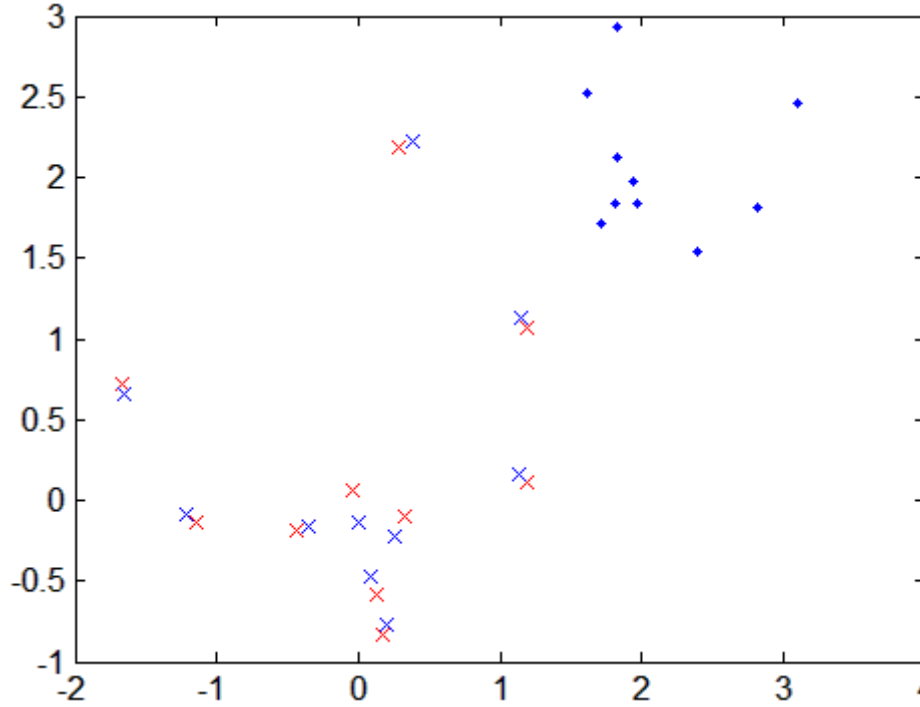
`[...] = procrustes(...,'scaling',flag)`, when *`flag`* is `false`, allows you to compute the transformation without a scale component (that is, with `b` equal to `1`). The default *`flag`* is `true`.

`[...] = procrustes(...,'reflection',flag)`, when *`flag`* is `false`, allows you to compute the transformation without a reflection component (that is, with `det(T)` equal to `1`). The default *`flag`* is `'best'`, which computes the best-fitting transformation, whether or not it includes a reflection component. A *`flag`* of `true` forces the transformation to be computed with a reflection component (that is, with `det(T)` equal to `-1`)

Examples

This example creates some random points in two dimensions, then rotates, scales, translates, and adds some noise to those points. It uses `procrustes` to conform `Y` to `X`, then plots the original `X` and `Y` with the transformed `Y`.

```
n = 10;
X = normrnd(0,1,[n 2]);
S = [0.5 -sqrt(3)/2; sqrt(3)/2 0.5];
Y = normrnd(0.5*X*S+2,0.05,n,2);
[d,Z,tr] = procrustes(X,Y);
plot(X(:,1),X(:,2),'rx',...
     Y(:,1),Y(:,2),'b.',...
     Z(:,1),Z(:,2),'bx');
```



References

[1] Kendall, David G. "A Survey of the Statistical Theory of Shape." *Statistical Science*. Vol. 4, No. 2, 1989, pp. 87–99.

[2] Bookstein, Fred L. *Morphometric Tools for Landmark Data*. Cambridge, UK: Cambridge University Press, 1991.

[3] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

See Also

`cmdscale` | `factoran`

Purpose

Proximity matrix for data

Syntax

```
prox = proximity(B,X)
```

Description

`prox = proximity(B,X)` computes a numeric matrix of size `Nobs`-by-`Nobs` of proximities for data `X`, where `Nobs` is the number of observations (rows) in `X`. Proximity between any two observations in the input data is defined as a fraction of trees in the ensemble `B` for which these two observations land on the same leaf. This is a symmetric matrix with ones on the diagonal and off-diagonal elements ranging from 0 to 1.

TreeBagger.Proximity property

Purpose

Proximity matrix for observations

Description

The `Proximity` property is a numeric matrix of size `Nobs`-by-`Nobs`, where `Nobs` is the number of observations in the training data, containing measures of the proximity between observations. For any two observations, their proximity is defined as the fraction of trees for which these observations land on the same leaf. This is a symmetric matrix with 1s on the diagonal and off-diagonal elements ranging from 0 to 1.

See Also

`CompactTreeBagger.proximity` | `classregtree.varimportance`

Purpose

Produce sequence of subtrees by pruning

Syntax

```
tree1 = prune(tree)
tree1 = prune(tree,Name,Value)
```

Description

`tree1 = prune(tree)` creates a copy of the classification tree `tree` with its optimal pruning sequence filled in.

`tree1 = prune(tree,Name,Value)` creates a pruned tree with additional options specified by one `Name,Value` pair argument. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Tips

- `tree1 = prune(tree)` returns the decision tree `tree1` that is the full, unpruned `tree`, but with optimal pruning information added. This is useful only if you created `tree` by pruning another tree, or by using the `ClassificationTree.fit` method with pruning set `'off'`. If you plan to prune a tree multiple times along the optimal pruning sequence, it is more efficient to create the optimal pruning sequence first.

Input Arguments

`tree`

A classification tree created with `ClassificationTree.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`alpha`

A numeric scalar. `prune` prunes `tree` to the specified value of the pruning cost.

`level`

A numeric scalar from `0` (no pruning) to the largest pruning level of this tree `max(tree.PruneList)`. `prune` returns the tree pruned to this level.

`nodes`

A numeric vector with elements from `1` to `tree.NumNodes`. Any `tree` branch nodes listed in `nodes` become leaf nodes in `tree1`, unless their parent nodes are also pruned.

Output Arguments

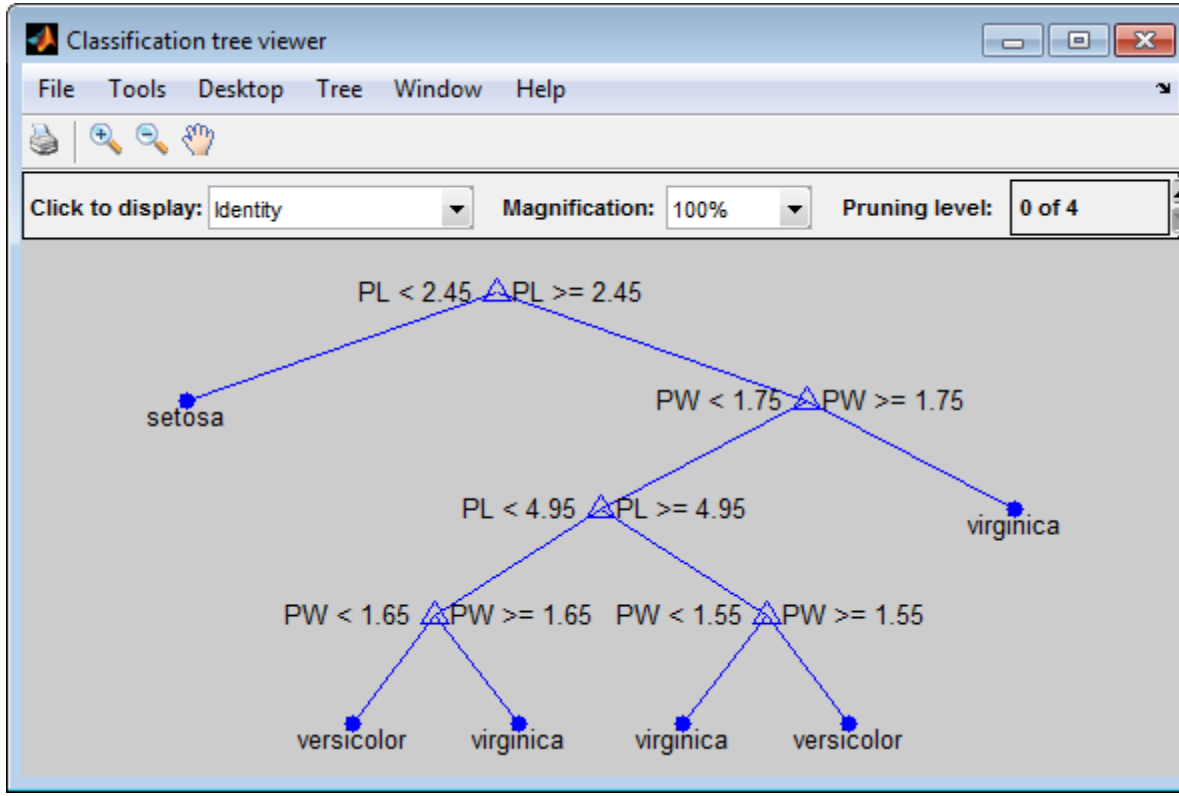
`tree1`

A classification tree.

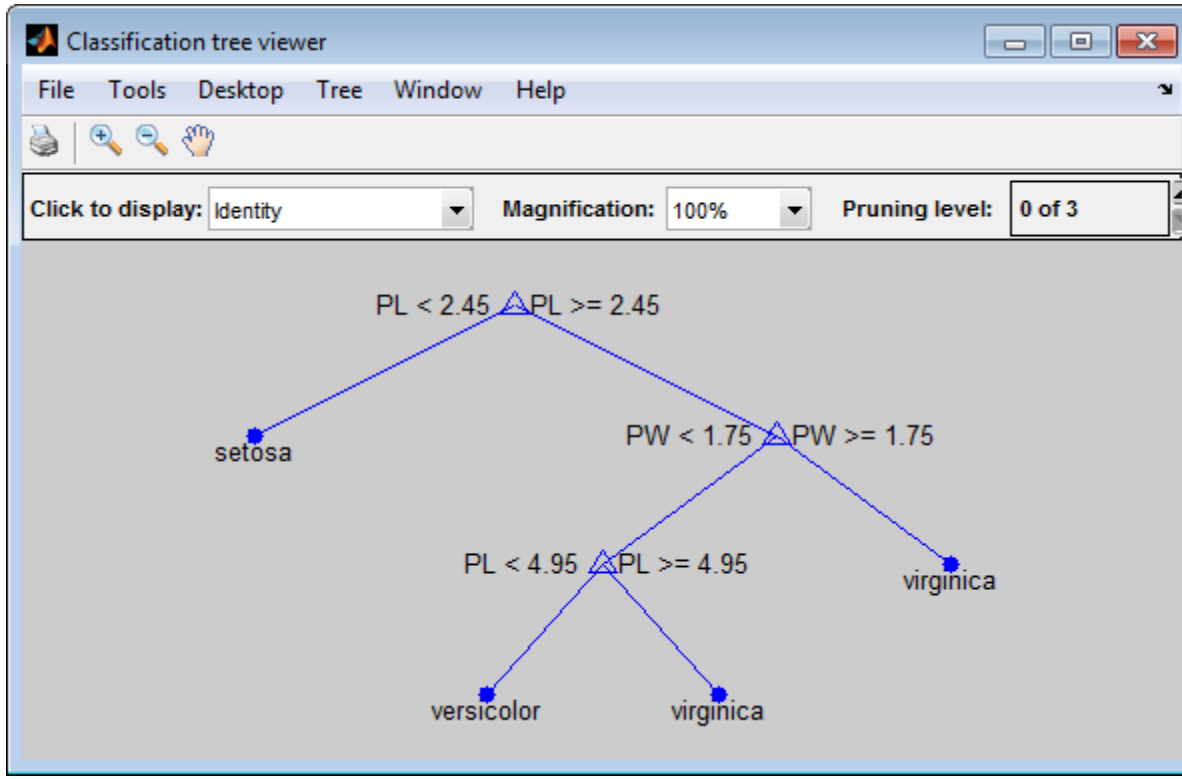
Examples

Display a full tree for Fisher's iris data, as well as the next largest tree from the optimal pruning sequence:

```
load fisheriris;
varnames = {'SL' 'SW' 'PL' 'PW'};
t1 = ClassificationTree.fit(meas,species,...
    'minparent',5,'predictornames',varnames);
view(t1,'mode','graph');
```




```
t2 = prune(t1,'level',1);
view(t2,'mode','graph');
```



See Also `ClassificationTree.fit`

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Purpose

Prune tree

Syntax

```
t2 = prune(t1,'level',level)
t2 = prune(t1,'nodes',nodes)
t2 = prune(t1)
```

Description

`t2 = prune(t1,'level',level)` takes a decision tree `t1` and a pruning level `level`, and returns the decision tree `t2` pruned to that level. If `level` is 0, there is no pruning. Trees are pruned based on an optimal pruning scheme that first prunes branches giving less improvement in error cost.

`t2 = prune(t1,'nodes',nodes)` prunes the nodes listed in the `nodes` vector from the tree. Any `t1` branch nodes listed in `nodes` become leaf nodes in `t2`, unless their parent nodes are also pruned. Use `view` to display the node numbers for any node you select.

`t2 = prune(t1)` returns the decision tree `t2` that is the full, unpruned `t1`, but with optimal pruning information added. This is useful only if `t1` is created by pruning another tree, or by using the `classregtree` function with the `'prune'` parameter set to `'off'`. If you plan to prune a tree multiple times along the optimal pruning sequence, it is more efficient to create the optimal pruning sequence first.

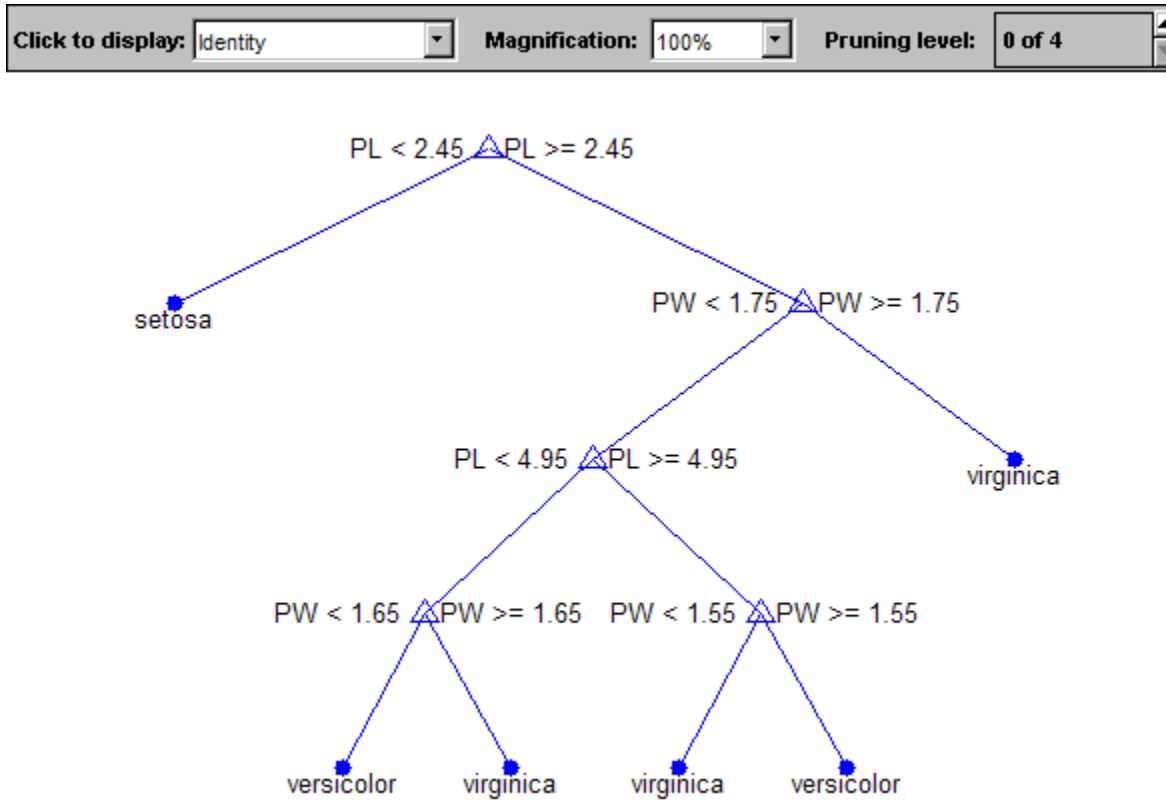
Pruning is the process of reducing a tree by turning some branch nodes into leaf nodes and removing the leaf nodes under the original branch.

Examples

Display the full tree for Fisher's iris data:

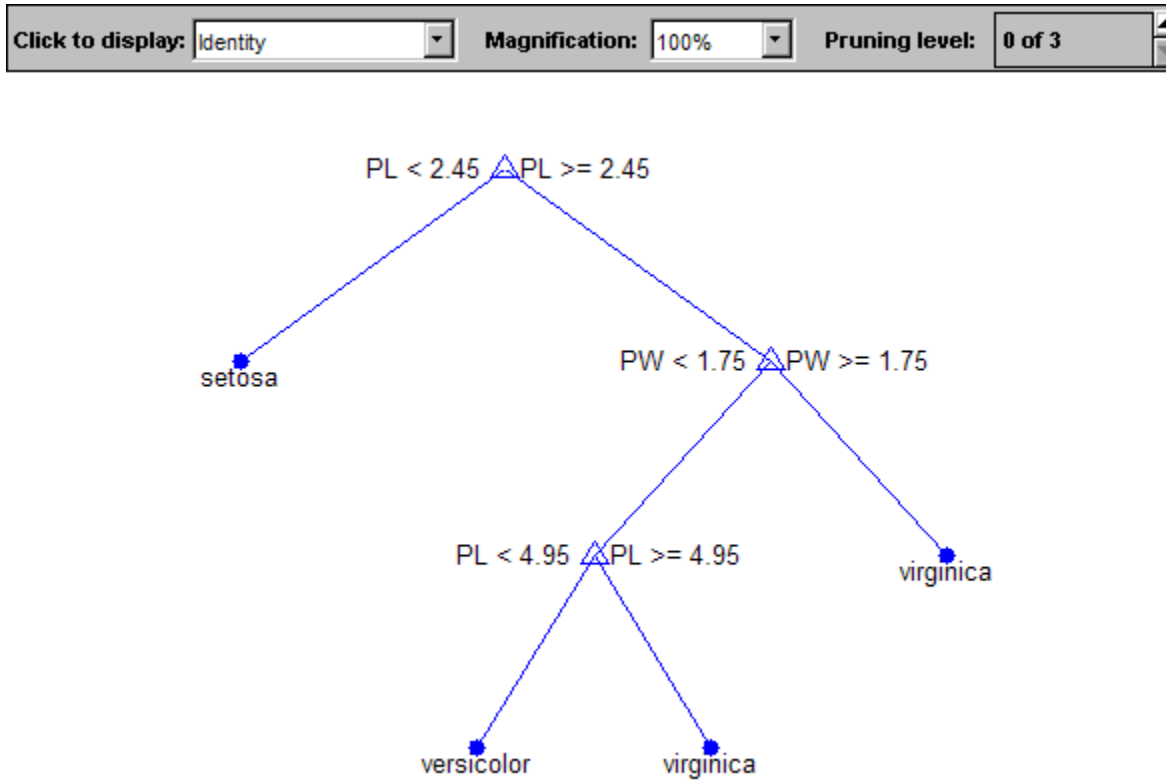
```
load fisheriris;

t1 = classregtree(meas,species,...
                  'names',{'SL' 'SW' 'PL' 'PW'},...
                  'splitmin',5)
t1 =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
```

```
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t1)
```



Display the next largest tree from the optimal pruning sequence:

```
t2 = prune(t1,'level',1)
t2 =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  class = versicolor
7  class = virginica

view(t2)
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree | test | view`

Purpose

Produce sequence of subtrees by pruning

Syntax

```
tree1 = prune(tree)
tree1 = prune(tree,Name,Value)
```

Description

`tree1 = prune(tree)` creates a copy of the regression tree `tree` with its optimal pruning sequence filled in.

`tree1 = prune(tree,Name,Value)` creates a pruned tree with additional options specified by one `Name,Value` pair argument. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Tips

- `tree1 = prune(tree)` returns the decision tree `tree1` that is the full, unpruned `tree`, but with optimal pruning information added. This is useful only if you created `tree` by pruning another tree, or by using the `RegressionTree.fit` with pruning set `'off'`. If you plan to prune a tree multiple times along the optimal pruning sequence, it is more efficient to create the optimal pruning sequence first.

Input Arguments

`tree`

A regression tree created with `RegressionTree.fit`.

Name-Value Pair Arguments

Optional comma-separated pair of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify only one name-value pair argument.

`alpha`

A numeric scalar from `0` (no pruning) to `1` (prune to one node). Prunes to minimize the sum of (`alpha` times the number of leaf nodes) and a cost (mean squared error).

`level`

A numeric scalar from `0` (no pruning) to the largest pruning level of this tree `max(tree.PruneList)`. `prune` returns the tree pruned to this level.

`nodes`

A numeric vector with elements from `1` to `tree.NumNodes`. Any `tree` branch nodes listed in `nodes` become leaf nodes in `tree1`, unless their parent nodes are also pruned.

Output Arguments

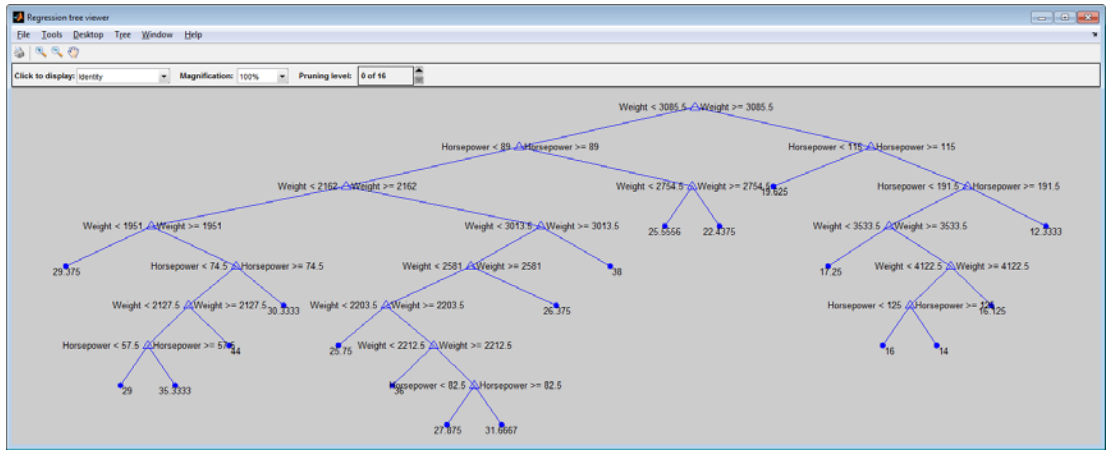
`tree1`

A regression tree.

Examples

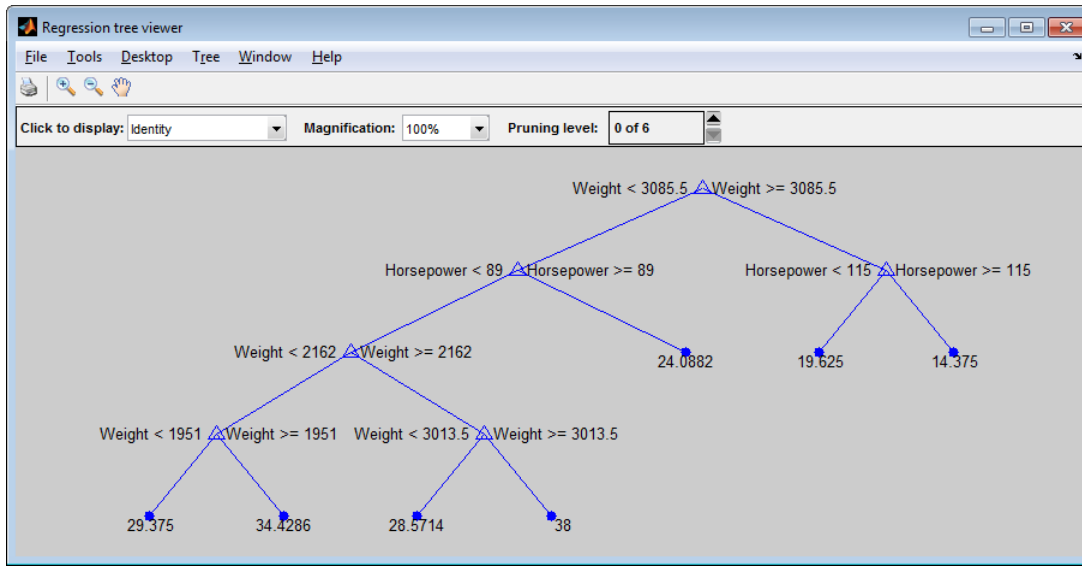
Display a full tree for the `carsmall` data, as well as the tree pruned to level `10`:

```
load carsmall;
varnames = {'Weight' 'Horsepower'};
t1 = RegressionTree.fit([Weight Horsepower],MPG,...
    'predictornames',varnames)
view(t1,'mode','graph');
```




```
t2 = prune(t1,'level',10);
```

```
view(t2,'mode','graph');
```



See Also

`RegressionTree.fit`

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TreeBagger.Prune property

Purpose

Flag to prune trees

Description

The `Prune` property is true if decision trees are pruned and false if they are not. Pruning decision trees is not recommended for ensembles. The default value is false.

See Also

`classregtree.prune`

Purpose

Pruning levels for decision tree nodes

Syntax

```
P = prunelist(T)
P = prunelist(T,J)
```

Description

`P = prunelist(T)` returns an n-element numeric vector with the pruning levels in each node of the tree `T`, where n is the number of nodes. When you call `prune(T,'level',level)`, nodes with the pruning levels below *`level`* are pruned, and nodes with the pruning levels greater or equal to *`level`* are not pruned.

`P = prunelist(T,J)` takes an array `J` of node numbers and returns the pruning levels for the specified nodes.

See Also

`classregtree` | `numnodes`

qrandstream.qrand

Purpose

Generate quasi-random points from stream

Syntax

```
x = qrand(q)
X = qrand(q,n)
```

Description

`x = qrand(q)` returns the next value `x` in the quasi-random number stream `q` of the `qrandstream` class. `x` is a 1-by-*d* vector, where *d* is the dimension of the stream. The command sets `q.State` to the index in the underlying point set of the next value to be returned.

`X = qrand(q,n)` returns the next `n` values `X` in an `n`-by-*d* matrix.

Objects `q` of the `qrandstream` class encapsulate properties of a specified quasi-random number stream. Values of the stream are not generated and stored in memory until `q` is accessed using `qrand`.

Examples

Use `qrandstream` to construct a 3-D Halton stream, based on a point set that skips the first 1000 values and then retains every 101st point:

```
q = qrandstream('halton',3,'Skip',1e3,'Leap',1e2)
q =
   Halton quasi-random stream in 3 dimensions
   Point set properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none

nextIdx = q.State
nextIdx =
     1
```

Use `qrand` to generate two samples of size four:

```
X1 = qrand(q,4)
X1 =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
```

```
    0.9087    0.5629    0.6166
nextIdx = q.State
nextIdx =
     5

X2 = qrand(q,4)
X2 =
    0.2446    0.0238    0.8102
    0.5298    0.7540    0.0438
    0.3843    0.5112    0.2758
    0.8335    0.2245    0.4694
nextIdx = q.State
nextIdx =
     9
```

Use `reset` to reset the stream, then generate another sample:

```
reset(q)
nextIdx = q.State
nextIdx =
     1

X = qrand(q,4)
X =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
```

See Also

`qrandstream | reset`

qrandset

Purpose

Quasi-random point sets

Description

`qrandset` is a base class that encapsulates a sequence of multi-dimensional quasi-random numbers. This base class is abstract and cannot be instantiated directly. Concrete subclasses include `sobolset` and `haltonset`.

Construction

qrandset	Abstract quasi-random point set class

Methods

disp	Display qrandset object
end	Last index in indexing expression for point set
length	Length of point set
ndims	Number of dimensions in matrix
net	Generate quasi-random point set
scramble	Scramble quasi-random point set
size	Number of dimensions in matrix
subsref	Subscripted reference for qrandset

Properties

Dimensions	Number of dimensions
Leap	Interval between points
ScrambleMethod	Settings that control scrambling

Skip	Number of initial points to omit from sequence
Type	Name of sequence on which point set `P` is based

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

See Also

`haltonset` | `sobolset`

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- “Quasi-Random Point Sets” on page 6-16

qrandset

Purpose

Abstract quasi-random point set class

Description

`qrandset` is an abstract class, and you cannot create instances of it directly. You must use `haltonset` or `sobolset` to create a `qrandset` object.

See Also

`haltonset` | `sobolset`

Purpose

Quasi-random number streams

Construction

qrandstream	Construct quasi-random number stream

Methods

addlistener	Add listener for event
delete	Delete handle object
disp	Display `qrandstream` object
eq	Test handle equality
findobj	Find objects matching specified conditions
findprop	Find property of MATLAB handle object
ge	Greater than or equal relation for handles
gt	Greater than relation for handles
isvalid	Test handle validity
le	Less than or equal relation for handles
lt	Less than relation for handles
ne	Not equal relation for handles
notify	Notify listeners of event
qrand	Generate quasi-random points from stream
rand	Generate quasi-random points from stream
reset	Reset state

Properties

PointSet	Point set from which stream is drawn
State	Current state of the stream

Copy Semantics

Handle. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

Purpose

Construct quasi-random number stream

Syntax

```
q = qrandstream(type,d)
q = qrandstream(type,d,prop1,val1,prop2,val2,...)
q = qrandstream(p)
```

Description

`q = qrandstream(type,d)` constructs a `d`-dimensional quasi-random number stream `q` of the `qrandstream` class, of type specified by the string *`type`*. *`type`* is either `'halton'` or `'sobol'`, and `q` is based on a point set from either the `haltonset` class or `sobolset` class, respectively, with default property settings.

`q = qrandstream(type,d,prop1,val1,prop2,val2,...)` specifies property name/value pairs for the point set on which the stream is based. Applicable properties depend on *`type`*.

`q = qrandstream(p)` constructs a stream based on the specified point set `p`. `p` must be a point set from either the `haltonset` class or `sobolset` class.

Examples

Construct a 3-D Halton stream, based on a point set that skips the first 1000 values and then retains every 101st point:

```
q = qrandstream('halton',3,'Skip',1e3,'Leap',1e2)
q =
   Halton quasi-random stream in 3 dimensions
   Point set properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none

nextIdx = q.State
nextIdx =
     1
```

Use `qrand` to generate two samples of size four:

```
X1 = qrand(q,4)
```

```
X1 =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
nextIdx = q.State
nextIdx =
     5

X2 = qrand(q,4)
X2 =
    0.2446    0.0238    0.8102
    0.5298    0.7540    0.0438
    0.3843    0.5112    0.2758
    0.8335    0.2245    0.4694
nextIdx = q.State
nextIdx =
     9
```

Use `reset` to reset the stream, and then generate another sample:

```
reset(q)
nextIdx = q.State
nextIdx =
     1

X = qrand(q,4)
X =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
```

See Also

`haltonset` | `qrand` | `reset` | `sobolset`

Purpose

Quantile-quantile plot

Syntax

```
qqplot(X)
qqplot(X,Y)
qqplot(X,PD)
qqplot(X,Y,pvec)
h = qqplot(X,Y,pvec)
```

Description

`qqplot(X)` displays a quantile-quantile plot of the sample quantiles of `X` versus theoretical quantiles from a normal distribution. If the distribution of `X` is normal, the plot will be close to linear.

`qqplot(X,Y)` displays a quantile-quantile plot of two samples. If the samples do come from the same distribution, the plot will be linear.

`qqplot(X,PD)` makes an empirical quantile-quantile plot of the quantiles of the data in the vector `X` versus the quantiles of the distribution specified by `PD`, a `ProbDist` object of the `ProbDistUnivParam` class or `ProbDistUnivKernel` class.

For matrix `X` and `Y`, `qqplot` displays a separate line for each pair of columns. The plotted quantiles are the quantiles of the smaller data set.

The plot has the sample data displayed with the plot symbol `'+'`. Superimposed on the plot is a line joining the first and third quartiles of each distribution (this is a robust linear fit of the order statistics of the two samples). This line is extrapolated out to the ends of the sample to help evaluate the linearity of the data.

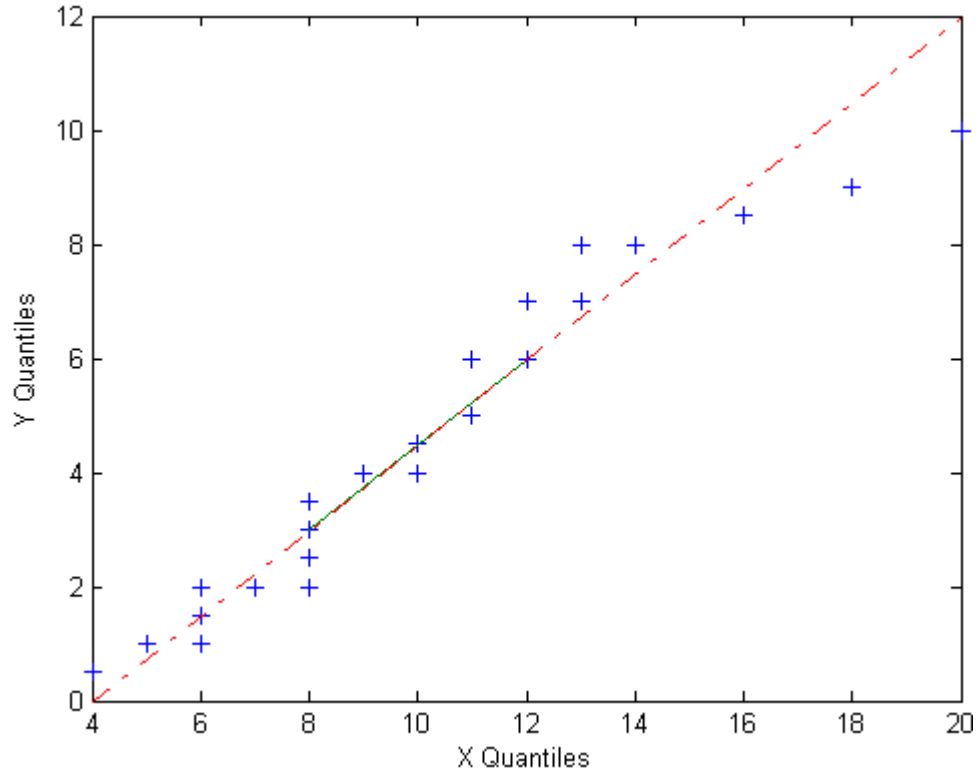
Use `qqplot(X,Y,pvec)` to specify the quantiles in the vector `pvec`.

`h = qqplot(X,Y,pvec)` returns handles to the lines in `h`.

Examples

The following example shows a quantile-quantile plot of two samples from Poisson distributions.

```
x = poissrnd(10,50,1);
y = poissrnd(5,100,1);
qqplot(x,y);
```



How To

- `normplot`

Purpose

Quantiles

Syntax

```
Y = quantile(X,p)
Y = quantile(X,p,dim)
Y = quantile(X,N,...)
```

Description

`Y = quantile(X,p)` returns quantiles of the values in `X`. `p` is a scalar or a vector of cumulative probability values. When `X` is a vector, `Y` is the same size as `p`, and `Y(i)` contains the `p(i)`th quantile. When `X` is a matrix, the *i*th row of `Y` contains the `p(i)`th quantiles of each column of `X`. For *n*-dimensional arrays, `quantile` operates along the first nonsingleton dimension of `X`.

`Y = quantile(X,p,dim)` calculates quantiles along dimension `dim`. The `dim`th dimension of `Y` has length `length(P)`.

Quantiles are specified using cumulative probabilities from 0 to 1. For an *n*-element vector `X`, quantile computes quantiles as follows:

1. The sorted values in `X` are taken as the (0.5/*n*), (1.5/*n*), ..., ([*n*–0.5]/*n*) quantiles.
2. Linear interpolation is used to compute quantiles for probabilities between (0.5/*n*) and ([*n*–0.5]/*n*).
3. The minimum or maximum values in `X` are assigned to quantiles for probabilities outside that range.

`quantile` treats `NaN`s as missing values and removes them.

`Y = quantile(X,N,...)` returns quantiles at the `N` evenly-spaced cumulative probabilities (1:`N`)/(`N`+1). `N` is a scalar positive integer value.

Examples

```
y = quantile(x,.50); % the median of x
y = quantile(x,[.025 .25 .50 .75 .975]); % Summary of x
y = quantile(x,[.25 .50 .75]); % the quartiles of x
y = quantile(x,3); % another way to get quartiles
```

See Also prctile | iqr | median

Purpose

Generate quasi-random points from stream

Syntax

```
rand
rand(q,n)
rand(q)
rand(q,m,n)
rand(q,[m,n])
rand(q,m,n,p,...)
rand(q,[m,n,p,...])
```

Description

`rand` returns a matrix of quasi-random values and is intended to allow objects of the `qrandstream` class to be used in code that contains calls to the `rand` method of the MATLAB pseudo-random `randstream` class. Due to the multidimensional nature of quasi-random numbers, only some syntaxes of `rand` are supported by the `qrandstream` class.

`rand(q,n)` returns an `n`-by-`n` matrix only when `n` is equal to the number of dimensions. Any other value of `n` produces an error.

`rand(q)` returns a scalar only when the stream is in one dimension. Having more than one dimension in `q` produces an error.

`rand(q,m,n)` or `rand(q,[m,n])` returns an `m`-by-`n` matrix only when `n` is equal to the number of dimensions in the stream. Any other value of `n` produces an error.

`rand(q,m,n,p,...)` or `rand(q,[m,n,p,...])` produces an error unless `p` and all following dimensions sizes are equal to one.

Examples

Generate the first 256 points from a 5-D Sobol sequence:

```
q = qrandstream('sobol',5);
X = rand(q,256,5);
```

See Also

`qrandstream` | `qrand` | `rand`

randg

Purpose

Gamma random numbers

Syntax

```
Y = randg
Y = randg(A)
Y = randg(A,m)
Y = randg(A,m,n,p,...)
Y = randg(A,[m,n,p,...])
```

Description

`Y = randg` returns a scalar random value chosen from a gamma distribution with unit scale and shape.

`Y = randg(A)` returns a matrix of random values chosen from gamma distributions with unit scale. `Y` is the same size as `A`, and `randg` generates each element of `Y` using a shape parameter equal to the corresponding element of `A`.

`Y = randg(A,m)` returns an `m`-by-`m` matrix of random values chosen from gamma distributions with shape parameters `A`. `A` is either an `m`-by-`m` matrix or a scalar. If `A` is a scalar, `randg` uses that single shape parameter value to generate all elements of `Y`.

`Y = randg(A,m,n,p,...)` or `Y = randg(A,[m,n,p,...])` returns an `m`-by-`n`-by-`p`-by-`...` array of random values chosen from gamma distributions with shape parameters `A`. `A` is either an `m`-by-`n`-by-`p`-by-`...` array or a scalar.

`randg` produces pseudo-random numbers using the MATLAB functions `rand` and `randn`. The sequence of numbers generated is determined by the state of the default random number stream. Since MATLAB resets the state at start-up, the sequence of numbers `randg` generates will be the same in each session unless those states are changed.

To create reproducible output from `randg`, reset the state of the random number stream before calling `randg`. For example:

```
s = rng % Obtain the current state of the random stream
% call randg
rng(s) % Reset the stream to the previous state
% call randg again, obtain identical results
```

See the `rng` documentation for more information.

Calling `randg` changes the current states of `rand`, `randn`, and `randi`, and therefore alters the outputs of subsequent calls to those functions.

To generate gamma random numbers and specify both the scale and shape parameters, you should call `gamrnd` rather than calling `randg` directly.

References

[1] Marsaglia, G., and W. W. Tsang. "A Simple Method for Generating Gamma Variables." *ACM Transactions on Mathematical Software.* Vol. 26, 2000, pp. 363–372.

See Also

`gamrnd`

random

Purpose

Random numbers

Syntax

```
Y = random(name,A)
Y = random(name,A,B)
Y = random(name,A,B,C)
Y = random(name,A,m,n,...)
Y = random(name,A,[m,n,...])
Y = random(name,A,B,m,n,...)
Y = random(name,A,B,[m,n,...])
Y = random(name,A,B,C,m,n,...)
Y = random(name,A,B,C,[m,n,...])
```

Description

`Y = random(name,A)` where `name` is the name of a distribution that takes a single parameter, returns random numbers `Y` from the one-parameter family of distributions specified by `name`. Parameter values for the distribution are given in `A`.

`Y` is the same size as `A`.

`Y = random(name,A,B)` returns random numbers `Y` from a two-parameter family of distributions. Parameter values for the distribution are given in `A` and `B`.

If `A` and `B` are arrays, they must be the same size. If either `A` or `B` are scalars, they are expanded to constant matrices of the same size.

`Y = random(name,A,B,C)` returns random numbers `Y` from a three-parameter family of distributions. Parameter values for the distribution are given in `A`, `B`, and `C`.

If `A`, `B`, and `C` are arrays, they must be the same size. If any of `A`, `B`, or `C` are scalars, they are expanded to constant matrices of the same size.

`Y = random(name,A,m,n,...)` or `Y = random(name,A,[m,n,...])` returns an `m`-by-`n`-by... matrix of random numbers.

Similarly, `Y = random(name,A,B,m,n,...)` or `Y = random(name,A,B,[m,n,...])` returns an `m`-by-`n`-by... matrix of random numbers for distributions that require two parameters. `Y = random(name,A,B,C,m,n,...)` or `Y =`

`random(name,A,B,C,[m,n,...])` returns an `m`-by-`n`-by... matrix of random numbers for distributions that require three parameters.

If any of `A`, `B`, or `C` are arrays, then the specified dimensions must match the common dimensions of `A`, `B`, and `C` after any necessary scalar expansion.

The following table denotes the acceptable strings for `name`, as well as the parameters for that distribution:

`name`	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
`'beta'` or `'Beta'`	"Beta Distribution" on page B-4	`a`	`b`	—
`'bino'` or `'Binomial'`	"Binomial Distribution" on page B-7	`n`: number of trials	`p`: probability of success for each trial	—
`'chi2'` or `'Chisquare'`	"Chi-Square Distribution" on page B-12	ν: degrees of freedom	—	—
`'exp'` or `'Exponential'`	"Exponential Distribution" on page B-16	μ: mean	—	—
`'ev'` or `'Extreme Value'`	"Extreme Value Distribution" on page B-19	μ: location parameter	σ: scale parameter	—
`'f'` or `'F'`	"F Distribution" on page B-25	$\nu 1$: numerator degrees of freedom	$\nu 2$: denominator degrees of freedom	—
`'gam'` or `'Gamma'`	"Gamma Distribution" on page B-27	`a`: shape parameter	`b`: scale parameter	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'gev' or 'Generalized Extreme Value'	"Generalized Extreme Value Distribution" on page B-32	k: shape parameter	σ: scale parameter	μ: location parameter
'gp' or 'Generalized Pareto'	"Generalized Pareto Distribution" on page B-37	k: tail index (shape) parameter	σ: scale parameter	μ: threshold (location) parameter
'geo' or 'Geometric'	"Geometric Distribution" on page B-41	p: probability parameter	—	—
'hyge' or 'Hypergeometric'	"Hypergeometric Distribution" on page B-43	M: size of the population	K: number of items with the desired characteristic in the population	n: number of samples drawn
'logn' or 'Lognormal'	"Lognormal Distribution" on page B-51	μ	σ	—
'nbin' or 'Negative Binomial'	"Negative Binomial Distribution" on page B-72	r: number of successes	p: probability of success in a single trial	—
'ncf' or 'Noncentral F'	"Noncentral F Distribution" on page B-78	ν1: numerator degrees of freedom	ν2: denominator degrees of freedom	δ: noncentrality parameter
'nct' or 'Noncentral t'	"Noncentral t Distribution" on page B-80	ν: degrees of freedom	δ: noncentrality parameter	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'ncx2' or 'Noncentral Chi-square'	"Noncentral Chi-Square Distribution" on page B-76	ν: degrees of freedom	δ: noncentrality parameter	—
'norm' or 'Normal'	"Normal Distribution" on page B-83	μ: mean	σ: standard deviation	—
'poiss' or 'Poisson'	"Poisson Distribution" on page B-89	λ: mean	—	—
'rayl' or 'Rayleigh'	"Rayleigh Distribution" on page B-91	b: scale parameter	—	—
't' or 'T'	"Student's t Distribution" on page B-95	ν: degrees of freedom	—	—
'unif' or 'Uniform'	"Uniform Distribution (Continuous)" on page B-99	a: lower endpoint (minimum)	b: upper endpoint (maximum)	—
'unid' or 'Discrete Uniform'	"Uniform Distribution (Discrete)" on page B-101	N: maximum observable value	—	—
'wbl' or 'Weibull'	"Weibull Distribution" on page B-103	a: scale parameter	b: shape parameter	—

Examples

Generate a 2-by-4 array of random values from the normal distribution with mean 0 and standard deviation 1:

```
x1 = random('Normal',0,1,2,4)
x1 =
  1.1650  0.0751  -0.6965  0.0591
  0.6268  0.3516  1.6961  1.7971
```

The order of the parameters is the same as for `normrnd`.

Generate a single random value from Poisson distributions with rate parameters 1, 2, ..., 6, respectively:

```
x2 = random('Poisson',1:6,1,6)
x2 =
   0   0   1   2   5   7
```

See Also

`cdf` | `pdf` | `icdf` | `mle`

Purpose

Random numbers from Gaussian mixture distribution

Syntax

```
y = random(obj)
Y = random(obj,n)
[Y,idx] = random(obj,n)
```

Description

`y = random(obj)` generates a 1-by-*d* vector `y` drawn at random from the *d*-dimensional Gaussian mixture distribution defined by `obj`. `obj` is an object created by `gmdistribution` or `fit`.

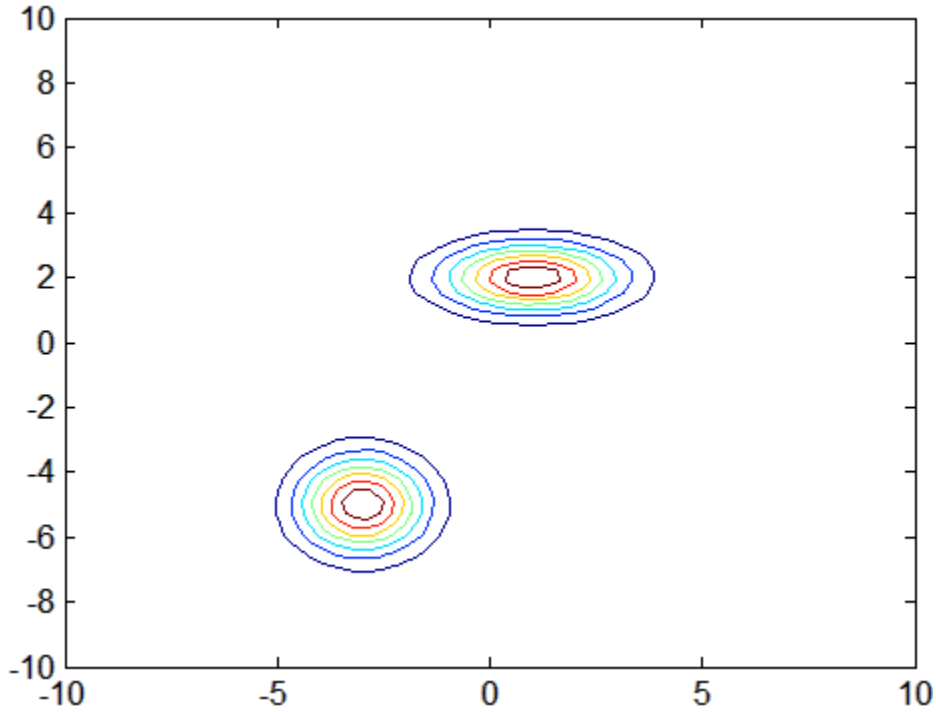
`Y = random(obj,n)` generates an `n`-by-*d* matrix `Y` of `n` *d*-dimensional random samples.

`[Y,idx] = random(obj,n)` also returns an `n`-by-1 vector `idx`, where `idx(I)` is the index of the component used to generate `Y(I,:)`.

Examples

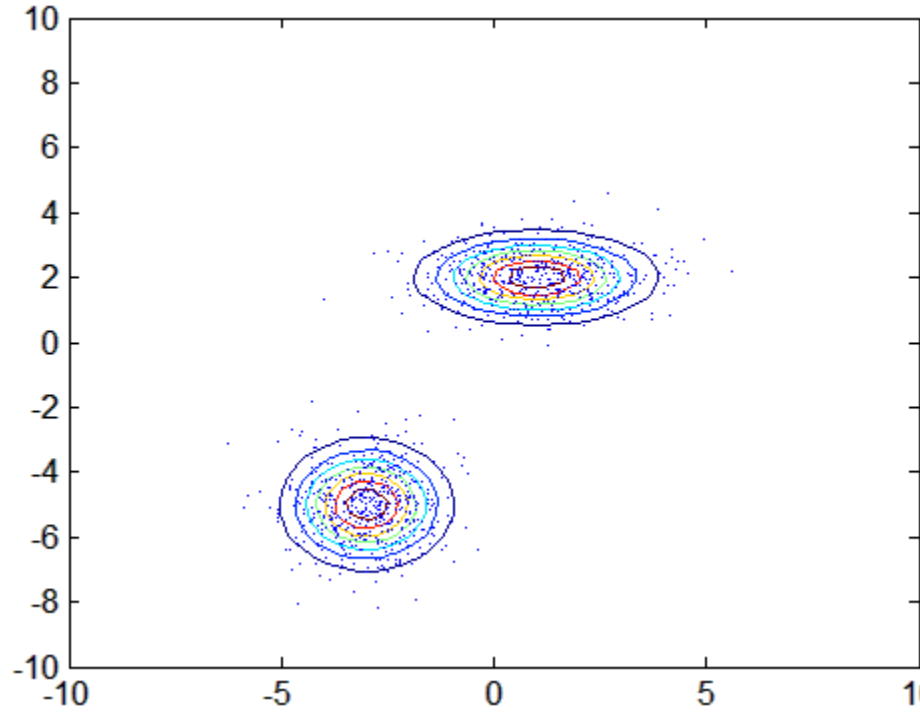
Create a `gmdistribution` object defining a two-component mixture of bivariate Gaussian distributions:

```
MU = [1 2;-3 -5];
SIGMA = cat(3,[2 0;0 .5],[1 0;0 1]);
p = ones(1,2)/2;
obj = gmdistribution(MU,SIGMA,p);

ezcontour(@(x,y)pdf(obj,[x y]),[-10 10],[-10 10])
hold on
```



Generate 1000 random values:

```
Y = random(obj,1000);

scatter(Y(:,1),Y(:,2),10,'.')
```



See Also

`gmdistribution` | `fit` | `mvnrnd`

piecewisedistribution.random

Purpose

Random numbers from piecewise distribution

Syntax

```
r = random(obj)
R = random(obj,n)
R = random(obj,m,n)
R = random(obj,[m,n])
R = random(obj,m,n,p,...)
R = random(obj,[m,n,p,...])
```

Description

`r = random(obj)` generates a pseudo-random number `r` drawn from the piecewise distribution object `obj`.

`R = random(obj,n)` generates an n-by-n matrix of pseudo-random numbers `R`.

`R = random(obj,m,n)` or `R = random(obj,[m,n])` generates an m-by-n matrix of pseudo-random numbers `R`.

`R = random(obj,m,n,p,...)` or `R = random(obj,[m,n,p,...])` generates an m-by-n-by-p-by-... array of pseudo-random numbers `R`.

Examples

Fit Pareto tails to a t distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);

r = random(obj)
r =
    0.8285
```

See Also

`paretotails` | `cdf` | `icdf`

Purpose

Generate random number drawn from ProbDist object

Syntax

```
Y = random(PD)
Y = random(PD, N)
Y = random(PD, N, M, ...)
```

Description

`Y = random(PD)` generates a random number drawn from the distribution specified by *PD*, a ProbDist object.

`Y = random(PD, N)` generates an *N*-by-*N* array of random numbers drawn from the distribution specified by *PD*, a ProbDist object.

`Y = random(PD, N, M, ...)` generates an *N*-by-*M*-by`...` array of random numbers drawn from the distribution specified by *PD*, a ProbDist object.

Input Arguments

PD	An object of the class `ProbDistUnivParam` or `ProbDistUnivKernel`.
N	A positive integer.
M	A positive integer.

Output Arguments

Y	A random number drawn from the distribution specified by *PD*.

See Also

`random`

randsample

Purpose

Random sample

Syntax

```
y = randsample(n,k)
y = randsample(population,k)
y = randsample(n,k,replacement)
y = randsample(population,k,replacement)
y = randsample(n,k,true,w)
y = randsample(population,k,true,w)
y = randsample(s,...)
```

Description

`y = randsample(n,k)` returns a `k`-by-`1` vector `y` of values sampled uniformly at random, without replacement, from the integers 1 to `n`.

`y = randsample(population,k)` returns a vector of `k` values sampled uniformly at random, without replacement, from the values in the vector `population`. The orientation of `y` (row or column) is the same as `population`.

`y = randsample(n,k,replacement)` or `y = randsample(population,k,replacement)` returns a sample taken with replacement if `replacement` is `true`, or without replacement if `replacement` is `false`. The default is `false`.

`y = randsample(n,k,true,w)` or `y = randsample(population,k,true,w)` returns a weighted sample taken with replacement, using a vector of positive weights `w`, whose length is `n`. The probability that the integer `i` is selected for an entry of `y` is `w(i)/sum(w)`. Usually, `w` is a vector of probabilities. `randsample` does not support weighted sampling without replacement.

`y = randsample(s,...)` uses the stream `s` for random number generation. `s` is a member of the `RandStream` class. Default is the MATLAB default random number stream.

Examples

Draw a single value from the integers `1` through `10`:

```
n = 10;
x = randsample(n,1);
```

Draw a single value from the population `1` through `n`, where `n > 1`:

```
y = randsample(1:n,1);
```

Note If `population` is a numeric vector containing only nonnegative integer values, and `population` can have length `1`, use

```
y = population(randsample(length(population),k))
```

instead of `y = randsample(population,k)`.

Generate a random sequence of the characters `A`, `C`, `G`, and `T`, with replacement, according to the specified probabilities.

```
R = randsample('ACGT',48,true,[0.15 0.35 0.35 0.15])
```

See Also

`rand` | `randperm` | `RandStream`

randtool

Purpose

Interactive random number generation

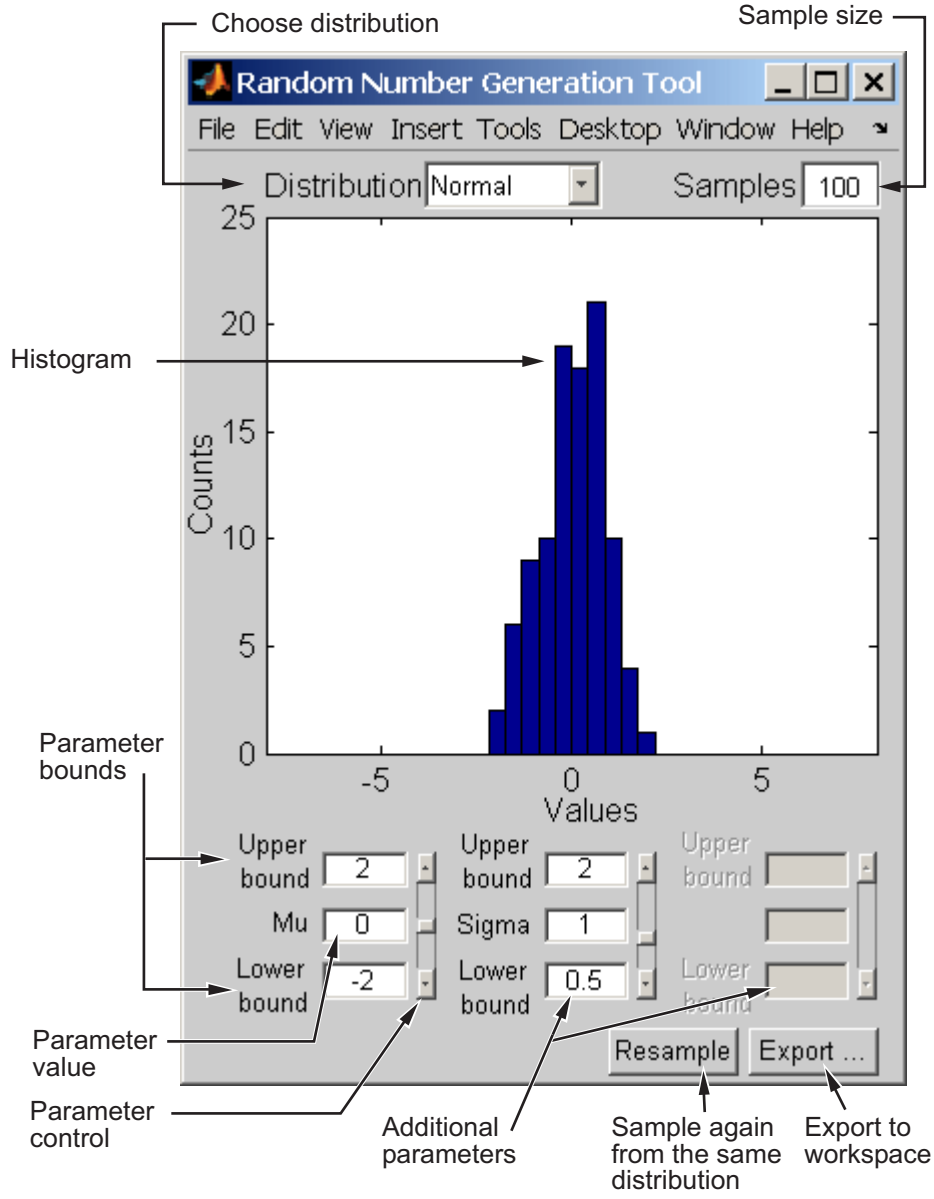
Syntax

```
randtool
```

Description

`randtool` opens the Random Number Generation Tool.

The Random Number Generation Tool is a graphical user interface that generates random samples from specified probability distributions and displays the samples as histograms. Use the tool to explore the effects of changing parameters and sample size on the distributions.


Choose distribution
Sample size
Random Number Generation Tool
File Edit View Insert Tools Desktop Window Help
Distribution Normal
Samples 100
Histogram
Counts
Values
Parameter bounds
Upper bound 2
Mu 0
Lower bound -2
Upper bound 2
Sigma 1
Lower bound 0.5
Upper bound
Lower bound
Resample
Export ...
Parameter value
Parameter control
Additional parameters
Sample again from the same distribution
Export to workspace

Start by selecting a distribution, then enter the desired sample size.

You can also

- Use the controls at the bottom of the window to set parameter values for the distribution and to change their upper and lower bounds.
- Draw another sample from the same distribution, with the same size and parameters.
- Export the current sample to your workspace. A dialog box enables you to provide a name for the sample.

See Also

`disttool` | `dfittool`

Purpose

Range of values

Syntax

```
range(X)
y = range(X,dim)
```

Description

`range(X)` returns the difference between the maximum and the minimum of a sample. For vectors, `range(x)` is the range of the elements. For matrices, `range(X)` is a row vector containing the range of each column of X. For N-dimensional arrays, `range` operates along the first nonsingleton dimension of `X`.

`y = range(X,dim)` operates along the dimension `dim` of `X`.

`range` treats `NaN`s as missing values and ignores them.

The range is an easily-calculated estimate of the spread of a sample. Outliers have an undue influence on this statistic, which makes it an unreliable estimator.

Examples

The range of a large sample of standard normal random numbers is approximately six. This is the motivation for the process capability indices C_p and C_{pk} in statistical quality control applications.

```
rv = normrnd(0,1,1000,5);
near6 = range(rv)
near6 =
  6.1451  6.4986  6.2909  5.8894  7.0002
```

See Also

`std` | `iqr` | `mad`

rangesearch

Purpose

Find all neighbors within specified distance

Syntax

```
idx = rangesearch(X,Y,r)
[idx,D]= rangesearch(X,Y,r)
[idx,D]= rangesearch(X,Y,r,Name,Value)
```

Description

`idx = rangesearch(X,Y,r)` finds all the `X` points that are within distance `r` of the `Y` points. Rows of `X` and `Y` correspond to observations, and columns correspond to variables.

`[idx,D]= rangesearch(X,Y,r)` returns the distances between each row of `Y` and the rows of `X` that are `r` or less distant.

`[idx,D]= rangesearch(X,Y,r,Name,Value)` finds nearby points with additional options specified by one or more `Name,Value` pair arguments.

Tips

- For a fixed positive integer `K`, `knnsearch` finds `K` points in `X` that are nearest each `Y` point. In contrast, for a fixed positive real value `r`, `rangesearch` finds all the `X` points that are within a distance `r` of each `Y` point.

Input Arguments

`X`

mx-by-*n* numeric matrix, where each row represents one *n*-dimensional point. The number of columns *n* must equal as the number of columns in `Y`.

`Y`

my-by-*n* numeric matrix, where each row represents one *n*-dimensional point. The number of columns *n* must equal as the number of columns in `X`.

`r`

Search radius, a scalar. `rangesearch` finds all `X` points (rows) that are within distance `r` of each `Y` point. The meaning of distance depends on the `Distance` name-value pair.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`BucketSize`

Maximum number of data points in the leaf node of the *k*d-tree. This argument is only meaningful when *k*d-tree is used for finding nearest neighbors.

Default: `50`

`Cov`

Positive definite matrix indicating the covariance matrix when computing the Mahalanobis distance. This argument is only valid when the `Distance` name-value pair is `'mahalanobis'`.

Default: `nancov(X)`

`Distance`

String or function handle specifying the distance metric.

Value	Description
`'euclidean'`	Euclidean distance.
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between `X` and a query point is scaled, meaning divided by a scale value `S`. The default value of `S` is the standard deviation computed from `X`, `S=nanstd(X)`. To specify another value for `S`, use the `Scale` name-value pair.

Value	Description
`'mahalanobis'`	Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is the sample covariance matrix of `X`, as computed by `nancov(X)`. To specify a different value for `C`, use the `'Cov'` name-value pair.
`'cityblock'`	City block distance.
`'minkowski'`	Minkowski distance. The default exponent is `2`. To specify a different exponent, use the `'P'` name-value pair.
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'cosine'`	One minus the cosine of the included angle between observations (treated as vectors).
`'correlation'`	One minus the sample linear correlation between observations (treated as sequences of values).
`'hamming'`	Hamming distance, percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.

Value	Description
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).

`@distfun`	Distance function handle. *`distfun`* has the form
	
	`function D2 = DISTFUN(ZI,ZJ)`
	`...`
	
	where
	
	• `ZI` is a `1`-by-`N` vector containing one row of `X` or `Y`.
	• `ZJ` is an `M2`-by-`N` matrix containing multiple rows of `X` or `Y`.
	• `D2` is an `M2`-by-`1` vector of distances, `D2(k)` is the distance between the observations `ZI` and `ZJ(J,:)`.

For definitions, see "Distance Metrics" on page 13-9.

Default: `'euclidean'`

`NSMethod`

Nearest neighbors search method.

Value	Meaning
`'kdtree'`	Creates and uses a *k*d-tree to find nearest neighbors. `'kdtree'` is only valid when the distance metric is one of: • `'chebyshev'` • `'cityblock'` • `'euclidean'` • `'minkowski'`
`'exhaustive'`	Uses the exhaustive search algorithm. The distances from all `X` points to each `Y` point are computed to find nearest neighbors.

Default: `'kdtree'` when the number of columns of `X` is not greater than `10`, `X` is not sparse, and the distance metric is one of the valid `'kdtree'` metrics. Otherwise, the default is `'exhaustive'`.

`P`

Positive scalar indicating the exponent of Minkowski distance. This argument is only valid when the `Distance` name-value pair is `'minkowski'`.

Default: `2`

`Scale`

Vector `S` containing nonnegative values, with length equal to the number of columns in `X`. Each coordinate difference between `X` and a query point is scaled by the corresponding element of `S`. This argument is only valid when the `Distance` name-value pair is `'seuclidean'`.

Default: `nanstd(X)`

Output Arguments

`idx`

my-by-1 cell array, where *my* is the number of rows in `Y`. `idx{I}` contains the indices of points (rows) in `X` whose distances to `Y(I,:)` are not greater than `r`. The entries in `idx{I}` are in ascending order of distance.

`D`

my-by-1 cell array, where *my* is the number of rows in `Y`. `D{I}` contains the distance values between `Y(I,:)` and the corresponding points in `idx{I}`.

Definitions

Distance Metrics

For definitions, see "Distance Metrics" on page 13-9.

Examples

Find the `X` points that are within a Euclidean distance `1.5` of each `Y` point. Both `X` and `Y` are samples of 5-D normally distributed variables.

```
rng('default') % for reproducibility
X = randn(100,5);
Y = randn(10,5);
[idx, dist] = rangesearch(X,Y,1.5)

idx =
    [1x7  double]
    [1x2  double]
    [1x11 double]
    [1x2  double]
    [1x12 double]
    [1x9  double]
    [         89]
    [1x0  double]
    [1x0  double]
    [1x0  double]

dist =
    [1x7  double]
```

```
[1x2  double]
[1x11 double]
[1x2  double]
[1x12 double]
[1x9  double]
[     1.1739]
[1x0  double]
[1x0  double]
[1x0  double]
```

In this case, the last three `Y` points are more than `1.5` distant from any `X` point. `X(89,:)` is `1.1739` distant from `Y(7,:)`, and there is no other `X` point that is within distance `1.5` of `Y(7,:)`. There are `12` points in `X` within distance `1.5` of `Y(5,:)`.

Algorithms

For an overview of the *k*d-tree algorithm, see "*k*-Nearest Neighbor Search Using a *k*d-Tree" on page 13-14.

The exhaustive search algorithm finds the distance of each point in `X` to each point in `Y`.

Alternatives

`rangesearch` is the `ExhaustiveSearcher` method for distance search. It is equivalent to the `rangesearch` function with the `NSMethod` name-value pair set to `'exhaustive'`.

`rangesearch` is the `KDTreeSearcher` method for distance search. It is equivalent to the `rangesearch` function with the `NSMethod` name-value pair set to `'kdtree'`.

See Also

`createns` | `ExhaustiveSearcher` | `KDTreeSearcher` | `knnsearch` | `pdist2`

How To

- "*k*-Nearest Neighbor Search and Radius Search" on page 13-12

Purpose

Find all neighbors within specified distance using `ExhaustiveSearcher` object

Syntax

```
idx = rangesearch(NS,Y,r)
[idx,D]= rangesearch(NS,Y,r)
[idx,D]= rangesearch(NS,Y,r,Name,Value)
```

Description

`idx = rangesearch(NS,Y,r)` finds all points in `NS.X` that are within distance `r` of the `Y` points. Rows of `NS.X` and `Y` correspond to observations, and columns correspond to variables.

`[idx,D]= rangesearch(NS,Y,r)` returns the distances between each row of `Y` and the rows of `NS.X` that are `r` or less distant.

`[idx,D]= rangesearch(NS,Y,r,Name,Value)` finds nearby points with additional options specified by one or more `Name,Value` pair arguments.

Tips

- For a fixed positive integer `K`, `knnsearch` finds the `K` points in `NS.X` that are nearest each `Y` point. In contrast, for a fixed positive real value `r`, `rangesearch` finds all the points in `NS.X` that are within a distance `r` of each `Y` point.

Input Arguments

`NS`

`ExhaustiveSearcher` object, constructed using `ExhaustiveSearcher` or `createns`.

`Y`

my-by-*n* numeric matrix, where each row represents one *n*-dimensional point. The number of columns *n* must equal the number of columns in `NS.X`.

`r`

Search radius, a scalar. `rangesearch` finds all `NS.X` points (rows) that are within distance `r` of each `Y` point. The meaning of distance depends on the `Distance` name-value pair.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`Cov`

Positive definite matrix indicating the covariance matrix when computing the Mahalanobis distance. This argument is only valid when the `Distance` name-value pair is `'mahalanobis'`.

Default: `nancov(X)`

`Distance`

String or function handle specifying the distance metric.

Value	Description
`'euclidean'`	Euclidean distance.
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between `X` and a query point is scaled, meaning divided by a scale value `S`. The default value of `S` is the standard deviation computed from `X`, `S=nanstd(X)`. To specify another value for `S`, use the `Scale` name-value pair.
`'mahalanobis'`	Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is the sample covariance matrix of `X`, as computed by `nancov(X)`. To specify a different value for `C`, use the `'Cov'` name-value pair.
`'cityblock'`	City block distance.

Value	Description
`'minkowski'`	Minkowski distance. The default exponent is `2`. To specify a different exponent, use the `'P'` name-value pair.
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'cosine'`	One minus the cosine of the included angle between observations (treated as vectors).
`'correlation'`	One minus the sample linear correlation between observations (treated as sequences of values).
`'hamming'`	Hamming distance, percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).

`@distfun`	Distance function handle. *`distfun`* has the form
	
	`function D2 = DISTFUN(ZI,ZJ)`
	`...`
	
	where
	
	• `ZI` is a `1`-by-`N` vector containing one row of `X` or `Y`.
	• `ZJ` is an `M2`-by-`N` matrix containing multiple rows of `X` or `Y`.

Value	Description
	• D2 is an M2-by-1 vector of distances, D2(k) is the distance between the observations ZI and ZJ(J,:).

For definitions, see “Distance Metrics” on page 13-9.

Default: `'euclidean'`

`P`

Positive scalar indicating the exponent of Minkowski distance. This argument is only valid when the `Distance` name-value pair is `'minkowski'`.

Default: `2`

`Scale`

Vector `S` containing nonnegative values, with length equal to the number of columns in `X`. Each coordinate difference between `X` and a query point is scaled by the corresponding element of `S`. This argument is only valid when the `Distance` name-value pair is `'seuclidean'`.

Default: `nanstd(X)`

Output Arguments

`idx`

my-by-1 cell array, where *my* is the number of rows in `Y`. `idx{I}` contains the indices of points (rows) in `NS.X` whose distances to `Y(I,:)` are not greater than `r`. The entries in `idx{I}` are in ascending order of distance.

`D`

my-by-1 cell array, where *my* is the number of rows in `Y`. `D{I}` contains the distance values between `Y(I,:)` and the corresponding points in `idx{I}`.

Definitions

Distance Metrics

For definitions, see "Distance Metrics" on page 13-9.

Examples

Create `X` and `Y` as samples of 5-D normally distributed variables. Create an `ExhaustiveSearcher` object `NS` from `X`. Find the points in `NS.X` that are within a Euclidean distance `1.5` of each point in `Y`.

```
rng('default') % for reproducibility
X = randn(100,5);
Y = randn(10,5);
NS = ExhaustiveSearcher(X);
[idx, dist] = rangesearch(NS,Y,1.5)

idx =
    [1x7  double]
    [1x2  double]
    [1x11 double]
    [1x2  double]
    [1x12 double]
    [1x9  double]
    [         89]
    [1x0  double]
    [1x0  double]
    [1x0  double]

dist =
    [1x7  double]
    [1x2  double]
    [1x11 double]
    [1x2  double]
    [1x12 double]
    [1x9  double]
```

```
[     1.1739]
[1x0  double]
[1x0  double]
[1x0  double]
```

In this case, the last three points in `Y` are more than `1.5` distant from any point in `NS.X`. `NS.X(89,:)` is `1.1739` distant from `Y(7,:)`, and there is no other point in `NS.X` that is within distance `1.5` of `Y(7,:)`. There are `12` points in `NS.X` within distance `1.5` of `Y(5,:)`.

Algorithms

The exhaustive search algorithm finds the distance of each point in `X` to each point in `Y`.

Alternatives

`rangesearch` is the `ExhaustiveSearcher` method for distance search. It is equivalent to the `rangesearch` function with the `NSMethod` name-value pair set to `'exhaustive'`.

`rangesearch` is the `KDTreeSearcher` method for distance search. It is equivalent to the `rangesearch` function with the `NSMethod` name-value pair set to `'kdtree'`.

See Also

`createns` | `ExhaustiveSearcher` | `knnsearch` | `pdist2` | `rangesearch`

Purpose

Find all neighbors within specified distance using `KDTreeSearcher` object

Syntax

```
idx = rangesearch(NS,Y,r)
[idx,D]= rangesearch(NS,Y,r)
[idx,D]= rangesearch(NS,Y,r,Name,Value)
```

Description

`idx = rangesearch(NS,Y,r)` finds all points in `NS.X` that are within distance `r` of the `Y` points. Rows of `NS.X` and `Y` correspond to observations, and columns correspond to variables.

`[idx,D]= rangesearch(NS,Y,r)` returns the distances between each row of `Y` and the rows of `NS.X` that are `r` or less distant.

`[idx,D]= rangesearch(NS,Y,r,Name,Value)` finds nearby points with additional options specified by one or more `Name,Value` pair arguments.

Tips

- For a fixed positive integer `K`, `knnsearch` finds the `K` points in `NS.X` that are nearest each `Y` point. In contrast, for a fixed positive real value `r`, `rangesearch` finds all the points in `NS.X` that are within a distance `r` of each `Y` point.

Input Arguments

`NS`

`KDTreeSearcher` object, constructed using `KDTreeSearcher` or `createns`.

`Y`

my-by-*n* numeric matrix, where each row represents one *n*-dimensional point. The number of columns *n* must equal the number of columns in `NS.X`.

`r`

Search radius, a scalar. `rangesearch` finds all `NS.X` points (rows) that are within distance `r` of each `Y` point. The meaning of distance depends on the `Distance` name-value pair.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`Distance`

String or function handle specifying the distance metric.

Value	Description
`'euclidean'`	Euclidean distance.
`'cityblock'`	City block distance.
`'minkowski'`	Minkowski distance. The default exponent is `2`. To specify a different exponent, use the `'P'` name-value pair.
`'chebychev'`	Chebychev distance (maximum coordinate difference).

For definitions, see "Distance Metrics" on page 13-9.

Default: `NS.Distance`

`P`

Positive scalar indicating the exponent of Minkowski distance. This argument is only valid when the `Distance` name-value pair is `'minkowski'`.

Default: `2`

Output Arguments

`idx`

my-by-`1` cell array, where *my* is the number of rows in `Y`. `idx{I}` contains the indices of points (rows) in `NS.X` whose distances

to `Y(I,:)` are not greater than `r`. The entries in `idx{I}` are in ascending order of distance.

`D`

my-by-1 cell array, where *my* is the number of rows in `Y`. `D{I}` contains the distance values between `Y(I,:)` and the corresponding points in `idx{I}`.

Definitions

Distance Metrics

For definitions, see "Distance Metrics" on page 13-9.

Examples

Create `X` and `Y` as samples of 5-D normally distributed variables. Create a `KDTreeSearcher` object `NS` from `X`. Find the points in `NS.X` that are within a Euclidean distance `1.5` of each point in `Y`.

```
rng('default') % for reproducibility
X = randn(100,5);
Y = randn(10,5);
NS = KDTreeSearcher(X);
[idx, dist] = rangesearch(NS,Y,1.5)

idx =
    [1x7  double]
    [1x2  double]
    [1x11 double]
    [1x2  double]
    [1x12 double]
    [1x9  double]
    [         89]
    [1x0  double]
    [1x0  double]
    [1x0  double]

dist =
    [1x7  double]
    [1x2  double]
```

```
[1x11 double]
[1x2  double]
[1x12 double]
[1x9  double]
[     1.1739]
[1x0  double]
[1x0  double]
[1x0  double]
```

In this case, the last three points in `Y` are more than `1.5` distant from any point in `NS.X`. `NS.X(89,:)` is `1.1739` distant from `Y(7,:)`, and there is no other point in `NS.X` that is within distance `1.5` of `Y(7,:)`. There are `12` points in `NS.X` within distance `1.5` of `Y(5,:)`.

Algorithms

For an overview of the *k*d-tree algorithm, see "*k*-Nearest Neighbor Search Using a *k*d-Tree" on page 13-14.

Alternatives

`rangesearch` is the `KDTreeSearcher` method for distance search. It is equivalent to the `rangesearch` function with the `NSMethod` name-value pair set to `'kdtree'`.

`rangesearch` is the `ExhaustiveSearcher` method for distance search. It is equivalent to the `rangesearch` function with the `NSMethod` name-value pair set to `'exhaustive'`.

See Also

`createns` | `KDTreeSearcher` | `knnsearch` | `pdist2` | `rangesearch`

Purpose

Wilcoxon rank sum test

Syntax

```
p = ranksum(x,y)
[p,h] = ranksum(x,y)
[p,h] = ranksum(x,y,'alpha',alpha)
[p,h] = ranksum(...,'method',method)
[p,h,stats] = ranksum(...)
```

Description

`p = ranksum(x,y)` performs a two-sided rank sum test of the null hypothesis that data in the vectors `x` and `y` are independent samples from identical continuous distributions with equal medians, against the alternative that they do not have equal medians. `x` and `y` can have different lengths. The *p* value of the test is returned in `p`. The test is equivalent to a Mann-Whitney *U*-test.

`[p,h] = ranksum(x,y)` returns the result of the test in `h`. `h = 1` indicates a rejection of the null hypothesis at the 5% significance level. `h = 0` indicates a failure to reject the null hypothesis at the 5% significance level.

`[p,h] = ranksum(x,y,'alpha',alpha)` performs the test at the (100*`alpha`)% significance level. The default, when unspecified, is `alpha = 0.05`.

`[p,h] = ranksum(...,'method',method)` computes the *p* value using either an exact algorithm, when *`method`* is `'exact'`, or a normal approximation, when *`method`* is `'approximate'`. Because the exact method can be very slow on large samples, the default is `exact` for small samples and `approximate` for large samples.

`[p,h,stats] = ranksum(...)` returns the structure `stats` with the following fields:

- `ranksum` — Value of the rank sum test statistic
- `zval` — Value of the *z*-statistic (computed only for large samples)

Examples

Test the hypothesis of equal medians for two independent unequal-sized samples. The sampling distributions are identical except for a shift of 0.25.

```
x = unifrnd(0,1,10,1);
y = unifrnd(0.25,1.25,15,1);
[p,h] = ranksum(x,y)
p =
  0.0375
h =
   1
```

The test rejects the null hypothesis of equal medians at the default 5% significance level.

References

[1] Gibbons, J. D. *Nonparametric Statistical Inference*. New York: Marcel Dekker, 1985.

[2] Hollander, M., and D. A. Wolfe. *Nonparametric Statistical Methods*. Hoboken, NJ: John Wiley & Sons, Inc., 1999.

See Also

`kruskalwallis` | `signrank` | `signtest` | `ttest2`

Purpose

Rayleigh cumulative distribution function

Syntax

```
P = raylcdf(X,B)
```

Description

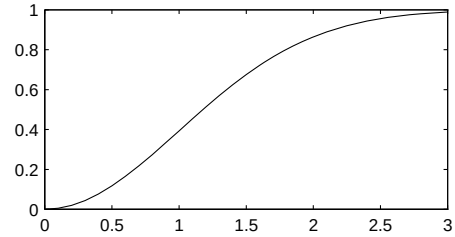
`P = raylcdf(X,B)` computes the Rayleigh cdf at each of the values in `X` using the corresponding scale parameter, `B`. `X` and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `X` or `B` is expanded to a constant array with the same dimensions as the other input.

The Rayleigh cdf is

$$y = F(x \mid b) = \int_0^x \frac{t}{b^2} e^{\left(\frac{-t^2}{2b^2}\right)} dt$$

Examples

```
x = 0:0.1:3;
p = raylcdf(x,1);
plot(x,p)
```



References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. Hoboken, NJ: Wiley-Interscience, 2000. pp. 134–136.

See Also

`cdf` | `raylpdf` | `raylinv` | `raylstat` | `raylfit` | `raylrnd`

How To

• "Rayleigh Distribution" on page B-91

raylfit

Purpose

Rayleigh parameter estimates

Syntax

```
raylfit(data,alpha)
[phat,pci] = raylfit(data,alpha)
```

Description

`raylfit(data,alpha)` returns the maximum likelihood estimates of the parameter of the Rayleigh distribution given the data in the vector `data`.

`[phat,pci] = raylfit(data,alpha)` returns the maximum likelihood estimate and 100(1 - `alpha`)% confidence interval given the data. The default value of the optional parameter `alpha` is 0.05, corresponding to 95% confidence intervals.

See Also

`mle` | `raylpdf` | `raylcdf` | `raylinv` | `raylstat` | `raylrnd`

How To

- “Rayleigh Distribution” on page B-91

Purpose

Rayleigh inverse cumulative distribution function

Syntax

```
X = raylinv(P,B)
```

Description

`X = raylinv(P,B)` returns the inverse of the Rayleigh cumulative distribution function using the corresponding scale parameter, `B` at the corresponding probabilities in `P`. `P` and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `P` or `B` is expanded to a constant array with the same dimensions as the other input.

Examples

```
x = raylinv(0.9,1)
x =
  2.1460
```

See Also

`raylcdf` | `raylpdf` | `raylrnd` | `raylstat`

How To

- `icdf`
- “Rayleigh Distribution” on page B-91

raylpdf

Purpose

Rayleigh probability density function

Syntax

```
Y = raylpdf(X,B)
```

Description

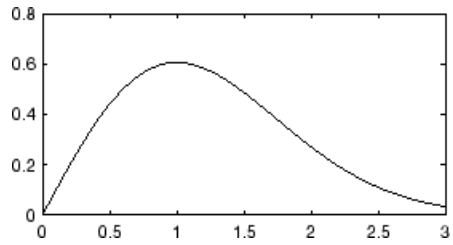
`Y = raylpdf(X,B)` computes the Rayleigh pdf at each of the values in `X` using the corresponding scale parameter, `B`. `X` and `B` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `Y`. A scalar input for `X` or `B` is expanded to a constant array with the same dimensions as the other input.

The Rayleigh pdf is

$$y = f(x \mid b) = \frac{x}{b^2} e^{\left(\frac{-x^2}{2b^2}\right)}$$

Examples

```
x = 0:0.1:3;
p = raylpdf(x,1);
plot(x,p)
```



See Also

`pdf` | `raylcdf` | `raylinv` | `raylstat` | `raylfit` | `raylrnd`

How To

- "Rayleigh Distribution" on page B-91

Purpose

Rayleigh random numbers

Syntax

```
R = raylrnd(B)
R = raylrnd(B,v)
R = raylrnd(B,m,n)
```

Description

`R = raylrnd(B)` returns a matrix of random numbers chosen from the Rayleigh distribution with scale parameter, `B`. `B` can be a vector, a matrix, or a multidimensional array. The size of `R` is the size of `B`.

`R = raylrnd(B,v)` returns a matrix of random numbers chosen from the Rayleigh distribution with parameter `B`, where `v` is a row vector. If `v` is a 1-by-2 vector, `R` is a matrix with `v(1)` rows and `v(2)` columns. If `v` is 1-by-n, `R` is an n-dimensional array.

`R = raylrnd(B,m,n)` returns a matrix of random numbers chosen from the Rayleigh distribution with parameter `B`, where scalars `m` and `n` are the row and column dimensions of `R`.

Examples

```
r = raylrnd(1:5)
r =
  1.7986  0.8795  3.3473  8.9159  3.5182
```

See Also

`random` | `raylpdf` | `raylcdf` | `raylinv` | `raylstat` | `raylfit`

How To

- “Rayleigh Distribution” on page B-91

Purpose

Rayleigh mean and variance

Syntax

```
[M,V] = raylstat(B)
```

Description

`[M,V] = raylstat(B)` returns the mean of and variance for the Rayleigh distribution with scale parameter `B`.

The mean of the Rayleigh distribution with parameter b is $b\sqrt{\pi / 2}$ and the variance is

$$\frac{4-\pi}{2}b^2$$

Examples

```
[mn,v] = raylstat(1)
mn =
  1.2533
v =
  0.4292
```

See Also

`raylpdf` | `raylcdf` | `raylinv` | `raylfit` | `raylrnd`

How To

- “Rayleigh Distribution” on page B-91

Purpose

Residual case order plot

Syntax

```
rcoplot(r,rint)
```

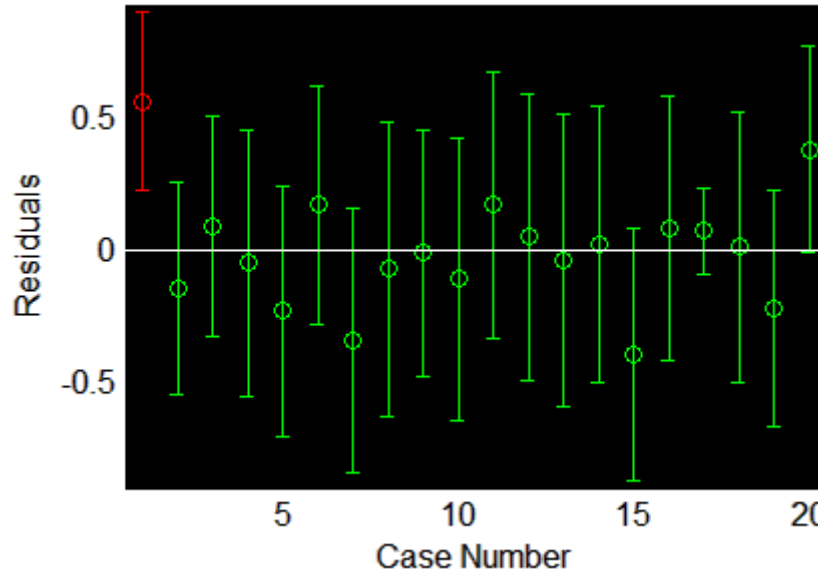
Description

`rcoplot(r,rint)` displays an errorbar plot of the confidence intervals on the residuals from a regression. The residuals appear in the plot in case order. Inputs `r` and `rint` are outputs from the `regress` function.

Examples

The following plots residuals and prediction intervals from a regression of a linearly additive model to the data in `moore.mat`:

```
load moore
X = [ones(size(moore,1),1) moore(:,1:5)];
y = moore(:,6);
alpha = 0.05;
[betahat,Ibeta,res,Ires,stats] = regress(y,X,alpha);
rcoplot(res,Ires)
```



The interval around the first residual, shown in red, does not contain zero. This indicates that the residual is larger than expected in 95% of new observations, and suggests the data point is an outlier.

See Also

`regress`

Purpose

Add reference curve to plot

Syntax

```
refcurve(p)
refcurve
hcurve = refcurve(...)
```

Description

`refcurve(p)` adds a polynomial reference curve with coefficients `p` to the current axes. If `p` is a vector with `n+1` elements, the curve is:

```
y = p(1)*x^n + p(2)*x^(n-1) + ... + p(n)*x + p(n+1)
```

`refcurve` with no input arguments adds a line along the *x* axis.

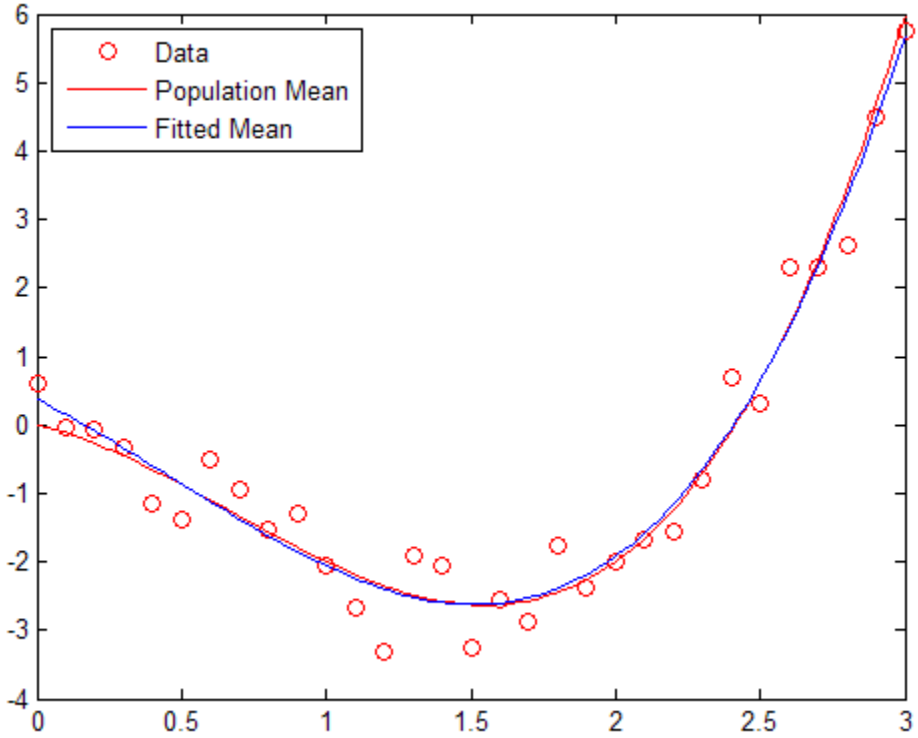
`hcurve = refcurve(...)` returns the handle `hcurve` to the curve.

Examples

Example 1

Plot data from a population with a polynomial trend and use `refcurve` to add both the population and fitted mean functions:

```
p = [1 -2 -1 0];
t = 0:0.1:3;
y = polyval(p,t) + 0.5*randn(size(t));

plot(t,y,'ro')
h = refcurve(p);
set(h,'Color','r')

q = polyfit(t,y,3);
refcurve(q)
legend('Data','Population Mean','Fitted Mean',...
  'Location','NW')
```



Example 2

Plot trajectories of a batted baseball, with and without air resistance.

Relevant physical constants are:

```
M = 0.145;      % Mass (kg)
R = 0.0366;     % Radius (m)
A = pi*R^2;     % Area (m^2)
rho = 1.2;      % Density of air (kg/m^3)
C = 0.5;        % Drag coefficient
```

```
D = rho*C*A/2;
% Drag proportional to the square of the speed
g = 9.8;        % Acceleration due to gravity (m/s^2)
```

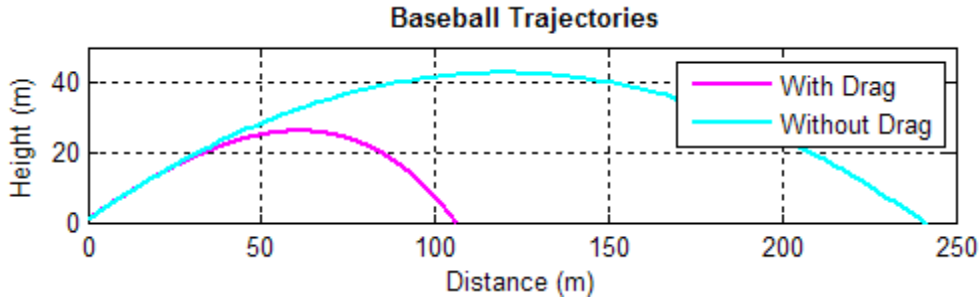
First, simulate the trajectory with drag proportional to the square of the speed, assuming constant acceleration in each time interval:

```
dt = 1e-2;      % Simulation time interval (s)
r0 = [0 1];     % Initial position (m)
s0 = 50;        % Initial speed (m/s)
alpha0 = 35;    % Initial angle (deg)
v0=s0*[cosd(alpha0) sind(alpha0)]; % Initial velocity (m/s)

r = r0;
v = v0;
trajectory = r0;
while r(2) > 0
    a = [0 -g]-(D/M)*norm(v)*v;
    v = v + a*dt;
    r = r + v*dt + (1/2)*a*(dt^2);
    trajectory = [trajectory;r];
end
```

Second, use `refcurve` to add the drag-free parabolic trajectory (found analytically) to a plot of `trajectory`:

```
plot(trajectory(:,1),trajectory(:,2),'m','LineWidth',2)
xlim([0,250])
h = refcurve([-g/(2*v0(1)^2),...
    (g*r0(1)/v0(1)^2)+(v0(2)/v0(1)),...
    (-g*r0(1)^2/(2*v0(1)^2))-(v0(2)*r0(1)/v0(1))+r0(2)]);
set(h,'Color','c','LineWidth',2)
axis equal
ylim([0,50])
grid on
xlabel('Distance (m)')
ylabel('Height (m)')
title('{\bf Baseball Trajectories}')
```

```
legend('With Drag','Without Drag')
```



See Also `refline` | `lsline` | `gline` | `polyfit`

Purpose

Add reference line to plot

Syntax

```
refline(m,b)
refline(coeffs)
refline
hline = refline(...)
```

Description

`refline(m,b)` adds a reference line with slope `m` and intercept `b` to the current axes.

`refline(coeffs)`, where `coeffs` is a two-element coefficient vector, adds the line

```
y = coeffs(1)*x + coeffs(2)
```

to the figure.

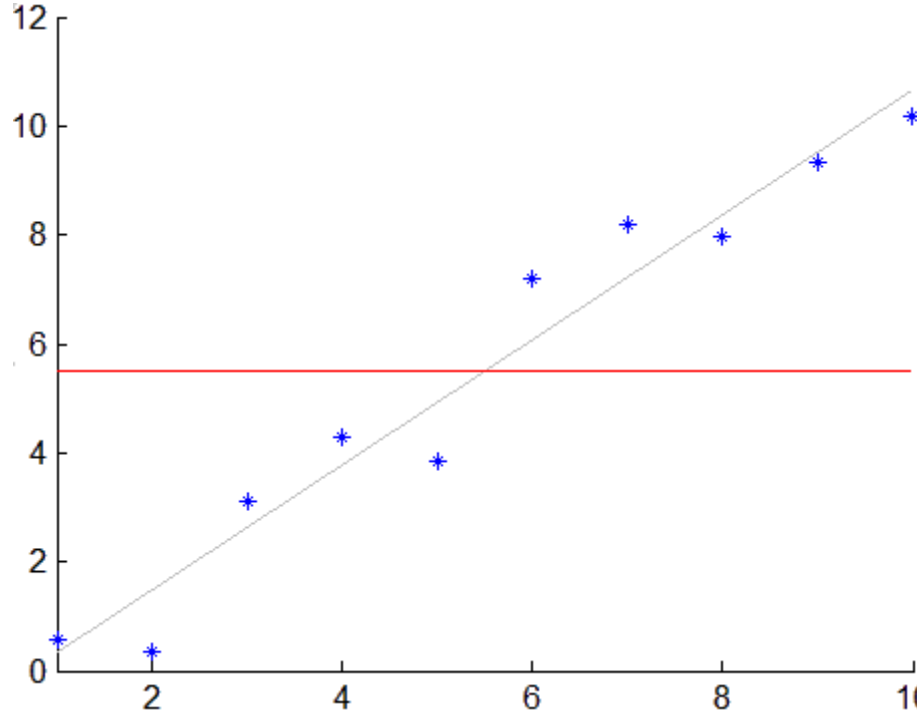
`refline` with no input arguments is equivalent to `lsline`.

`hline = refline(...)` returns the handle `hline` to the line.

Examples

Add a reference line at the mean of a data scatter and its least-squares line:

```
x = 1:10;

y = x + randn(1,10);
scatter(x,y,25,'b','*')

lsline

mu = mean(y);
hline = refline([0 mu]);
set(hline,'Color','r')
```



See Also

`refcurve` | `lsline` | `gline`

Purpose

Multiple linear regression

Syntax

```
b = regress(y,X)
[b,bint] = regress(y,X)
[b,bint,r] = regress(y,X)
[b,bint,r,rint] = regress(y,X)
[b,bint,r,rint,stats] = regress(y,X)
[...] = regress(y,X,alpha)
```

Description

`b = regress(y,X)` returns a p-by-1 vector `b` of coefficient estimates for a multilinear regression of the responses in `y` on the predictors in `X`. `X` is an n-by-p matrix of p predictors at each of n observations. `y` is an n-by-1 vector of observed responses.

`regress` treats `NaN`s in `X` or `y` as missing values, and ignores them.

If the columns of `X` are linearly dependent, `regress` obtains a basic solution by setting the maximum number of elements of `b` to zero.

`[b,bint] = regress(y,X)` returns a p-by-2 matrix `bint` of 95% confidence intervals for the coefficient estimates. The first column of `bint` contains lower confidence bounds for each of the p coefficient estimates; the second column contains upper confidence bounds.

If the columns of `X` are linearly dependent, `regress` returns zeros in elements of `bint` corresponding to the zero elements of `b`.

`[b,bint,r] = regress(y,X)` returns an n-by-1 vector `r` of residuals.

`[b,bint,r,rint] = regress(y,X)` returns an n-by-2 matrix `rint` of intervals that can be used to diagnose outliers. If the interval `rint(i,:)` for observation `i` does not contain zero, the corresponding residual is larger than expected in 95% of new observations, suggesting an outlier.

In a linear model, observed values of `y` are random variables, and so are their residuals. Residuals have normal distributions with zero mean but with different variances at different values of the predictors. To put residuals on a comparable scale, they are "Studentized," that is, they are divided by an estimate of their standard deviation that is independent of their value. Studentized residuals have t distributions with known

degrees of freedom. The intervals returned in `rint` are shifts of the 95% confidence intervals of these t distributions, centered at the residuals.

`[b,bint,r,rint,stats] = regress(y,X)` returns a 1-by-4 vector `stats` that contains, in order, the R^2 statistic, the F statistic and its p value, and an estimate of the error variance.

Note When computing statistics, `X` should include a column of 1s so that the model contains a constant term. The F statistic and its p value are computed under this assumption, and they are not correct for models without a constant. The R^2 statistic can be negative for models without a constant, indicating that the model is not appropriate for the data.

`[...] = regress(y,X,alpha)` uses a `100*(1-alpha)`% confidence level to compute `bint` and `rint`.

Examples

Load data on cars; identify weight and horsepower as predictors, mileage as the response:

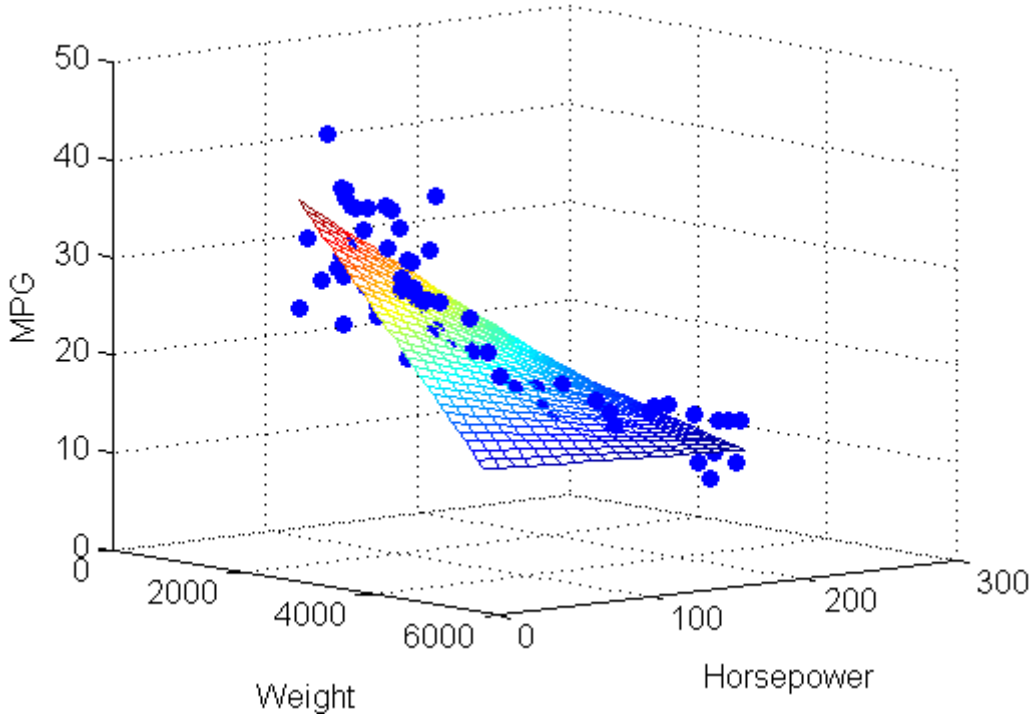
```
load carsmall
x1 = Weight;
x2 = Horsepower; % Contains NaN data
y = MPG;
```

Compute regression coefficients for a linear model with an interaction term:

```
X = [ones(size(x1)) x1 x2 x1.*x2];
b = regress(y,X) % Removes NaN data
b =
  60.7104
  -0.0102
  -0.1882
   0.0000
```

Plot the data and the model:

```
scatter3(x1,x2,y,'filled')
hold on
x1fit = min(x1):100:max(x1);
x2fit = min(x2):10:max(x2);
[X1FIT,X2FIT] = meshgrid(x1fit,x2fit);
YFIT = b(1) + b(2)*X1FIT + b(3)*X2FIT + b(4)*X1FIT.*X2FIT;
mesh(X1FIT,X2FIT,YFIT)
xlabel('Weight')
ylabel('Horsepower')
zlabel('MPG')
view(50,10)
```



References

[1] Chatterjee, S., and A. S. Hadi. "Influential Observations, High Leverage Points, and Outliers in Linear Regression." *Statistical Science*. Vol. 1, 1986, pp. 379–416.

See Also

`regstats` | `mvregress` | `robustfit` | `stepwisefit` | `rcoplot`

Superclasses

RegressionEnsemble

Purpose

Regression ensemble grown by resampling

Description

`RegressionBaggedEnsemble` combines a set of trained weak learner models and data on which these learners were trained. It can predict ensemble response for new data by aggregating predictions from its weak learners.

Construction

`ens = fitensemble(X,Y,'bag',nlearn,learners,'type','regression')` creates a bagged regression ensemble. For more information on the syntax, see the `fitensemble` function reference page.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CombineWeights`

A string describing how the ensemble combines learner predictions.

`FitInfo`

A numeric array of fit information. The `FitInfoDescription` property describes the content of this array.

`FitInfoDescription`

String describing the meaning of the `FitInfo` array.

`FResample`

A numeric scalar between `0` and `1`. `FResample` is the fraction of training data `fitensemble` resampled at random for every weak learner when constructing the ensemble.

`LearnerNames`

Cell array of strings with names of the weak learners in the ensemble. The name of each learner appears just once. For example, if you have an ensemble of 100 trees, `LearnerNames` is `{'Tree'}`.

`Method`

A string with the name of the algorithm `fitensemble` used for training the ensemble.

`ModelParams`

Parameters used in training `ens`.

`NObservations`

Numeric scalar containing the number of observations in the training data.

`NTrained`

Number of trained learners in the ensemble, a positive scalar.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`ReasonForTermination`

A string describing the reason `fitensemble` stopped adding weak learners to the ensemble.

`Regularization`

A structure containing the result of the `regularize` method. Use `Regularization` with `shrink` to lower resubstitution error and shrink the ensemble.

`Replace`

Boolean flag indicating if training data for weak learners in this ensemble were sampled with replacement. `Replace` is `true` for sampling with replacement, `false` otherwise.

`ResponseName`

A string with the name of the response variable `Y`.

`ResponseTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`.

Add or change a `ResponseTransform` function by dot addressing:

```
ens.ResponseTransform = @function
```

`Trained`

The trained learners, a cell array of compact regression models.

`TrainedWeights`

A numeric vector of weights the ensemble assigns to its learners. The ensemble computes predicted response by aggregating weighted predictions from its learners.

`UseObsForLearner`

A logical matrix of size `N`-by-`NTrained`, where `N` is the number of rows (observations) in the training data `X`, and `NTrained` is the number of trained weak learners. `UseObsForLearner(I,J)` is `true` if observation `I` was used for training learner `J`, and is `false` otherwise.

`W`

The scaled `weights`, a vector with length `n`, the number of rows in `X`. The sum of the elements of `W` is `1`.

`X`

The matrix of predictor values that trained the ensemble. Each column of `X` represents one variable, and each row represents one observation.

`Y`

The numeric column vector with the same number of rows as `X` that trained the ensemble. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

oobLoss	Out-of-bag regression error
oobPredict	Predict out-of-bag response of ensemble

Inherited Methods

compact	Create compact regression ensemble
crossval	Cross validate ensemble
cvshrink	Cross validate shrinking (pruning) ensemble
regularize	Find weights to minimize resubstitution error plus penalty term
resubLoss	Regression error by resubstitution
resubPredict	Predict response of ensemble by resubstitution
resume	Resume training ensemble
shrink	Prune ensemble
loss	Regression error
predict	Predict response of ensemble
predictorImportance	Estimates of predictor importance

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Create a bagged regression ensemble to predict the mileage of cars in the `carsmall` data set based on their engine displacement, horsepower, and weight:

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'bag',100,'Tree',...
    'type','regression')

ens =

classreg.learning.regr.RegressionBaggedEnsemble:
           PredictorNames: {'x1'  'x2'  'x3'}
    CategoricalPredictors: []
             ResponseName: 'Y'
        ResponseTransform: 'none'
            NObservations: 94
                 NTrained: 100
                   Method: 'Bag'
             LearnerNames: {'Tree'}
     ReasonForTermination: [1x77 char]
                  FitInfo: []
       FitInfoDescription: 'None'
           Regularization: []
                FResample: 1
                  Replace: 1
          UseObsForLearner: [94x100 logical]
```

Predict the mileage of a car whose characteristics are the average of those of the first 10 cars:

```
car10 = mean(X(1:10,:));
predict(ens,car10)

ans =
   14.6569
```

See Also

`RegressionEnsemble` | `fitensemble`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Superclasses

CompactRegressionEnsemble

Purpose

Ensemble regression

Description

`RegressionEnsemble` combines a set of trained weak learner models and data on which these learners were trained. It can predict ensemble response for new data by aggregating predictions from its weak learners.

Construction

`ens = fitensemble(X,Y,method,nlearn,learners)` returns an ensemble model that can predict responses to data. The ensemble consists of models listed in `learners`. For more information on the syntax, see the `fitensemble` function reference page.

`ens = fitensemble(X,Y,method,nlearn,learners,Name,Value)` returns an ensemble model with additional options specified by one or more `Name,Value` pair arguments. For more information on the syntax, see the `fitensemble` function reference page.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CombineWeights`

A string describing how the ensemble combines learner predictions.

`FitInfo`

A numeric array of fit information. The `FitInfoDescription` property describes the content of this array.

`FitInfoDescription`

String describing the meaning of the `FitInfo` array.

`LearnerNames`

Cell array of strings with names of the weak learners in the ensemble. The name of each learner appears just once. For example, if you have an ensemble of 100 trees, `LearnerNames` is `{'Tree'}`.

`Method`

A string with the name of the algorithm `fitensemble` used for training the ensemble.

`ModelParams`

Parameters used in training `ens`.

`NObservations`

Numeric scalar containing the number of observations in the training data.

`NTrained`

Number of trained learners in the ensemble, a positive scalar.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`ReasonForTermination`

A string describing the reason `fitensemble` stopped adding weak learners to the ensemble.

`Regularization`

A structure containing the result of the `regularize` method. Use `Regularization` with `shrink` to lower resubstitution error and shrink the ensemble.

`ResponseName`

A string with the name of the response variable `Y`.

`ResponseTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`.

Add or change a `ResponseTransform` function by dot addressing:

```
ens.ResponseTransform = @function
```

`Trained`

The trained learners, a cell array of compact regression models.

`TrainedWeights`

A numeric vector of weights the ensemble assigns to its learners. The ensemble computes predicted response by aggregating weighted predictions from its learners.

`W`

The scaled `weights`, a vector with length `n`, the number of rows in `X`. The sum of the elements of `W` is `1`.

`X`

The matrix of predictor values that trained the ensemble. Each column of `X` represents one variable, and each row represents one observation.

`Y`

The numeric column vector with the same number of rows as `X` that trained the ensemble. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

compact	Create compact regression ensemble
crossval	Cross validate ensemble
cvshrink	Cross validate shrinking (pruning) ensemble

regularize	Find weights to minimize resubstitution error plus penalty term
resubLoss	Regression error by resubstitution
resubPredict	Predict response of ensemble by resubstitution
resume	Resume training ensemble
shrink	Prune ensemble

Inherited Methods

loss	Regression error
predict	Predict response of ensemble
predictorImportance	Estimates of predictor importance

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Create a boosted regression ensemble to predict the mileage of cars in the `carsmall` data set based on their weights and numbers of cylinders:

```
load carsmall
learner = RegressionTree.template('MinParent',20);
ens = fitensemble([Weight, Cylinders],MPG,...
    'LSBoost',100,learner,'PredictorNames',{'W','C'},...
    'categoricalpredictors',2)

ens =
classreg.learning.regr.RegressionEnsemble:
           PredictorNames: {'W'  'C'}
    CategoricalPredictors: 2
             ResponseName: 'Response'
        ResponseTransform: 'none'
```

```
                NObservations: 94
                     NTrained: 100
                       Method: 'LSBoost'
                  LearnerNames: {'Tree'}
            ReasonForTermination: [1x77 char]
                      FitInfo: [100x1 double]
              FitInfoDescription: [2x83 char]
                  Regularization: []
```

Predict the mileage of 4,000-pound cars with 4, 6, and 8 cylinders:

```
mileage4K = predict(ens,[4000 4; 4000 6; 4000 8])

mileage4K =
   20.0294
   19.4206
   15.5000
```

See Also

`ClassificationEnsemble` | `fitensemble` | `CompactRegressionEnsemble`

How To

- Chapter 13, "Nonparametric Supervised Learning"

RegressionPartitionedEnsemble

Superclasses

RegressionPartitionedModel

Purpose

Cross-validated regression ensemble

Description

`RegressionPartitionedEnsemble` is a set of regression ensembles trained on cross-validated folds. Estimate the quality of classification by cross validation using one or more "kfold" methods: `kfoldfun`, `kfoldLoss`, or `kfoldPredict`. Every "kfold" method uses models trained on in-fold observations to predict response for out-of-fold observations. For example, suppose you cross validate using five folds. In this case, every training fold contains roughly 4/5 of the data and every test fold contains roughly 1/5 of the data. The first model stored in `Trained{1}` was trained on `X` and `Y` with the first 1/5 excluded, the second model stored in `Trained{2}` was trained on `X` and `Y` with the second 1/5 excluded, and so on. When you call `kfoldPredict`, it computes predictions for the first 1/5 of the data using the first model, for the second 1/5 of data using the second model and so on. In short, response for every observation is computed by `kfoldPredict` using the model trained without this observation.

Construction

`cvens = crossval(ens)` creates a cross-validated ensemble from `ens`, a regression ensemble. For syntax details, see the `crossval` method reference page.

`cvens = fitensemble(X,Y,method,nlearn,learners,name,value)` creates a cross-validated ensemble when `name` is one of `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. For syntax details, see the `fitensemble` function reference page.

Input Arguments

`ens`

A regression ensemble constructed with `fitensemble`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CrossValidatedModel`

Name of the cross-validated model, a string.

`Kfold`

Number of folds used in a cross-validated tree, a positive integer.

`ModelParams`

Object holding parameters of `tree`.

`NObservations`

Numeric scalar containing the number of observations in the training data.

`NTrainedPerFold`

Vector of `Kfold` elements. Each entry contains the number of trained learners in this cross-validation fold.

`Partition`

The partition of class `cvpartition` used in creating the cross-validated ensemble.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`ResponseName`

Name of the response variable `Y`, a string.

`ResponseTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`.

Add or change a `ResponseTransform` function by dot addressing:

```
ens.ResponseTransform = @function
```

`Trainable`

Cell array of ensembles trained on cross-validation folds. Every ensemble is full, meaning it contains its training data and weights.

`Trained`

Cell array of compact ensembles trained on cross-validation folds.

`W`

The scaled `weights`, a vector with length `n`, the number of rows in `X`.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

kfoldLoss	Cross-validation loss of partitioned regression ensemble
resume	Resume training ensemble

Inherited Methods

kfoldfun	Cross validate function
kfoldLoss	Cross-validation loss of partitioned regression model
kfoldPredict	Predict response for observations not used for training.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Construct a partitioned regression ensemble, and examine the cross-validation losses for the folds:

```
load carsmall
XX = [Cylinders Displacement Horsepower Weight];
YY = MPG;
rens = fitensemble(XX,YY,'LSBoost',100,'Tree');
cvrens = crossval(rens);
L = kfoldLoss(cvrens,'mode','individual')

L =
   42.4468
   12.3158
   65.9432
   39.0019
   30.5908
   16.6225
   17.3071
   46.1769
    8.0561
   12.9689
```

See Also

`ClassificationPartitionedEnsemble` | `RegressionPartitionedModel` | `RegressionEnsemble`

How To

- Chapter 13, “Nonparametric Supervised Learning”

RegressionPartitionedModel

Purpose

Cross-validated regression model

Description

`RegressionPartitionedModel` is a set of regression models trained on cross-validated folds. Estimate the quality of regression by cross validation using one or more "kfold" methods: `kfoldPredict`, `kfoldLoss`, and `kfoldfun`. Every "kfold" method uses models trained on in-fold observations to predict response for out-of-fold observations. For example, suppose you cross validate using five folds. In this case, every training fold contains roughly 4/5 of the data and every test fold contains roughly 1/5 of the data. The first model stored in `Trained{1}` was trained on `X` and `Y` with the first 1/5 excluded, the second model stored in `Trained{2}` was trained on `X` and `Y` with the second 1/5 excluded, and so on. When you call `kfoldPredict`, it computes predictions for the first 1/5 of the data using the first model, for the second 1/5 of data using the second model and so on. In short, response for every observation is computed by `kfoldPredict` using the model trained without this observation.

Construction

`cvmodel = crossval(tree)` creates a cross-validated classification model from a regression tree. For syntax details, see the `crossval` method reference page.

`cvmodel = RegressionTree.fit(X,Y,name,value)` creates a cross-validated model when `name` is one of `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. For syntax details, see the `RegressionTree.fit` function reference page.

Input Arguments

`tree`

A regression tree constructed with `RegressionTree.fit`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CrossValidatedModel`

Name of the cross-validated model, a string.

`Kfold`

Number of folds used in a cross-validated tree, a positive integer.

`ModelParams`

Object holding parameters of `tree`.

`Partition`

The partition of class `cvpartition` used in the cross-validated model.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`ResponseName`

Name of the response variable `Y`, a string.

`ResponseTransform`

Function handle for transforming the raw response values (mean squared error). The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function by dot addressing:

```
ctree.ResponseTransform = @function
```

`Trained`

The trained learners, a cell array of compact regression models.

`W`

The scaled `weights`, a vector with length `n`, the number of rows in `X`.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

kfoldfun	Cross validate function
kfoldLoss	Cross-validation loss of partitioned regression model
kfoldPredict	Predict response for observations not used for training.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Evaluate the cross-validation error of the `carsmall` data using `Horsepower` and `Weight` as predictor variables for mileage (`MPG`):

```
load carsmall
X = [Horsepower Weight];
tree = RegressionTree.fit(X,MPG);
cvtree = crossval(tree);
L = kfoldLoss(cvtree)

L =

   26.4414
```

See Also

`RegressionPartitionedEnsemble` | `ClassificationPartitionedModel`

How To

- Chapter 13, “Nonparametric Supervised Learning”

RegressionTree

Superclasses

CompactRegressionTree

Purpose

Regression tree

Description

A decision tree with binary splits for regression. An object of class `RegressionTree` can predict responses for new data with the `predict` method. The object contains the data used for training, so can compute resubstitution predictions.

Construction

`tree = RegressionTree.fit(X,Y)` returns a regression tree based on the input variables (also known as predictors, features, or attributes) `X` and output (response) `Y`. `tree` is a binary tree where each branching node is split based on the values of a column of `X`.

`tree = RegressionTree.fit(X,Y,Name,Value)` fits a tree with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`RegressionTree.fit` considers `NaN` values in `X` as missing values. `RegressionTree.fit` does not use observations with all missing values for `X` the fit. `RegressionTree.fit` uses observations with some missing values for `X` to find splits on variables for which these observations have valid values.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

`RegressionTree.fit` considers `NaN` values in `Y` to be missing values. `RegressionTree.fit` does not use observations with missing values for `Y` in the fit.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`CategoricalPredictors`

List of categorical predictors. Pass `CategoricalPredictors` as one of:

- A numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of `X` is a categorical variable.
- `'all'`, meaning all predictors are categorical.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in the `PredictorNames` property.
- A character matrix, where each row of the matrix is a name of a predictor variable. Pad the names with extra blanks so each row of the character matrix has the same length.

Default: `[]`

`crossval`

If `'on'`, grows a cross-validated decision tree with 10 folds. You can use `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'` parameters to override this cross-validation setting. You can only use one of these four parameters (`'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`) at a time when creating a cross-validated tree.

Alternatively, cross-validate `tree` later using the `crossval` method.

Default: `'off'`

`cvpartition`

A partition created with `cvpartition` to use in cross-validated tree. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'` and `'cvpartition'`.

`holdout`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'` and `'cvpartition'`.

`kfold`

Number of folds to use in a cross-validated tree, a positive integer. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: `10`

`leaveout`

Use leave-one-out cross validation by setting to `'on'`. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`MergeLeaves`

When `'on'`, `RegressionTree` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, `RegressionTree` does not merge leaves.

Default: `'on'`

`MinLeaf`

Each leaf has at least `MinLeaf` observations per tree leaf. If you supply both `MinParent` and `MinLeaf`, `RegressionTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: `1`

`MinParent`

Each branch node in the tree has at least `MinParent` observations. If you supply both `MinParent` and `MinLeaf`, `RegressionTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: `10`

`NVarToSample`

Number of predictors to select at random for each split. Can be a positive integer or `'all'`, which means use all available predictors.

Default: `'all'`

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

Default: `{'x1','x2',...}`

`Prune`

When `'on'`, `RegressionTree` computes the full tree and the optimal sequence of pruned subtrees. When `'off'` `RegressionTree` computes the full tree without pruning.

Default: `'on'`

`PruneCriterion`

String with the pruning criterion, always `'error'`.

Default: `'error'`

`ResponseName`

Name of the response variable `Y`, a string.

Default: `'Y'`

`ResponseTransform`

Function handle for transforming the raw response values (mean squared error). The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function by dot addressing:

```
tree.ResponseTransform = @function
```

Default: `'none'`

`SplitCriterion`

Criterion for choosing a split, always the string `'MSE'`, meaning mean squared error.

Default: `'MSE'`

`Weights`

Vector of observation weights. The length of `weights` is the number of rows in `X`.

Default: `ones(size(X,1),1)`

Properties

`CategoricalPredictors`

List of categorical predictors, a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CatSplit`

An *n*-by-2 cell array, where `n` is the number of nodes in `tree`. Each row in `CatSplit` gives left and right values for a categorical split. For each branch node `j` based on a categorical predictor variable `z`, the left child is chosen if `z` is in `CatSplit(j,1)` and the right child is chosen if `z` is in `CatSplit(j,2)`. The splits are in the same order as nodes of the tree. Nodes for these splits can be found by running `cuttype` and selecting `'categorical'` cuts from top to bottom.

`Children`

An *n*-by-2 array containing the numbers of the child nodes for each node in `tree`, where *n* is the number of nodes. Leaf nodes have child node `0`.

`CutCategories`

An *n*-by-2 cell array of the categories used at branches in `tree`, where *n* is the number of nodes. For each branch node `i` based on a categorical predictor variable `x`, the left child is chosen if `x` is among the categories listed in `CutCategories{i,1}`, and the right child is chosen if `x` is among those listed in `CutCategories{i,2}`. Both columns of `CutCategories` are empty for branch nodes based on continuous predictors and for leaf nodes.

`CutVar` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutPoint`

An *n*-element vector of the values used as cut points in `tree`, where *n* is the number of nodes. For each branch node `i` based on a continuous predictor variable `x`, the left child is chosen if `x<CutPoint(i)` and the right child is chosen if `x>=CutPoint(i)`.

`CutPoint` is `NaN` for branch nodes based on categorical predictors and for leaf nodes.

`CutType`

An *n*-element cell array indicating the type of cut at each node in `tree`, where *n* is the number of nodes. For each node `i`, `CutType{i}` is:

- `'continuous'` — If the cut is defined in the form `x < v` for a variable `x` and cut point `v`.
- `'categorical'` — If the cut is defined by whether a variable `x` takes a value in a set of categories.
- `''` — If `i` is a leaf node.

`CutVar` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutVar`

An *n*-element cell array of the names of the variables used for branching in each node in `tree`, where *n* is the number of nodes. These variables are sometimes known as *cut variables*. For leaf nodes, `CutVar` contains an empty string.

`CutVar` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`IsBranch`

An *n*-element logical vector `ib` that is `true` for each branch node and `false` for each leaf node of `tree`.

`ModelParams`

Object holding parameters of `tree`.

`NObservations`

Number of observations in the training data, a numeric scalar. `NObservations` can be less than the number of rows of input data `X` when there are missing values in `X` or response `Y`.

`NodeErr`

An n-element vector `e` of the errors of the nodes in `tree`, where n is the number of nodes. `e(i)` is the misclassification probability for node `i`.

`NodeMean`

An n-element numeric array with mean values in each node of `tree`, where n is the number of nodes in the tree. Every element in `NodeMean` is the average of the true `Y` values over all observations in the node.

`NodeProb`

An n-element vector `p` of the probabilities of the nodes in `tree`, where n is the number of nodes. The probability of a node is computed as the proportion of observations from the original data that satisfy the conditions for the node. This proportion is adjusted for any prior probabilities assigned to each class.

`NodeSize`

An n-element vector `sizes` of the sizes of the nodes in `tree`, where n is the number of nodes. The size of a node is defined as the number of observations from the data used to create the tree that satisfy the conditions for the node.

`NumNodes`

The number of nodes `n` in `tree`.

`Parent`

An n-element vector `p` containing the number of the parent node for each node in `tree`, where n is the number of nodes. The parent of the root node is `0`.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`PruneList`

An *n*-element numeric vector with the pruning levels in each node of `tree`, where *n* is the number of nodes.

`ResponseName`

Name of the response variable `Y`, a string.

`ResponseTransform`

Function handle for transforming the raw response values (mean squared error). The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function by dot addressing:

```
tree.ResponseTransform = @function
```

`Risk`

An *n*-element vector `r` of the risk of the nodes in `tree`, where *n* is the number of nodes. The risk `r(i)` for node `i` is the node error `NodeErr(i)` multiplied by the node probability `NodeProb(i)`.

`SurrCutCategories`

An *n*-element cell array of the categories used for surrogate splits in `tree`, where *n* is the number of nodes in `tree`. For each node `k`, `SurrCutCategories{k}` is a cell array. The length of `SurrCutCategories{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutCategories{k}` is either an empty string for a continuous surrogate predictor, or is a two-element cell array with categories for a categorical surrogate predictor. The first element of this two-element cell array lists categories assigned to the left child by this surrogate split, and the second element of this two-element cell array lists categories assigned to the right child by this

surrogate split. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutCategories` contains an empty cell.

`SurrCutFlip`

An n-element cell array of the numeric cut assignments used for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutFlip{k}` is a numeric vector. The length of `SurrCutFlip{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutFlip{k}` is either zero for a categorical surrogate predictor, or a numeric cut assignment for a continuous surrogate predictor. The numeric cut assignment can be either –1 or +1. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z < C$ and the cut assignment for this surrogate split is +1, or if $Z \geq C$ and the cut assignment for this surrogate split is –1. Similarly, the right child is chosen if $Z \geq C$ and the cut assignment for this surrogate split is +1, or if $Z < C$ and the cut assignment for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutFlip` contains an empty array.

`SurrCutPoint`

An n-element cell array of the numeric values used for surrogate splits in `tree`, where n is the number of nodes in `tree`. For each node `k`, `SurrCutPoint{k}` is a numeric vector. The length of `SurrCutPoint{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrCutPoint{k}` is either `NaN` for a categorical surrogate predictor, or a numeric cut for a continuous surrogate predictor. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z < C$ and `SurrCutFlip` for this surrogate split is –1. Similarly, the right child is chosen if $Z \geq C$ and `SurrCutFlip` for this surrogate split is +1, or if $Z < C$ and `SurrCutFlip` for this

surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables returned by `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutPoint` contains an empty cell.

`SurrCutType`

An *n*-element cell array indicating types of surrogate splits at each node in `tree`, where *n* is the number of nodes in `tree`. For each node `k`, `SurrCutType{k}` is a cell array with the types of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The order of the surrogate split variables at each node is matched to the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutType` contains an empty cell. A surrogate split type can be either `'continuous'` if the cut is defined in the form `Z < V` for a variable `Z` and cut point `V` or `'categorical'` if the cut is defined by whether `Z` takes a value in a set of categories.

`SurrCutVar`

An *n*-element cell array of the names of the variables used for surrogate splits in each node in `tree`, where *n* is the number of nodes in `tree`. Every element of `SurrCutVar` is a cell array with the names of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrCutVar` contains an empty cell.

`SurrVarAssoc`

An *n*-element cell array of the predictive measures of association for surrogate splits in `tree`, where *n* is the number of nodes in `tree`. For each node `k`, `SurrVarAssoc{k}` is a numeric vector. The

length of `SurrVarAssoc{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrVarAssoc{k}` gives the predictive measure of association between the optimal split and this surrogate split. The order of the surrogate split variables at each node is the order of variables in `SurrCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrVarAssoc` contains an empty cell.

`W`

The scaled `weights`, a vector with length `n`, the number of rows in `X`.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

compact	Compact regression tree
crossval	Cross-validated decision tree
cvloss	Regression error by cross validation
fit	Binary decision tree for regression
prune	Produce sequence of subtrees by pruning
resubLoss	Regression error by resubstitution
resubPredict	Predict resubstitution response of tree
template	Create regression template

Inherited Methods

loss	Regression error
meanSurrVarAssoc	Mean predictive measure of association for surrogate splits in decision tree
predict	Predict response of regression tree
predictorImportance	Estimates of predictor importance
view	View tree

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

Examples

Load the data in `carsmall.mat`, and make a regression tree to predict the mileage of cars based on their weights and numbers of cylinders:

```
load carsmall
tree = RegressionTree.fit([Weight, Cylinders],MPG,...
                'categoricalpredictors',2,'MinParent',20,...
                'PredictorNames',{'W','C'})

tree =

RegressionTree:
           PredictorNames: {'W'  'C'}
    CategoricalPredictors: 2
             ResponseName: 'Response'
        ResponseTransform: 'none'
                        X: [94x2 double]
                        Y: [94x1 double]
                        W: [94x1 double]
              ModelParams: [1x1 classreg.learning.modelparams.TreeParams]
```

Predict the mileage of 4,000-pound cars with 4, 6, and 8 cylinders:

```
mileage4K = predict(tree,[4000 4; 4000 6; 4000 8])

mileage4K =
   19.2778
   19.2778
   14.3889
```

See Also

`ClassificationTree` | `RegressionEnsemble` | `RegressionTree.fit` | `CompactRegressionTree` | `predict`

Tutorials

- “Classification Trees and Regression Trees” on page 13-27

regstats

Purpose

Regression diagnostics

Syntax

```
regstats(y,X,model)
stats = regstats(...)
stats = regstats(y,X,model,whichstats)
```

Description

`regstats(y,X,model)` performs a multilinear regression of the responses in `y` on the predictors in `X`. `X` is an n-by-p matrix of p predictors at each of n observations. `y` is an n-by-1 vector of observed responses.

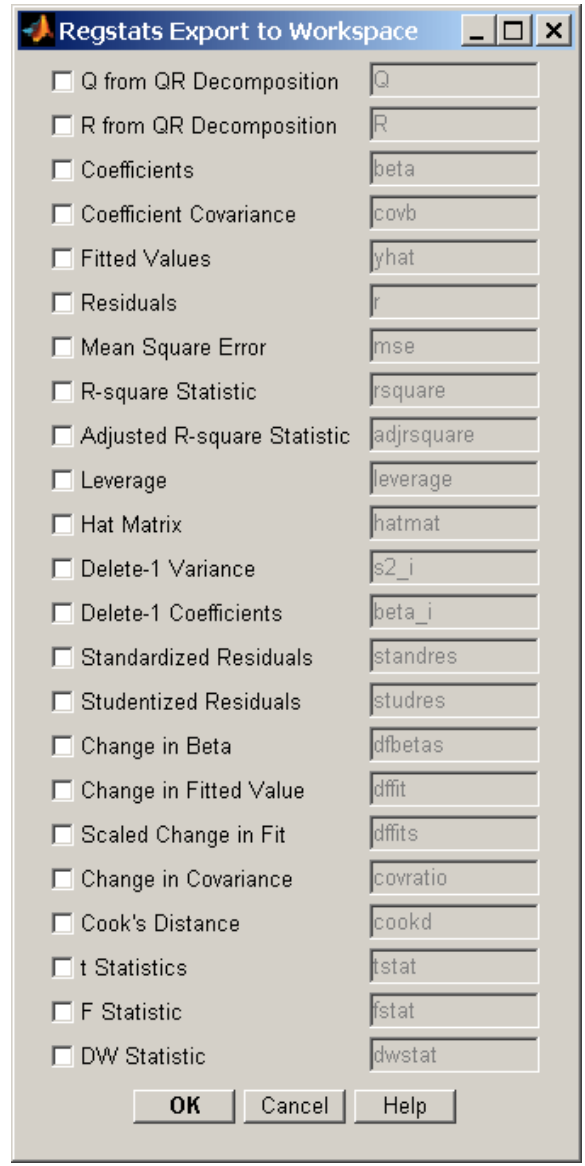
Note By default, `regstats` adds a first column of 1s to `X`, corresponding to a constant term in the model. Do not enter a column of 1s directly into `X`.

The optional input *`model`* controls the regression model. By default, `regstats` uses a linear additive model with a constant term. *`model`* can be any one of the following strings:

- `'linear'` — Constant and linear terms (the default)
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms
- `'purequadratic'` — Constant, linear, and squared terms

Alternatively, `model` can be a matrix of model terms accepted by the `x2fx` function. See `x2fx` for a description of this matrix and for a description of the order in which terms appear. You can use this matrix to specify other models including ones without a constant term.

With this syntax, the function displays a graphical user interface (GUI) with a list of diagnostic statistics, as shown in the following figure.


Regstats Export to Workspace
Q from QR Decomposition
Q
R from QR Decomposition
R
Coefficients
beta
Coefficient Covariance
covb
Fitted Values
yhat
Residuals
r
Mean Square Error
mse
R-square Statistic
rsquare
Adjusted R-square Statistic
adjrsquare
Leverage
leverage
Hat Matrix
hatmat
Delete-1 Variance
s2_i
Delete-1 Coefficients
beta_i
Standardized Residuals
standres
Studentized Residuals
studres
Change in Beta
dfbetas
Change in Fitted Value
dffit
Scaled Change in Fit
dffits
Change in Covariance
covratio
Cook's Distance
cookd
t Statistics
tstat
F Statistic
fstat
DW Statistic
dwstat
OK
Cancel
Help

When you select check boxes corresponding to the statistics you want to compute and click **OK**, `regstats` returns the selected statistics to the MATLAB workspace. The names of the workspace variables are displayed on the right-hand side of the interface. You can change the name of the workspace variable to any valid MATLAB variable name.

`stats = regstats(...)` creates the structure `stats`, whose fields contain all of the diagnostic statistics for the regression. This syntax does not open the GUI. The fields of `stats` are listed in the following table.

Field	Description
`Q`	Q from the QR decomposition of the design matrix
`R`	R from the QR decomposition of the design matrix
`beta`	Regression coefficients
`covb`	Covariance of regression coefficients
`yhat`	Fitted values of the response data
`r`	Residuals
`mse`	Mean squared error
`rsquare`	R^2 statistic
`adjrsquare`	Adjusted R^2 statistic
`leverage`	Leverage
`hatmat`	Hat matrix
`s2_i`	Delete-1 variance
`beta_i`	Delete-1 coefficients
`standres`	Standardized residuals
`studres`	Studentized residuals
`dfbetas`	Scaled change in regression coefficients
`dffit`	Change in fitted values

Field	Description
`dffits`	Scaled change in fitted values
`covratio`	Change in covariance
`cookd`	Cook's distance
`tstat`	t statistics and p-values for coefficients
`fstat`	F statistic and p-value
`dwstat`	Durbin-Watson statistic and p-value

Note that the fields names of `stats` correspond to the names of the variables returned to the MATLAB workspace when you use the GUI. For example, `stats.beta` corresponds to the variable `beta` that is returned when you select **Coefficients** in the GUI and click **OK**.

`stats = regstats(y,X,model,whichstats)` returns only the statistics that you specify in *`whichstats`*. *`whichstats`* can be a single string such as `'leverage'` or a cell array of strings such as `{'leverage' 'standres' 'studres'}`. Set *`whichstats`* to `'all'` to return all of the statistics.

Note The F statistic is computed under the assumption that the model contains a constant term. It is not correct for models without a constant. The R^2 statistic can be negative for models without a constant, which indicates that the model is not appropriate for the data.

Examples

Open the `regstats` GUI using data from `hald.mat`:

```
load hald
regstats(heat,ingredients,'linear');
```

Select **Fitted Values** and **Residuals** in the GUI:

Click **OK** to export the fitted values and residuals to the MATLAB workspace in variables named `yhat` and `r`, respectively.

You can create the same variables using the `stats` output, without opening the GUI:

```
whichstats = {'yhat','r'};
stats = regstats(heat,ingredients,'linear',whichstats);
yhat = stats.yhat;
r = stats.r;
```

References

[1] Belsley, D. A., E. Kuh, and R. E. Welsch. *Regression Diagnostics*. Hoboken, NJ: John Wiley & Sons, Inc., 1980.

[2] Chatterjee, S., and A. S. Hadi. "Influential Observations, High Leverage Points, and Outliers in Linear Regression." *Statistical Science*. Vol. 1, 1986, pp. 379–416.

[3] Cook, R. D., and S. Weisberg. *Residuals and Influence in Regression*. New York: Chapman & Hall/CRC Press, 1983.

[4] Goodall, C. R. "Computation Using the QR Decomposition." *Handbook in Statistics*. Vol. 9, Amsterdam: Elsevier/North-Holland, 1993.

See Also

`x2fx` | `regress` | `stepwise` | `leverage`

Purpose

Find weights to minimize resubstitution error plus penalty term

Syntax

```
ens1 = regularize(ens)
ens1 = regularize(ens,Name,Value)
```

Description

`ens1 = regularize(ens)` finds optimal weights for learners in `ens` by lasso regularization. `regularize` returns a regression ensemble identical to `ens`, but with a populated `Regularization` property.

`ens1 = regularize(ens,Name,Value)` computes optimal weights with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A regression ensemble, created by `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`lambda`

Vector of nonnegative regularization parameter values for lasso. For the default setting of `lambda`, `regularize` calculates the smallest value `lambda_max` for which all optimal weights for learners are `0`. The default value of `lambda` is a vector including `0` and nine exponentially-spaced numbers from `lambda_max/1000` to `lambda_max`.

Default: `[0 logspace(log10(lambda_max/1000),log10(lambda_max),9)]`

`npass`

Maximal number of passes for lasso optimization, a positive integer.

Default: `10`

`reltol`

Relative tolerance on the regularized loss for lasso, a numeric positive scalar.

Default: `1e-3`

`verbose`

Verbosity level, either `0` or `1`. When set to `1`, `regularize` displays more information as it runs.

Default: `0`

Output Arguments

`ens1`

A regression ensemble. Usually you set `ens1` to the same name as `ens`.

Definitions

Lasso

The lasso algorithm finds an optimal set of learner weights a_t that minimize

$$\sum_{n=1}^{N} w_n g\left(\left(\sum_{t=1}^{T}\alpha_t h_t\left(x_n\right)\right), y_n\right) + \lambda\sum_{t=1}^{T}|\alpha_t|.$$

Here

- $\lambda \geq 0$ is a parameter you provide, called the lasso parameter.
- h_t is a weak learner in the ensemble trained on N observations with predictors x_n, responses y_n, and weights w_n.

- $g(f,y) = (f - y)^2$ is the squared error.

Examples

Regularize an ensemble of bagged trees:

```
X = rand(2000,20);
Y = repmat(-1,2000,1);
Y(sum(X(:,1:5),2)>2.5) = 1;
bag = fitensemble(X,Y,'Bag',300,'Tree',...
    'type','regression');
bag = regularize(bag,'lambda',[0.001 0.1],'verbose',1);
```

`regularize` reports on its progress.

To see the resulting regularization structure:

```
bag.Regularization
ans =
            Method: 'Lasso'
    TrainedWeights: [300x2 double]
            Lambda: [1.0000e-003 0.1000]
 ResubstitutionMSE: [0.0616 0.0812]
    CombineWeights: @classreg.learning.combiner.WeightedSum
```

See how many learners in the regularized ensemble have positive weights (so would be included in a shrunken ensemble):

```
sum(bag.Regularization.TrainedWeights > 0)

ans =
   116    91
```

To shrink the ensemble using the weights from `Lambda = 0.1`:

```
cmp = shrink(bag,'weightcolumn',2)

cmp =

classreg.learning.regr.CompactRegressionEnsemble:
           PredictorNames: {1x20 cell}
```

```
    CategoricalPredictors: []
             ResponseName: 'Y'
        ResponseTransform: 'none'
                 NTrained: 91
```

There are 91 members in the regularized ensemble, which is less than 1/3 of the original 300.

See Also

shrink | cvshrink

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Value of `'Regularize'` parameter

Description

The value of the parameter `'Regularize'`.

Note This property applies only to gmdistribution objects constructed with `fit`.

relieff

Purpose

Importance of attributes (predictors) using ReliefF algorithm

Syntax

```
[RANKED,WEIGHT] = relieff(X,Y,K)
[RANKED,WEIGHT] = relieff(X,Y,K,'PARAM1',val1,'PARAM2',val2,
   ...)
```

Description

`[RANKED,WEIGHT] = relieff(X,Y,K)` computes ranks and weights of attributes (predictors) for input data matrix `X` and response vector `Y` using the ReliefF algorithm for classification or RReliefF for regression with `K` nearest neighbors. For classification, `relieff` uses `K` nearest neighbors per class. `RANKED` are indices of columns in `X` ordered by attribute importance, meaning `RANKED(1)` is the index of the most important predictor. `WEIGHT` are attribute weights ranging from `-1` to `1` with large positive weights assigned to important attributes.

If `Y` is numeric, `relieff` by default performs RReliefF analysis for regression. If `Y` is categorical, logical, a character array, or a cell array of strings, `relieff` by default performs ReliefF analysis for classification.

Attribute ranks and weights computed by `relieff` usually depend on `K`. If you set `K` to 1, the estimates computed by `relieff` can be unreliable for noisy data. If you set `K` to a value comparable with the number of observations (rows) in `X`, `relieff` can fail to find important attributes. You can start with `K = 10` and investigate the stability and reliability of `relieff` ranks and weights for various values of `K`.

`[RANKED,WEIGHT] = relieff(X,Y,K,'PARAM1',val1,'PARAM2',val2,...)` specifies optional parameter name/value pairs.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`method`

Either `'regression'` (default if `Y` is numeric) or `'classification'` (default if `Y` is not numeric).

`prior`

Prior probabilities for each class, specified as a string (`'empirical'` or `'uniform'`) or as a vector (one value for each distinct group name) or as a structure `S` with two fields:

- `S.group` containing the group names as a categorical variable, character array, or cell array of strings
- `S.prob` containing a vector of corresponding probabilities

If the input value is `'empirical'` (default), class probabilities are determined from class frequencies in `Y`. If the input value is `'uniform'`, all class probabilities are set equal.

`updates`

Number of observations to select at random for computing the weight of every attribute. By default all observations are used.

`categoricalx`

`'on'` or `'off'`, `'off'` by default. If `'on'`, treat all predictors in `X` as categorical. If `'off'`, treat all predictors in `X` as numerical. You cannot mix numerical and categorical predictors.

`sigma`

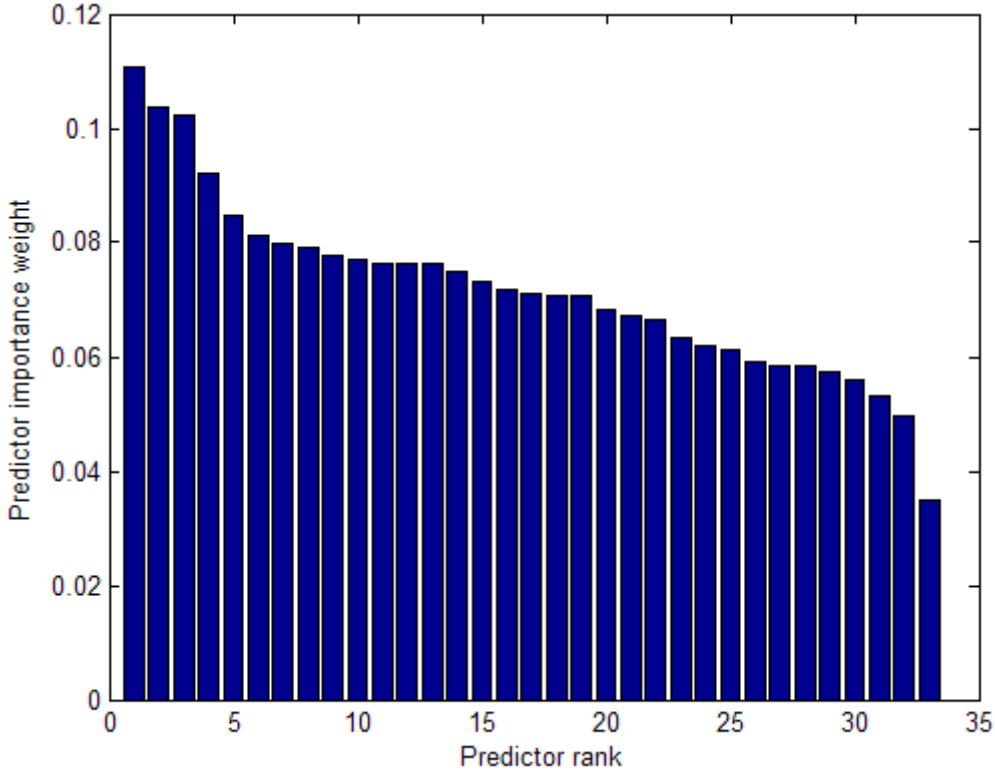
Distance scaling factor. For observation *i*, influence on the attribute weight from its nearest neighbor *j* is multiplied by exp((-`rank`(*i*,*j*)/`sigma`)^2), where `rank`(*i*,*j*) is the position of *j* in the list of nearest neighbors of *i* sorted by distance in the ascending order. Default is `Inf` (all nearest neighbors have the same influence) for classification and 50 for regression.

Examples

Identify important predictors in the ionosphere dataset:

```
load ionosphere;
```

```
[ranked,weights] = relieff(X,Y,10);
bar(weights(ranked));
xlabel('Predictor rank');
ylabel('Predictor importance weight');
```



Examine the Fisher iris data to find the important predictors:

```
load fisheriris
[ranked,weight] = relieff(meas,species,10)

ranked =
```

```
      4     3     1     2

  weight =
      0.1399    0.1226    0.3590    0.3754
```

The fourth predictor is the most important, and the second predictor is the least important.

References

[1] Kononenko, I., Simec, E., & Robnik-Sikonja, M. (1997). *Overcoming the myopia of inductive learning algorithms with RELIEFF*. Retrieved from CiteSeerX: http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.56.4740

[2] Robnik-Sikonja, M., & Kononenko, I. (1997). *An adaptation of Relief for attribute estimation in regression*. Retrieved from CiteSeerX: http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.34.8381

[3] Robnik-Sikonja, M., & Kononenko, I. (2003). *Theoretical and empirical analysis of ReliefF and RReliefF*. Machine Learning , 53, 23–69.

See Also

`knnsearch` | `pdist2`

categorical.reorderlevels

Purpose

Reorder levels

Syntax

```
B = reorderlevels(A,newlevels)
```

Description

`B = reorderlevels(A,newlevels)` reorders the levels of the categorical array `A`. `newlevels` is a cell array of strings or a 2-D character matrix that specifies the new order. `newlevels` must be a reordering of `getlabels(A)`.

The order of the levels of an ordinal array has significance for relational operators, minimum and maximum, and for sorting.

Examples

Reorder hockey standings:

```
standings = ordinal(1:3,{'Leafs','Canadiens','Bruins'});
getlabels(standings)
ans =
    'Leafs'  'Canadiens'  'Bruins'

standings = reorderlevels(standings,...
            {'Canadiens','Leafs','Bruins'});
getlabels(standings)
ans =
    'Canadiens'  'Leafs'  'Bruins'
```

See Also

`addlevels` | `droplevels` | `getlabels` | `islevel` | `mergelevels`

Purpose

Repartition data for cross-validation

Syntax

```
cnew = repartition(c)
```

Description

`cnew = repartition(c)` constructs an object `cnew` of the `cvpartition` class defining a random partition of the same type as `c`, where `c` is also an object of the `cvpartition` class.

Repartitioning is useful for Monte-Carlo repetitions of cross-validation analyses. `repartition` is called by `crossval` when the `'mcreps'` parameter is specified.

Examples

Partition and repartition 100 observations for 3-fold cross-validation:

```
c = cvpartition(100,'kfold',3)
c =
K-fold cross validation partition
             N: 100
   NumTestSets: 3
     TrainSize: 67  66  67
      TestSize: 33  34  33

cnew = repartition(c)
cnew =
K-fold cross validation partition
             N: 100
   NumTestSets: 3
     TrainSize: 67  66  67
      TestSize: 33  34  33
```

Check for equality of the test data in the first fold:

```
isequal(test(c,1),test(cnew,1))
ans =
     0
```

See Also

`cvpartition`

dataset.replacedata

Purpose

Replace dataset variables

Syntax

```
B = replacedata(A,X)
B = replacedata(A,X,vars)
B = replacedata(A,fun)
B = replacedata(A,fun,vars)
```

Description

`B = replacedata(A,X)` creates a dataset array `B` with the same variables as the dataset array `A`, but with the data for those variables replaced by the data in the array `X`. `replacedata` creates each variable in `B` using one or more columns from `X`, in order. `X` must have as many columns as the total number of columns in all of the variables in `A`, and as many rows as `A` has observations.

`B = replacedata(A,X,vars)` creates a dataset array `B` with the same variables as the dataset array `A`, but with the data for the variables specified in `vars` replaced by the data in the array `X`. The remaining variables in `B` are copies of the corresponding variables in `A`. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. Each variable in `B` has as many columns as the corresponding variable in `A`. `X` must have as many columns as the total number of columns in all the variables specified in `vars`.

`B = replacedata(A,fun)` or `B = replacedata(A,fun,vars)` creates a dataset array `B` by applying the function `fun` to the values in `A`'s variables. `replacedata` first horizontally concatenates `A`'s variables into a single array, then applies the function `fun`. The specified variables in `A` must have types and sizes compatible with the concatenation. `fun` is a function handle that accepts a single input array and returns an array with the same number of rows and columns as the input.

Examples

```
data = dataset({rand(3,3),'Var1','Var2','Var3'})

% Use ZSCORE to normalize each variable in a dataset array
% separately, by explicitly extracting and transforming the
% data, and then replacing it.
```

```
X = double(data);
X = zscore(X);
data = replacedata(data,X)

% Equivalently, provide a handle to ZSCORE.
data = replacedata(data,@zscore)

% Use ZSCORE to normalize each observation in a dataset
% array separately by creating an anonymous function.
data = replacedata(data,@(x) zscore(x,[],2))
```

See Also

dataset

categorical.repmat

Purpose

Replicate and tile categorical array

Syntax

```
B = repmat(A,m,n)
B = repmat(A,[m n p ...])
```

Description

`B = repmat(A,m,n)` creates a large array `B` consisting of an `m`-by-`n` tiling of copies of the categorical array `A`. The size of `B` is `[size(A,1)*M size(A,2)*N, size(A,3), ...]`. `repmat(A,n)` creates an `n`-by-`n` tiling.

`B = repmat(A,[m n p ...])` tiles the categorical array `A` to produce a multidimensional array `B` composed of copies of `A`. The size of `B` is `[size(A,1)*M, size(A,2)*N, size(A,3)*P, ...]`.

See Also

`ndims` | `size`

Purpose

Reset state

Syntax

```
reset(q)
```

Description

`reset(q)` resets the state of the quasi-random number stream `q` of the `qrandstream` class back to its initial state, `1`. Subsequent points drawn from the stream will be the same as those drawn from a new stream. The command is equivalent to `q.State = 1`.

Examples

Use `qrandstream` to construct a 3-D Halton stream, based on a point set that skips the first 1000 values and then retains every 101st point:

```
q = qrandstream('halton',3,'Skip',1e3,'Leap',1e2)
q =
   Halton quasi-random stream in 3 dimensions
   Point set properties:
              Skip : 1000
              Leap : 100
     ScrambleMethod : none

nextIdx = q.State
nextIdx =
     1
```

Use `qrand` to generate two samples of size four:

```
X1 = qrand(q,4)
X1 =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
nextIdx = q.State
nextIdx =
     5

X2 = qrand(q,4)
```

```
X2 =
    0.2446    0.0238    0.8102
    0.5298    0.7540    0.0438
    0.3843    0.5112    0.2758
    0.8335    0.2245    0.4694
nextIdx = q.State
nextIdx =
     9
```

Use `reset` to reset the stream, then generate another sample:

```
reset(q)
nextIdx = q.State
nextIdx =
     1

X = qrand(q,4)
X =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
```

See Also

`qrandstream` | `qrand`

Purpose

Resize categorical array

Syntax

```
B = reshape(A,M,N)
B = reshape(A,m,n,p,...)
reshape(A,[m n p ...])
B = reshape(A,...,[],...)
```

Description

`B = reshape(A,M,N)` returns an `m`-by-`n` categorical matrix whose elements are taken columnwise from the categorical array `A`. An error results if `A` does not have `m*n` elements.

`B = reshape(A,m,n,p,...)` or `reshape(A,[m n p ...])` returns an array with the same elements as `A` but reshaped to have the size `m`-by-`n`-by-`p`-by-`...` . `m*n*p*...` must be the same as `numel(A)`.

`B = reshape(A,...,[],...)` calculates the length of the dimension represented by`[]`, such that the product of the dimensions equals `numel(A)`. `numel(A)` must be evenly divisible by the product of the known dimensions. You can use only one occurrence of `[]`.

In general, `reshape(A,siz)` returns an array with the same elements as `A` but reshaped to the size `siz`. `prod(siz)` must be the same as `numel(A)`.

See Also

`shiftdim` | `squeeze`

ClassificationDiscriminant.resubEdge

Purpose

Classification edge by resubstitution

Syntax

```
edge = resubEdge(obj)
```

Description

`edge = resubEdge(obj)` returns the classification edge obtained by `obj` on its training data.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `ClassificationDiscriminant.fit`.

Output Arguments

`edge`

Classification edge obtained by resubstituting the training data into the calculation of edge.

Definitions

Edge

The *edge* is the weighted mean value of the classification *margin*. The weights are the class probabilities in `obj.Prior`. If you supply weights in the `weights` name-value pair, those weights are normalized to sum to the prior probabilities in the respective classes, and are then used to compute the weighted average.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `obj.X`. A high value of margin indicates a more reliable prediction than a low value.

Score (discriminant analysis)

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see “Posterior Probability” on page 12-7.

Examples

Estimate the quality of a discriminant analysis classifier for the Fisher iris data by resubstitution:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species);
redge = resubEdge(obj)

redge =
    0.9454
```

See Also

`ClassificationDiscriminant` | `edge` | `resubMargin`

How To

- "Discriminant Analysis" on page 12-3

ClassificationEnsemble.resubEdge

Purpose

Classification edge by resubstitution

Syntax

```
edge = resubEdge(ens)
edge = resubEdge(ens,Name,Value)
```

Description

`edge = resubEdge(ens)` returns the classification edge obtained by `ens` on its training data.

`edge = resubEdge(ens,Name,Value)` calculates edge with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `NTrained`. `resubEdge` uses only these learners for calculating edge.

Default: `1:NTrained`

`mode`

String representing the meaning of the output `edge`:

- `'ensemble'` — `edge` is a scalar value, the loss for the entire ensemble.

- `'individual'` — `edge` is a vector with one element per trained learner.
- `'cumulative'` — `edge` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`edge`

Classification edge obtained by `ens` by resubstituting the training data into the calculation of edge. Classification edge is classification margin averaged over the entire data. `edge` can be a scalar or vector, depending on the setting of the `mode` name-value pair.

Definitions

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in `ens.Prior`.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `ens.X`.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Find the resubstitution edge for an ensemble that classifies the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
edge = resubEdge(ens)

edge =
    3.2486
```

See Also

`resubMargin` | `resubLoss` | `resubPredict` | `resubEdge`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Classification edge by resubstitution

Syntax

```
edge = resubEdge(tree)
```

Description

`edge = resubEdge(tree)` returns the classification edge obtained by `tree` on its training data.

Input Arguments

`tree`

A classification tree created by `ClassificationTree.fit`.

Output Arguments

`edge`

Classification edge obtained by resubstituting the training data into the calculation of edge.

Definitions

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in `tree.Prior`.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `X`.

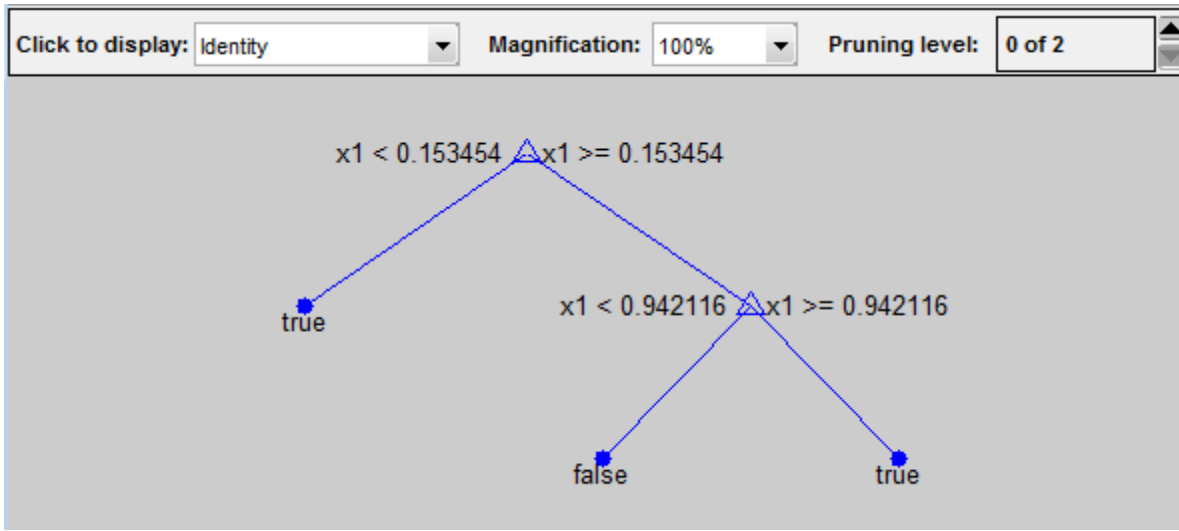
Score (tree)

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

Generate 100 random points and classify them:

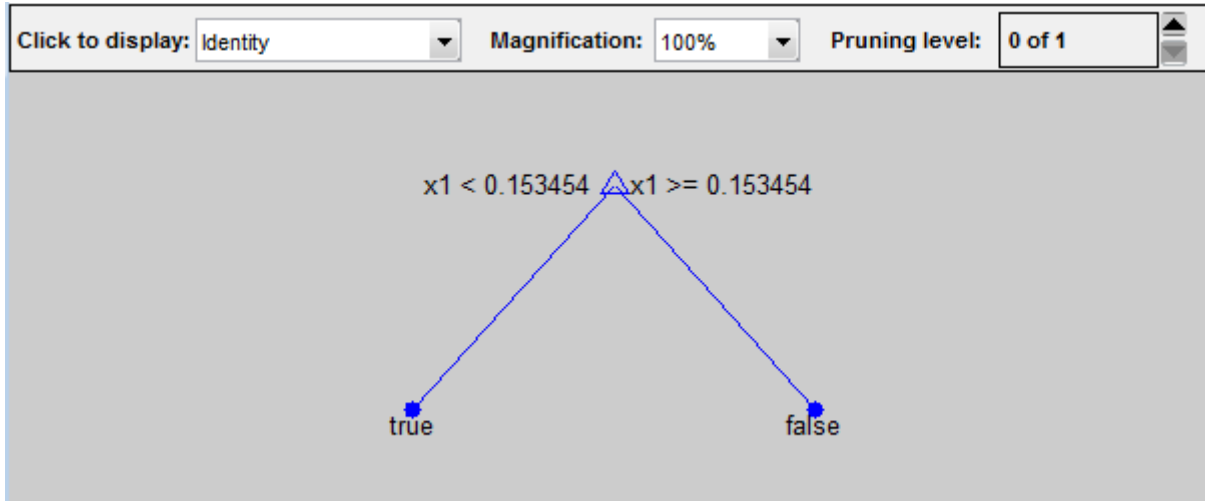
```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = ClassificationTree.fit(X,Y);
view(tree,'mode','graph')
```



2

Prune the tree:

```
tree1 = prune(tree,'level',1);
view(tree1,'mode','graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

3

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]

ans =
    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
```

```
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the rightmost column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Estimate the quality of a classification tree for the Fisher iris data by resubstitution:

```
load fisheriris
tree = ClassificationTree.fit(meas,species);
redge = resubEdge(tree)

redge =
    0.9384
```

See Also

`edge` | `resubMargin` | `resubLoss` | `resubPredict`

How To

- Chapter 13, "Nonparametric Supervised Learning"

Purpose

Classification error by resubstitution

Syntax

```
L = resubLoss(obj)
L = resubLoss(obj,Name,Value)
```

Description

`L = resubLoss(obj)` returns the resubstitution loss, meaning the loss computed for the data that `ClassificationDiscriminant.fit` used to create `obj`.

`L = resubLoss(obj,Name,Value)` returns loss statistics with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `ClassificationDiscriminant.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`lossfun`

Function handle or string representing a loss function. Built-in loss functions are:

- `'binodeviance'` — See "Loss Functions" on page 20-1640.
- `'exponential'` — See "Loss Functions" on page 20-1640.
- `'mincost'` — Smallest misclassification cost as given by the `obj.Cost` matrix.

You can write your own loss function using the syntax described in "Loss Functions" on page 20-1640.

Default: `'mincost'`

`weights`

Numeric vector of length `N`, where `N` is the number of rows of `obj.X`. `weights` are nonnegative. When you supply `weights`, `resubLoss` computes weighted classification error.

Default: `ones(N,1)`

Output Arguments

`L`

Classification error, a scalar. The meaning of the error depends on the values in `weights` and `lossfun`. See "Classification Error" on page 20-1640.

Definitions

Classification Error

The default classification error is the fraction of the training data `X` that `obj` misclassifies.

Weighted classification error is the sum of weight i times the Boolean value that is `1` when `obj` misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'mincost'` — Smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `obj.Cost` matrix.

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of `obj.X`.
- `K` is the number of classes in `obj`, represented in `obj.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `obj.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` gives a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Compute the resubstituted classification error for the Fisher iris data:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species);
L = resubLoss(obj)

L =
    0.0200
```

See Also

`ClassificationDiscriminant` | `loss`

How To

- “Discriminant Analysis” on page 12-3

Purpose

Classification error by resubstitution

Syntax

```
L = resubLoss(ens)
L = resubLoss(ens,Name,Value)
```

Description

`L = resubLoss(ens)` returns the resubstitution loss, meaning the loss computed for the data that `fitensemble` used to create `ens`.

`L = resubLoss(ens,Name,Value)` calculates loss with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `NTrained`. `resubLoss` uses only these learners for calculating loss.

Default: `1:NTrained`

`lossfun`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See “Loss Functions” on page 20-1644
- `'classiferror'` — Fraction of misclassified data

- `'exponential'` — See “Loss Functions” on page 20-1644

You can write your own loss function in the syntax described in “Loss Functions” on page 20-1644.

Default: `'classiferror'`

`mode`

String representing the meaning of the output `L`:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`L`

Loss, by default the fraction of misclassified data. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Definitions

Classification Error

The default classification error is the fraction of the training data `X` that `ens` misclassifies.

Weighted classification error is the sum of weight *i* times the Boolean value that is `1` when `tree` misclassifies the *i*th row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.
- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of `ens.X`.
- `K` is the number of classes in `ens`, represented in `ens.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `tree.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `score` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` gives a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Compute the resubstitution loss for a classification ensemble for the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
loss = resubLoss(ens)

loss =
    0.0333
```

See Also

`resubEdge` | `resubMargin` | `resubPredict` | `resubLoss`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Classification error by resubstitution

Syntax

```
L = resubLoss(tree)
L = resubLoss(tree,Name,Value)
L = resubLoss(tree,'subtrees',subtreevector)
[L,se] = resubLoss(tree,'subtrees',subtreevector)
[L,se,NLeaf] = resubLoss(tree,'subtrees',subtreevector)
[L,se,NLeaf,bestlevel] = resubLoss(tree,'subtrees',
   subtreevector)
[L,...] =
resubLoss(tree,'subtrees',subtreevector,Name,Value)
```

Description

`L = resubLoss(tree)` returns the resubstitution loss, meaning the loss computed for the data that `ClassificationTree.fit` used to create `tree`.

`L = resubLoss(tree,Name,Value)` returns the loss with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`L = resubLoss(tree,'subtrees',subtreevector)` returns a vector of classification errors for the trees in the pruning sequence `subtreevector`.

`[L,se] = resubLoss(tree,'subtrees',subtreevector)` returns the vector of standard errors of the classification errors.

`[L,se,NLeaf] = resubLoss(tree,'subtrees',subtreevector)` returns the vector of numbers of leaf nodes in the trees of the pruning sequence.

`[L,se,NLeaf,bestlevel] = resubLoss(tree,'subtrees',subtreevector)` returns the best pruning level as defined in the `treesize` name-value pair. By default, `bestlevel` is the pruning level that gives loss within one standard deviation of minimal loss.

`[L,...] = resubLoss(tree,'subtrees',subtreevector,Name,Value)` returns

loss statistics with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`tree`

A classification tree constructed by `ClassificationTree.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`lossfun`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 20-1650
- `'classiferror'` — Fraction of misclassified data
- `'exponential'` — See "Loss Functions" on page 20-1650

You can write your own loss function in the syntax described in "Loss Functions" on page 20-1650.

Default: `'classiferror'`

`weights`

A numeric vector of length `N`, where `N` is the number of rows of `tree.X`. `weights` are nonnegative. When you supply `weights`, `loss` computes weighted classification error.

Default: `ones(N,1)`

`Name,Value` arguments associated with pruning subtrees:

`subtrees`

A vector with integer values from `0` (full unpruned tree) to the maximal pruning level `max(tree.PruneList)`.

Default: `0`

`treesize`

One of the following strings:

- `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L+se`, where `L` and `se` relate to the smallest value in `subtrees`).
- `'min'` — `loss` returns the element of `subtrees` with smallest loss, usually the smallest element of `subtrees`.

Output Arguments

`L`

Classification error, a vector the length of `subtrees`. The meaning of the error depends on the values in `weights` and `lossfun`; see "Classification Error" on page 20-1650.

`se`

Standard error of loss, a vector the length of `subtrees`.

`NLeaf`

Number of leaves (terminal nodes) in the pruned subtrees, a vector the length of `subtrees`.

`bestlevel`

A scalar whose value depends on `treesize`:

- `treesize` = `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L+se`, where `L` and `se` relate to the smallest value in `subtrees`).

- `treesize` = `'min'` — `loss` returns the element of `subtrees` with smallest loss, usually the smallest element of `subtrees`.

Definitions

Classification Error

The default classification error is the fraction of the training data `X` that `tree` misclassifies.

Weighted classification error is the sum of weight i times the Boolean value that is `1` when `tree` misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.
- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of `tree.X`.
- `K` is the number of classes in `tree`, represented in `tree.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `tree.ClassNames`.

- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` gives a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Compute the resubstituted classification error for the `ionosphere` data:

```
load ionosphere
tree = ClassificationTree.fit(X,Y);
L = resubLoss(tree)

L =
    0.0114
```

See Also

`loss` | `resubEdge` | `resubMargin` | `resubPredict`

How To

- Chapter 13, “Nonparametric Supervised Learning”

RegressionEnsemble.resubLoss

Purpose

Regression error by resubstitution

Syntax

```
L = resubLoss(ens)
L = resubLoss(ens,Name,Value)
```

Description

`L = resubLoss(ens)` returns the resubstitution loss, meaning the mean squared error computed for the data that `fitensemble` used to create `ens`.

`L = resubLoss(ens,Name,Value)` calculates loss with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `NTrained`. `resubLoss` uses only these learners for calculating loss.

Default: `1:NTrained`

`lossfun`

Function handle for loss function, or the string `'mse'`, meaning mean squared error. If you pass a function handle `fun`, `resubLoss` calls it as

```
FUN(Y,Yfit,W)
```

where `Y`, `Yfit`, and `W` are numeric vectors of the same length. `Y` is the observed response, `Yfit` is the predicted response, and `W` is the observation weights.

Default: `'mse'`

`mode`

String representing the meaning of the output `L`:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`L`

Loss, by default the mean squared error. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Examples

Find the resubstitution predictions of mileage from the `carsmall` data based on horsepower and weight, and look at their mean square difference from the training data.

```
load carsmall
X = [Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',100,'Tree');
MSE = resubLoss(ens)

MSE =
    6.4336
```

See Also

`resubPredict` | `resubLoss` | `loss`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Regression error by resubstitution

Syntax

```
L = resubLoss(tree)
L = resubLoss(tree,Name,Value)
L = resubLoss(tree,'subtrees',subtreevector)
[L,se] = resubLoss(tree,'subtrees',subtreevector)
[L,se,NLeaf] = resubLoss(tree,'subtrees',subtreevector)
[L,se,NLeaf,bestlevel] = resubLoss(tree,'subtrees',
   subtreevector)
[L,...] =
resubLoss(tree,'subtrees',subtreevector,Name,Value)
```

Description

`L = resubLoss(tree)` returns the resubstitution loss, meaning the loss computed for the data that `RegressionTree.fit` used to create `tree`.

`L = resubLoss(tree,Name,Value)` returns the loss with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`L = resubLoss(tree,'subtrees',subtreevector)` returns a vector of mean squared errors for the trees in the pruning sequence `subtreevector`.

`[L,se] = resubLoss(tree,'subtrees',subtreevector)` returns the vector of standard errors of the classification errors.

`[L,se,NLeaf] = resubLoss(tree,'subtrees',subtreevector)` returns the vector of numbers of leaf nodes in the trees of the pruning sequence.

`[L,se,NLeaf,bestlevel] = resubLoss(tree,'subtrees',subtreevector)` returns the best pruning level as defined in the `treesize` name-value pair. By default, `bestlevel` is the pruning level that gives loss within one standard deviation of minimal loss.

`[L,...] = resubLoss(tree,'subtrees',subtreevector,Name,Value)` returns loss statistics with additional options specified by one or more

`Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`tree`

A regression tree constructed by `RegressionTree.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`lossfun`

Function handle, or the string `'mse'` meaning mean squared error.

You can write your own loss function in the syntax described in "Loss Functions" on page 20-1657.

Default: `'mse'`

`weights`

A numeric vector of length `N`, where `N` is the number of rows of `tree.X`. `weights` are nonnegative. When you supply `weights`, `loss` computes weighted classification error.

Default: `ones(N,1)`

`Name,Value` arguments associated with pruning subtrees:

`subtrees`

A vector with integer values from `0` (full unpruned tree) to the maximal pruning level `max(tree.PruneList)`.

Default: `0`

`treesize`

One of the following strings:

- `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L + se`, where `L` and `se` relate to the smallest value in `subtrees`).
- `'min'` — `loss` returns the element of `subtrees` with smallest loss, usually the smallest element of `subtrees`.

Output Arguments

`L`

Mean squared error, a vector the length of `subtrees`. The meaning of the error depends on the values in `weights` and `lossfun`.

`se`

Standard error of loss, a vector the length of `subtrees`.

`NLeaf`

Number of leaves (terminal nodes) in the pruned subtrees, a vector the length of `subtrees`.

`bestlevel`

A scalar whose value depends on `treesize`:

- `treesize` = `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L + se`, where `L` and `se` relate to the smallest value in `subtrees`).
- `treesize` = `'min'` — `loss` returns the element of `subtrees` with smallest loss, usually the smallest element of `subtrees`.

Definitions

Loss Functions

The built-in loss function is `'mse'`, meaning mean squared error.

To write your own loss function, create a function file of the form

```
function loss = lossfun(Y,Yfit,W)
```

- `N` is the number of rows of `tree.X`.
- `Y` is an `N`-element vector representing the observed response.
- `Yfit` is an `N`-element vector representing the predicted responses.
- `W` is an `N`-element vector representing the observation weights.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Find the mean square error of a model of the `carsmall` data:

```
load carsmall
X = [Displacement Horsepower Weight];
tree = RegressionTree.fit(X,MPG);
resubLoss(tree)

ans =
    4.8952
```

See Also

`resubPredict` | `loss`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Classification margins by resubstitution

Syntax

```
M = resubMargin(obj)
```

Description

`M = resubMargin(obj)` returns resubstitution classification margins for `obj`.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `ClassificationDiscriminant.fit`.

Output Arguments

`M`

Numeric column-vector of length `size(obj.X,1)` containing the classification margins.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `obj.X`. A high value of margin indicates a more reliable prediction than a low value.

Score (discriminant analysis)

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see "Posterior Probability" on page 12-7.

Examples

Find the margins for a classification tree for the Fisher iris data by resubstitution. Examine several entries:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species);
M = resubMargin(obj);
M(1:25:end)
```

```
ans =
    1.0000
    1.0000
    0.9998
    0.9998
    1.0000
    0.9946
```

See Also

`ClassificationDiscriminant` | `margin`

How To

- “Discriminant Analysis” on page 12-3

Purpose

Classification margins by resubstitution

Syntax

```
margin = resubMargin(ens)
margin = resubMargin(ens,Name,Value)
```

Description

`margin = resubMargin(ens)` returns the classification margin obtained by `ens` on its training data.

`margin = resubMargin(ens,Name,Value)` calculates margins with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `NTrained`. `resubMargin` uses only these learners for calculating margin.

Default: `1:NTrained`

Output Arguments

`margin`

A numeric column-vector of length `size(ens.X,1)` containing the classification margins.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false

classes. Margin is a column vector with the same number of rows as in the matrix `ens.X`.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Find the resubstitution margins for an ensemble that classifies the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
margin = resubMargin(ens);
[min(margin) mean(margin) max(margin)]

ans =
   -0.5674    3.2486    4.6245
```

See Also

`resubEdge` | `resubLoss` | `resubPredict` | `resubMargin`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Classification margins by resubstitution

Syntax

```
M = resubMargin(tree)
```

Description

`M = resubMargin(tree)` returns resubstitution classification margins for `tree`.

Input Arguments

`tree`

A classification tree created by `ClassificationTree.fit`.

Output Arguments

`M`

A numeric column-vector of length `size(tree.X,1)` containing the classification margins.

Definitions

Margin

Classification *margin* is the difference between classification *score* for the true class and maximal classification score for the false classes. A high value of margin indicates a more reliable prediction than a low value.

Score (tree)

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

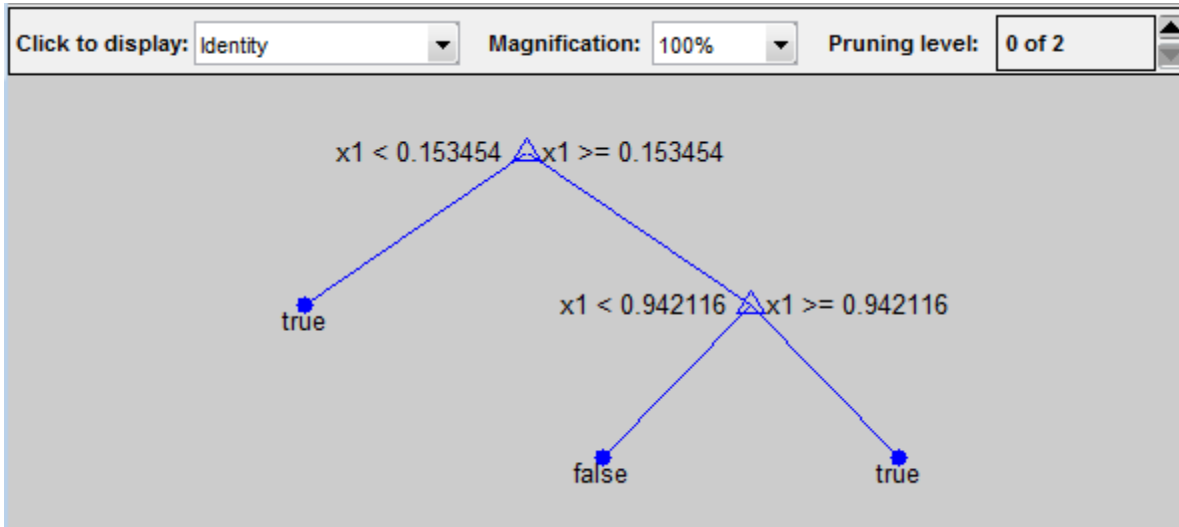
For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

1

Generate 100 random points and classify them:

```
rng(0,'twister') % for reproducibility
X = rand(100,1);
```

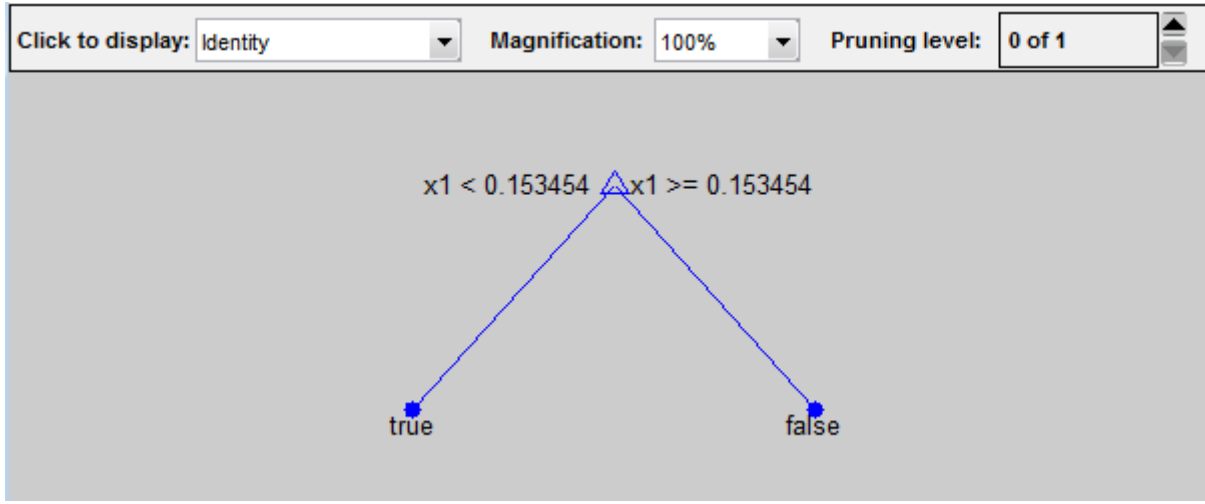
```
Y = (abs(X - .55) > .4);
tree = ClassificationTree.fit(X,Y);
view(tree,'mode','graph')
```



2

Prune the tree:

```
tree1 = prune(tree,'level',1);
view(tree1,'mode','graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

3

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]

ans =
    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
```

```
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the rightmost column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Find the margins for a classification tree for the Fisher iris data by resubstitution. Examine several entries:

```
load fisheriris
tree = ClassificationTree.fit(meas,species);
M = resubMargin(tree);
M(1:25:end)

ans =
    1.0000
    1.0000
    1.0000
    1.0000
    0.9565
    0.9565
```

See Also

`margin` | `resubLoss` | `resubPredict` | `resubEdge`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Predict resubstitution response of classifier

Syntax

```
label = resubPredict(obj)
[label,posterior] = resubPredict(obj)
[label,posterior,cost] = resubPredict(obj)
```

Description

`label = resubPredict(obj)` returns the labels `obj` predicts for the data `obj.X`. `label` is the predictions of `obj` on the data that `ClassificationDiscriminant.fit` used to create `obj`.

`[label,posterior] = resubPredict(obj)` returns the posterior class probabilities for the predictions.

`[label,posterior,cost] = resubPredict(obj)` returns the predicted misclassification costs per class for the resubstituted data.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `ClassificationDiscriminant.fit`.

Output Arguments

`label`

Response `obj` predicts for the training data. `label` is the same data type as the training response data `obj.Y`. The predicted class labels are those with minimal expected misclassification cost; see "How the predict Method Classifies" on page 12-6.

`posterior`

`N`-by-`K` matrix of posterior probabilities for classes `obj` predicts, where `N` is the number of observations and `K` is the number of classes.

`cost`

`N`-by-`K` matrix of predicted misclassification costs. Each cost is the average misclassification cost with respect to the posterior probability.

Definitions

Posterior Probability

`posterior(i,k)` is the posterior probability of class `k` for observation `i`. For the mathematical definition, see "Posterior Probability" on page 12-7.

Examples

Find the total number of misclassifications of the Fisher iris data for a discriminant analysis classifier:

```
load fisheriris
obj = ClassificationDiscriminant.fit(meas,species);
Ypredict = resubPredict(obj); % the predictions
Ysame = strcmp(Ypredict,species); % true when ==
sum(~Ysame) % how many are different?

ans =
     3
```

See Also

`ClassificationDiscriminant | predict`

How To

- "Discriminant Analysis" on page 12-3

Purpose

Predict ensemble response by resubstitution

Syntax

```
label = resubPredict(ens)
[label,score] = resubPredict(ens)
[label,score] = resubPredict(ens,Name,Value)
```

Description

`label = resubPredict(ens)` returns the labels `ens` predicts for the data `ens.X`. `label` is the predictions of `ens` on the data that `fitensemble` used to create `ens`.

`[label,score] = resubPredict(ens)` also returns scores for all classes.

`[label,score] = resubPredict(ens,Name,Value)` finds resubstitution predictions with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `NTrained`. `oobLoss` uses only these learners for calculating loss.

Default: `1:NTrained`

Output Arguments

`label`

The response `ens` predicts for the training data. `label` is the same data type as the training response data `ens.Y`, and has the same number of entries as the number of rows in `ens.X`.

`score`

An `N`-by-`K` matrix, where `N` is the number of rows in `ens.X`, and `K` is the number of classes in `ens`. High score value indicates that an observation likely comes from this class.

Definitions

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Find the total number of misclassifications of the Fisher iris data for a classification ensemble:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
Ypredict = resubPredict(ens); % the predictions
Ysame = strcmp(Ypredict,species); % true when ==
sum(~Ysame) % how many are different?

ans =
     5
```

See Also

`resubEdge` | `resubMargin` | `resubLoss` | `resubPredict`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Predict resubstitution response of tree

Syntax

```
label = resubPredict(tree)
[label,posterior] = resubPredict(tree)
[label,posterior,node] = resubPredict(tree)
[label,posterior,node,cnum] = resubPredict(tree)
[label,...] = resubPredict(tree,Name,Value)
```

Description

`label = resubPredict(tree)` returns the labels `tree` predicts for the data `tree.X`. `label` is the predictions of `tree` on the data that `ClassificationTree.fit` used to create `tree`.

`[label,posterior] = resubPredict(tree)` returns the posterior class probabilities for the predictions.

`[label,posterior,node] = resubPredict(tree)` returns the node numbers of `tree` for the resubstituted data.

`[label,posterior,node,cnum] = resubPredict(tree)` returns the predicted class numbers for the predictions.

`[label,...] = resubPredict(tree,Name,Value)` returns resubstitution predictions with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`tree`

A classification tree constructed by `ClassificationTree.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`subtrees`

A vector with integer values from `0` (full unpruned tree) to the maximal pruning level `max(tree.PruneList)`. `subtrees` must be in ascending order.

Default: `0`

Output Arguments

`label`

The response `tree` predicts for the training data. `label` is the same data type as the training response data `tree.Y`.

If the `subtrees` name-value argument contains `m>1` entries, `label` has `m` columns, each of which represents the predictions of the corresponding subtree. Otherwise, `label` is a vector.

`posterior`

Matrix or array of posterior probabilities for classes `tree` predicts.

If the `subtrees` name-value argument is a scalar or is missing, `posterior` is an `n`-by-`k` matrix, where `n` is the number of rows in the training data `tree.X`, and `k` is the number of classes.

If `subtrees` contains `m>1` entries, `posterior` is an `n`-by-`k`-by-`m` array, where the matrix for each `m` gives posterior probabilities for the corresponding subtree.

`node`

The node numbers of `tree` where each data row resolves.

If the `subtrees` name-value argument is a scalar or is missing, `node` is a numeric column vector with `n` rows, the same number of rows as `tree.X`.

If `subtrees` contains `m>1` entries, `node` is a `n`-by-`m` matrix. Each column represents the node predictions of the corresponding subtree.

`cnum`

The class numbers that `tree` predicts for the resubstituted data.

If the `subtrees` name-value argument is a scalar or is missing, `cnum` is a numeric column vector with `n` rows, the same number of rows as `tree.X`.

If `subtrees` contains `m>1` entries, `cnum` is a `n`-by-`m` matrix. Each column represents the class predictions of the corresponding subtree.

Definitions

Posterior Probability

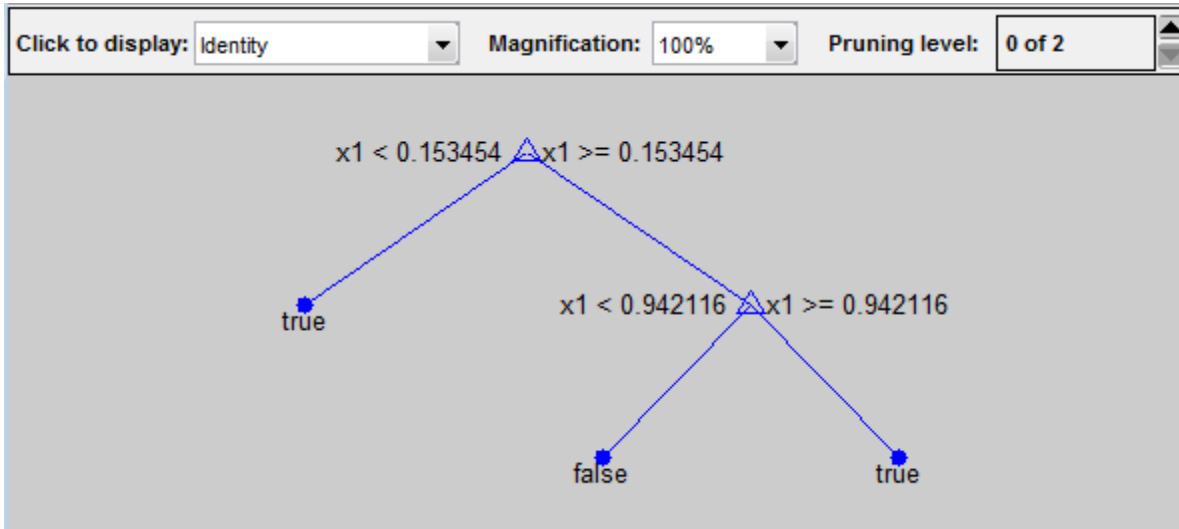
The posterior probability of the classification at a node is the number of training sequences that lead to that node with this classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X<0.15` or `X>0.95`, and `X` is false otherwise.

1

Generate 100 random points and classify them:

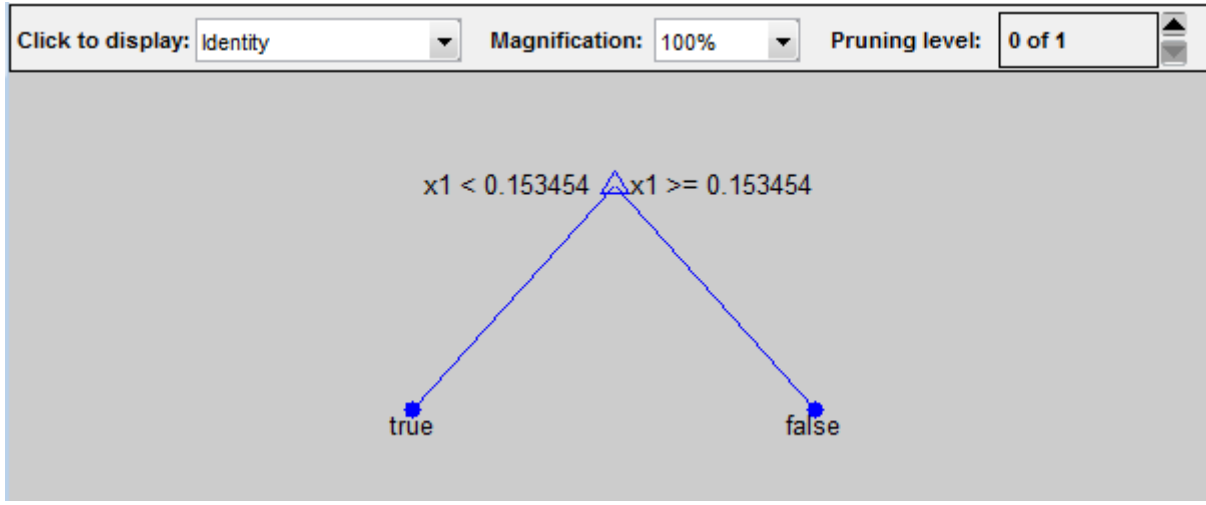
```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = ClassificationTree.fit(X,Y);
view(tree,'mode','graph')
```



2

Prune the tree:

```
tree1 = prune(tree,'level',1);
view(tree1,'mode','graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations between .15 and .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

3

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]

ans =
    0.9405    0.0595    0.6555
    0.9405    0.0595    0.1712
    0.9405    0.0595    0.7060
         0    1.0000    0.0318
    0.9405    0.0595    0.2769
         0    1.0000    0.0462
```

```
     0    1.0000    0.0971
0.9405    0.0595    0.8235
0.9405    0.0595    0.6948
0.9405    0.0595    0.3171
```

Indeed, every value of `X` (the rightmost column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.94` and `0.06`.

Examples

Find the total number of misclassifications of the Fisher iris data for a classification tree:

```
load fisheriris
tree = ClassificationTree.fit(meas,species);
Ypredict = resubPredict(tree); % the predictions
Ysame = strcmp(Ypredict,species); % true when ==
sum(~Ysame) % how many are different?

ans =
     3
```

See Also

`resubEdge` | `resubMargin` | `resubLoss` | `predict`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Predict response of ensemble by resubstitution

Syntax

```
Yfit = resubPredict(ens)
Yfit = resubPredict(ens,Name,Value)
```

Description

`Yfit = resubPredict(ens)` returns the response `ens` predicts for the data `ens.X`. `Yfit` is the predictions of `ens` on the data that `fitensemble` used to create `ens`.

`Yfit = resubPredict(ens,Name,Value)` predicts responses with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`learners`

Indices of weak learners in the ensemble ranging from `1` to `NTrained`. `oobLoss` uses only these learners for calculating loss.

Default: `1:NTrained`

Output Arguments

`Yfit`

A vector of predicted responses to the training data, with `ens.X` elements.

Examples

Find the resubstitution predictions of mileage from the `carsmall` data based on horsepower and weight, and look at their mean square difference from the training data.

```
load carsmall
X = [Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',100,'Tree');
Yfit = resubPredict(ens);
MSE = mean((Yfit - ens.Y).^2)

MSE =
    6.4336
```

This is the same as the result of `resubLoss`:

```
resubLoss(ens)

ans =
    6.4336
```

See Also

`resubLoss` | `resubPredict` | `predict`

How To

- Chapter 13, "Nonparametric Supervised Learning"

Purpose

Predict resubstitution response of tree

Syntax

```
Yfit = resubPredict(tree)
[Yfit,node] = resubPredict(tree)
[Yfit,node] = resubPredict(tree,Name,Value)
```

Description

`Yfit = resubPredict(tree)` returns the responses `tree` predicts for the data `tree.X`. `Yfit` is the predictions of `tree` on the data that `RegressionTree.fit` used to create `tree`.

`[Yfit,node] = resubPredict(tree)` returns the node numbers of `tree` for the resubstituted data.

`[Yfit,node] = resubPredict(tree,Name,Value)` predicts with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`tree`

A regression tree constructed by `RegressionTree.fit`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`subtrees`

A vector with integer values from `0` (full unpruned tree) to the maximal pruning level `max(tree.PruneList)`. `subtrees` must be in ascending order.

Default: `0`

Output Arguments

`Yfit`

The response `tree` predicts for the training data.

If the `subtrees` name-value argument is a scalar or is missing, `label` is the same data type as the training response data `tree.Y`.

If `subtrees` contains `m>1` entries, `label` has `m` columns, each of which represents the predictions of the corresponding subtree.

`node`

The `tree` node numbers where `tree` sends each data row.

If the `subtrees` name-value argument is a scalar or is missing, `node` is a numeric column vector with `n` rows, the same number of rows as `tree.X`.

If `subtrees` contains `m>1` entries, `node` is a `n`-by-`m` matrix. Each column represents the node predictions of the corresponding subtree.

Examples

Find the mean square error of a model of the `carsmall` data:

```
load carsmall
X = [Displacement Horsepower Weight];
tree = RegressionTree.fit(X,MPG);
Yfit = resubPredict(tree);
mean((Yfit - tree.Y).^2)

ans =
    4.8952
```

You can get the same answer using `resubLoss`:

```
resubLoss(tree)

ans =
    4.8952
```

See Also

`resubLoss | predict`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Resume training ensemble

Syntax

```
ens1 = resume(ens,nlearn)
ens1 = resume(ens,nlearn,Name,Value)
```

Description

`ens1 = resume(ens,nlearn)` trains `ens` for `nlearn` more cycles. `resume` uses the same training options `fitensemble` used to create `ens`.

`ens1 = resume(ens,nlearn,Name,Value)` trains `ens` with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A classification ensemble, created with `fitensemble`.

`nlearn`

A positive integer, the number of cycles for additional training of `ens`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`nprint`

Printout frequency, a positive integer scalar or `'off'` (no printouts). Returns to the command line the number of weak learners trained so far. Useful when you train ensembles with many learners on large data sets.

Default: `'off'`

Output Arguments

`ens1`

The classification ensemble `ens`, augmented with additional training.

Examples

Train a classification ensemble for 10 cycles. Examine the resubstitution error. Then train for 10 more cycles and examine the new resubstitution error.

```
load ionosphere
ens = fitensemble(X,Y,'GentleBoost',10,'Tree');
L = resubLoss(ens)

L =
    0.0484

ens1 = resume(ens,10);
L = resubLoss(ens1)

L =
    0.0256
```

The new ensemble has much less resubstitution error than the original.

See Also

`fitensemble`

How To

- Chapter 13, "Nonparametric Supervised Learning"

Purpose

Resume training learners on cross-validation folds

Syntax

```
ens1 = resume(ens,nlearn)
ens1 = resume(ens,nlearn,Name,Value)
```

Description

`ens1 = resume(ens,nlearn)` trains `ens` in every fold for `nlearn` more cycles. `resume` uses the same training options `fitensemble` used to create `ens`.

`ens1 = resume(ens,nlearn,Name,Value)` trains `ens` with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A cross-validated classification ensemble. `ens` is the result of either:

- The `fitensemble` function with a cross-validation name-value pair. The names are `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.
- The `crossval` method applied to a classification ensemble.

`nlearn`

A positive integer, the number of cycles for additional training of `ens`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`nprint`

Printout frequency, a positive integer scalar or `'off'` (no printouts). Returns to the command line the number of weak

learners trained so far. Useful when you train ensembles with many learners on large data sets.

Default: `'off'`

Output Arguments

`ens1`

The cross-validated classification ensemble `ens`, augmented with additional training.

Examples

Train a partitioned classification ensemble for 10 cycles. Examine the error. Then train for 10 more cycles and examine the new error.

```
load ionosphere
cvens = fitensemble(X,Y,'GentleBoost',10,'Tree',...
    'crossval','on');
L = kfoldLoss(cvens)

L =
    0.0883

cvens = resume(cvens,10);
L = kfoldLoss(cvens)

L =
    0.0769
```

The ensemble has less cross-validation error after training for ten more cycles.

See Also

`kfoldPredict` | `kfoldEdge` | `kfoldMargin` | `kfoldLoss`

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Purpose

Resume training ensemble

Syntax

```
ens1 = resume(ens,nlearn)
ens1 = resume(ens,nlearn,Name,Value)
```

Description

`ens1 = resume(ens,nlearn)` trains `ens` for `nlearn` more cycles. `resume` uses the same training options `fitensemble` used to create `ens`.

`ens1 = resume(ens,nlearn,Name,Value)` trains `ens` with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A regression ensemble, created with `fitensemble`.

`nlearn`

A positive integer, the number of cycles for additional training of `ens`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`nprint`

Printout frequency, a positive integer scalar or `'off'` (no printouts). Returns to the command line the number of weak learners trained so far. Useful when you train ensembles with many learners on large data sets.

Default: `'off'`

Output Arguments

`ens1`

The regression ensemble `ens`, augmented with additional training.

Examples

Train a regression ensemble for 50 cycles. Examine the resubstitution error. Then train for 50 more cycles and examine the new resubstitution error.

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',50,'Tree');
 L = resubLoss(ens)

L =
    6.2681

ens = resume(ens,50);
L = resubLoss(ens)

L =
    4.3904
```

The new ensemble has much less resubstitution error than the original.

See Also

`fitensemble`

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Purpose

Resume training ensemble

Syntax

```
ens1 = resume(ens,nlearn)
ens1 = resume(ens,nlearn,Name,Value)
```

Description

`ens1 = resume(ens,nlearn)` trains `ens` in every fold for `nlearn` more cycles. `resume` uses the same training options `fitensemble` used to create `ens`.

`ens1 = resume(ens,nlearn,Name,Value)` trains `ens` with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`ens`

A cross-validated regression ensemble. `ens` is the result of either:

- The `fitensemble` function with a cross-validation name-value pair. The names are `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.
- The `crossval` method applied to a regression ensemble.

`nlearn`

A positive integer, the number of cycles for additional training of `ens`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`nprint`

Printout frequency, a positive integer scalar or `'off'` (no printouts). Returns to the command line the number of weak learners trained so far. Useful when you train ensembles with many learners on large data sets.

Default: `'off'`

Output Arguments

`ens1`

The cross-validated regression ensemble `ens`, augmented with additional training.

Examples

Train a regression ensemble for 50 cycles, and cross validate it. Examine the cross-validation error. Then train for 50 more cycles and examine the new cross-validation error.

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',50,'Tree');
cvens = crossval(ens);
L = kfoldLoss(cvens)

L =
   25.6573

cvens = resume(cvens,50);
L = kfoldLoss(cvens)

L =
   26.7563
```

The additional training did not improve the cross-validation error.

See Also

`fitensemble` | `kfoldLoss`

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- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Ridge regression

Syntax

```
b = ridge(y,X,k)
b = ridge(y,X,k,scaled)
```

Description

`b = ridge(y,X,k)` returns a vector `b` of coefficient estimates for a multilinear ridge regression of the responses in `y` on the predictors in `X`. `X` is an n-by-p matrix of p predictors at each of n observations. `y` is an n-by-1 vector of observed responses. `k` is a vector of ridge parameters. If `k` has m elements, `b` is p-by-m. By default, `b` is computed after centering and scaling the predictors to have mean 0 and standard deviation 1. The model does not include a constant term, and `X` should not contain a column of 1s.

`b = ridge(y,X,k,scaled)` uses the {0,1}-valued flag `scaled` to determine if the coefficient estimates in `b` are restored to the scale of the original data. `ridge(y,X,k,0)` performs this additional transformation. In this case, `b` contains p+1 coefficients for each value of `k`, with the first row corresponding to a constant term in the model. `ridge(y,X,k,1)` is the same as `ridge(y,X,k)`. In this case, `b` contains p coefficients, without a coefficient for a constant term.

The relationship between `b0 = ridge(y,X,k,0)` and `b1 = ridge(y,X,k,1)` is given by

```
m = mean(X);
s = std(X,0,1)';
b1_scaled = b1./s;
b0 = [mean(y)-m*b1_scaled; b1_scaled]
```

This can be seen by replacing the x_i (i = 1, ..., n) in the multilinear model $y = b_0{}^0 + b_1{}^0 x_1 + \ldots + b_n{}^0 x_n$ with the z-scores $z_i = (x_i - \mu_i)/\sigma_i$, and replacing y with $y - \mu_y$.

In general, `b1` is more useful for producing plots in which the coefficients are to be displayed on the same scale, such as a *ridge trace* (a plot of the regression coefficients as a function of the ridge parameter). `b0` is more useful for making predictions.

Coefficient estimates for multiple linear regression models rely on the independence of the model terms. When terms are correlated and the columns of the design matrix X have an approximate linear dependence, the matrix $(X^TX)^{-1}$ becomes close to singular. As a result, the least-squares estimate

$$\hat{\beta} = (X^T X)^{-1} X^T y$$

becomes highly sensitive to random errors in the observed response y, producing a large variance. This situation of *multicollinearity* can arise, for example, when data are collected without an experimental design.

Ridge regression addresses the problem by estimating regression coefficients using

$$\hat{\beta} = (X^T X + kI)^{-1} X^T y$$

where k is the *ridge parameter* and I is the identity matrix. Small positive values of k improve the conditioning of the problem and reduce the variance of the estimates. While biased, the reduced variance of ridge estimates often result in a smaller mean square error when compared to least-squares estimates.

Examples

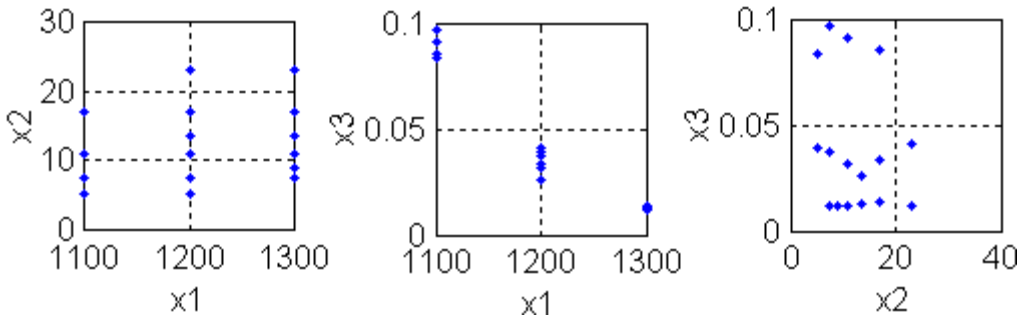
Load the data in `acetylene.mat`, with observations of the predictor variables `x1`, `x2`, `x3`, and the response variable `y`:

```
load acetylene
```

Plot the predictor variables against each other:

```
subplot(1,3,1)
plot(x1,x2,'.')
xlabel('x1'); ylabel('x2'); grid on; axis square

subplot(1,3,2)
plot(x1,x3,'.')
xlabel('x1'); ylabel('x3'); grid on; axis square
```

```
subplot(1,3,3)
plot(x2,x3,'.')
xlabel('x2'); ylabel('x3'); grid on; axis square
```



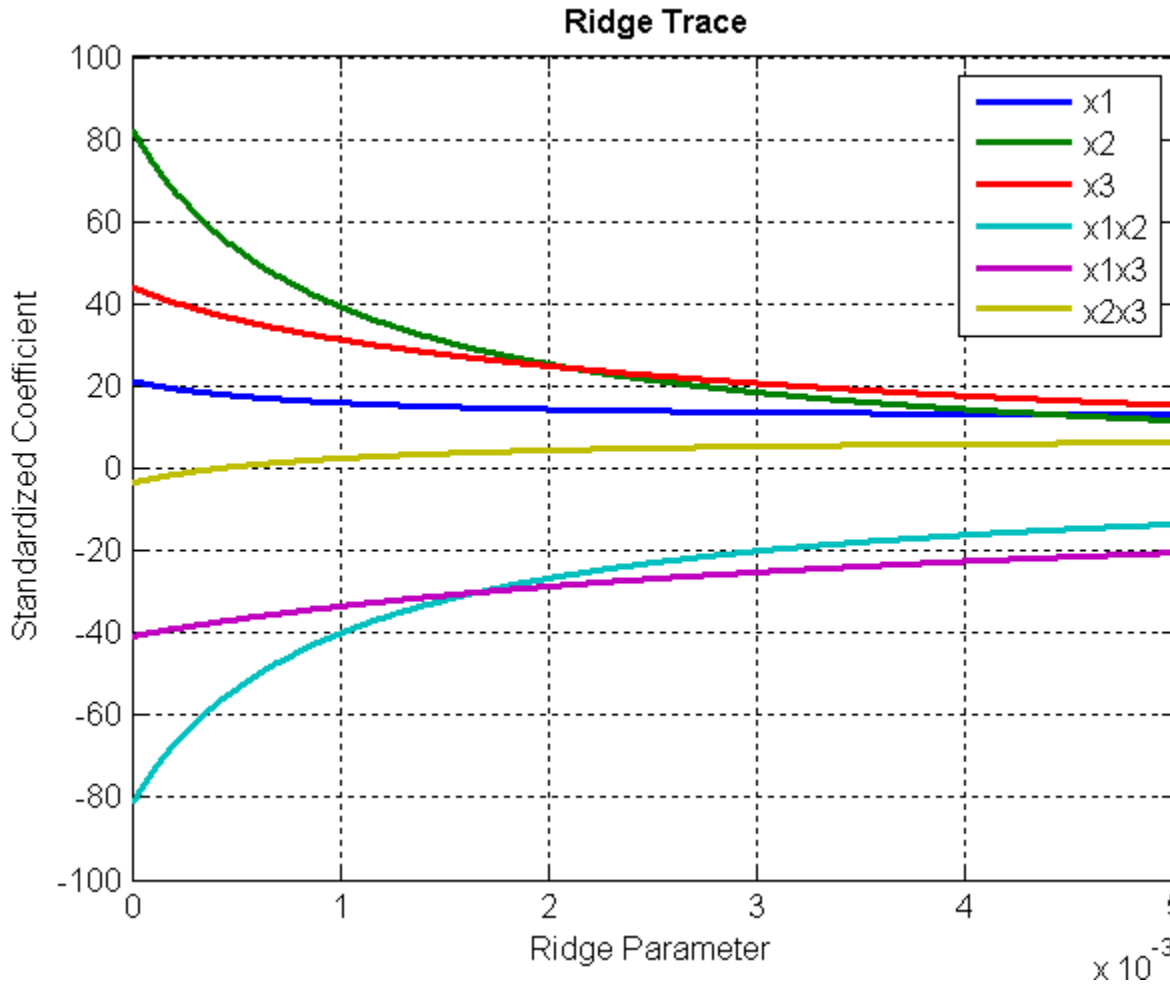
Note the correlation between `x1` and the other two predictor variables.

Use `ridge` and `x2fx` to compute coefficient estimates for a multilinear model with interaction terms, for a range of ridge parameters:

```
X = [x1 x2 x3];
D = x2fx(X,'interaction');
D(:,1) = []; % No constant term
k = 0:1e-5:5e-3;
b = ridge(y,D,k);
```

Plot the ridge trace:

```
figure
plot(k,b,'LineWidth',2)
ylim([-100 100])
grid on
xlabel('Ridge Parameter')
ylabel('Standardized Coefficient')
title('{\bf Ridge Trace}')
legend('x1','x2','x3','x1x2','x1x3','x2x3')
```



The estimates stabilize to the right of the plot. Note that the coefficient of the `x2x3` interaction term changes sign at a value of the ridge parameter $\approx 5 \times 10^{-4}$.

References

[1] Hoerl, A. E., and R. W. Kennard. "Ridge Regression: Biased Estimation for Nonorthogonal Problems." *Technometrics*. Vol. 12, No. 1, 1970, pp. 55–67.

[2] Hoerl, A. E., and R. W. Kennard. "Ridge Regression: Applications to Nonorthogonal Problems." *Technometrics*. Vol. 12, No. 1, 1970, pp. 69–82.

[3] Marquardt, D.W. "Generalized Inverses, Ridge Regression, Biased Linear Estimation, and Nonlinear Estimation." *Technometrics*. Vol. 12, No. 3, 1970, pp. 591–612.

[4] Marquardt, D. W., and R.D. Snee. "Ridge Regression in Practice." *The American Statistician*. Vol. 29, No. 1, 1975, pp. 3–20.

See Also

`regress` | `stepwise`

classregtree.risk

Purpose

Node risks

Syntax

```
r = risk(t)
r = risk(t,nodes)
```

Description

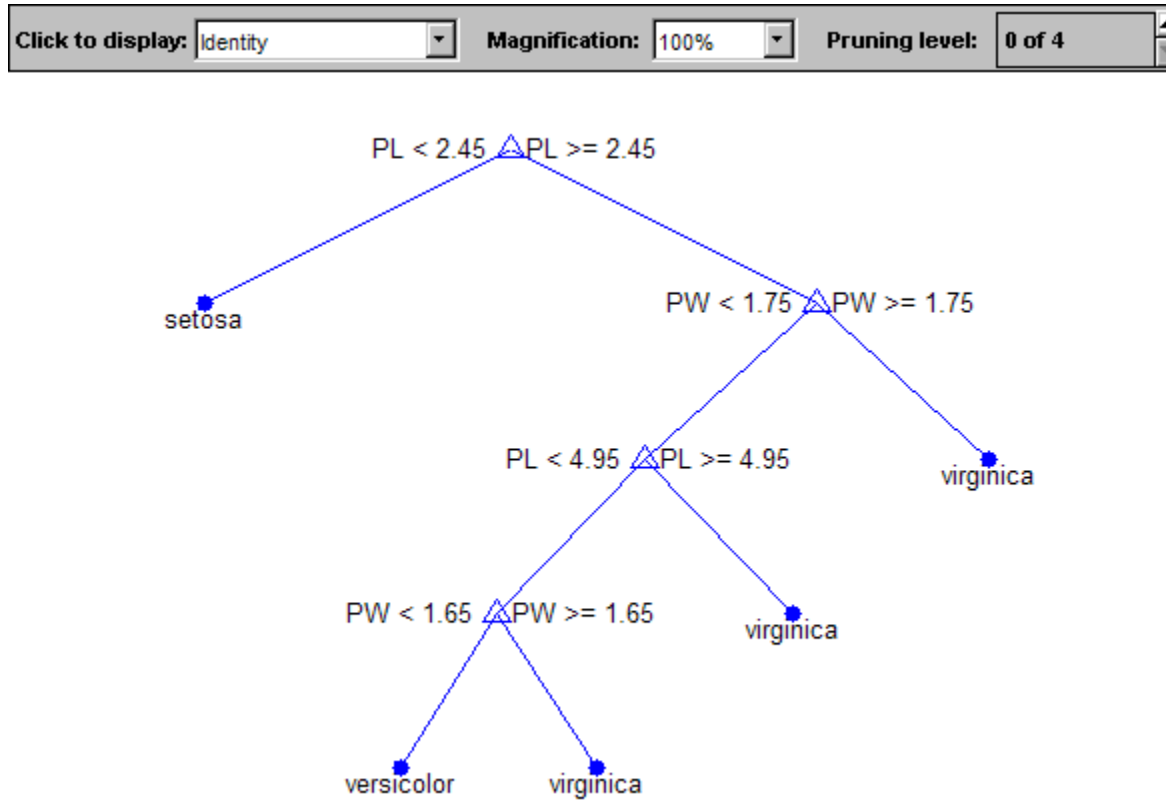
`r = risk(t)` returns an n-element vector `r` of the risk of the nodes in the tree `t`, where n is the number of nodes. The risk `r(i)` for node `i` is the node error `e(i)` (computed by `nodeerr`) weighted by the node probability `p(i)` (computed by `nodeprob`).

`r = risk(t,nodes)` takes a vector `nodes` of node numbers and returns the risk values for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
e = nodeerr(t);
p = nodeprob(t);
r = risk(t);

r
r =
    0.6667
         0
    0.3333
    0.0333
```

```
    0.0067
    0.0067
    0.0133
         0
         0

e.*p
ans =
    0.6667
         0
    0.3333
    0.0333
    0.0067
    0.0067
    0.0133
         0
         0
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `nodeerr` | `nodeprob`

Purpose

Interactive robust regression

Syntax

```
robustdemo
robustdemo(x,y)
```

Description

`robustdemo` shows the difference between ordinary least squares and robust regression for data with a single predictor. With no input arguments, `robustdemo` displays a scatter plot of a sample of roughly linear data with one outlier. The bottom of the figure displays equations of lines fitted to the data using ordinary least squares and robust methods, together with estimates of the root mean squared errors.

Use the right mouse button to click on a point and view its least-squares leverage and robust weight.

Use the left mouse button to click-and-drag a point. The displays will update.

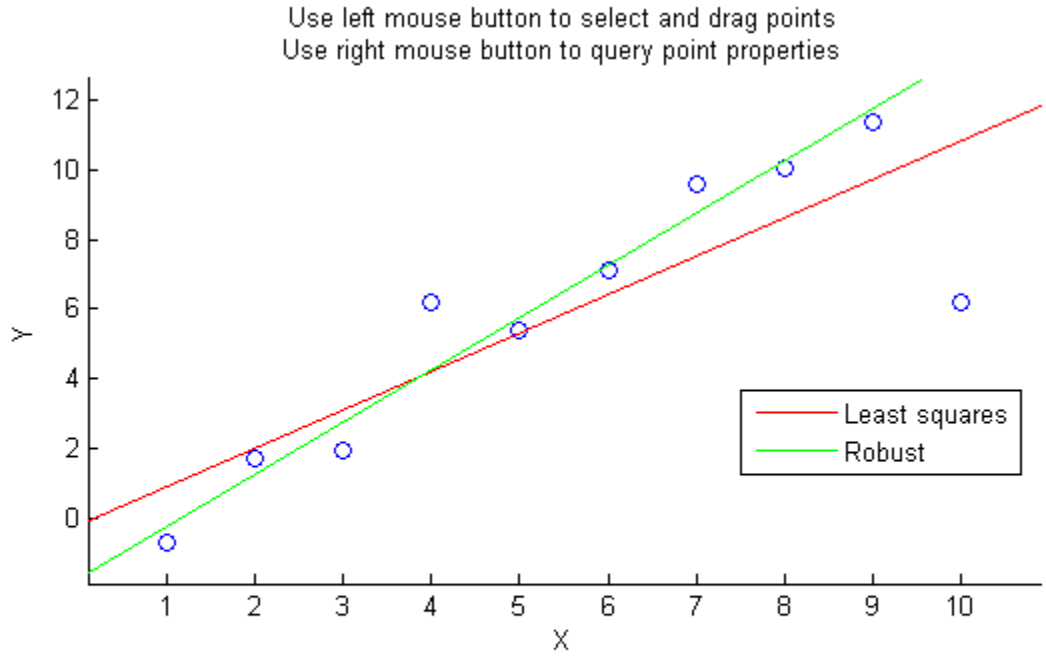
`robustdemo(x,y)` uses `x` and `y` data vectors you supply, in place of the sample data supplied with the function.

Examples

The following steps show you how to use `robustdemo`.

1. **Start the demo.** To begin using `robustdemo` with the built-in data, simply type the function name:

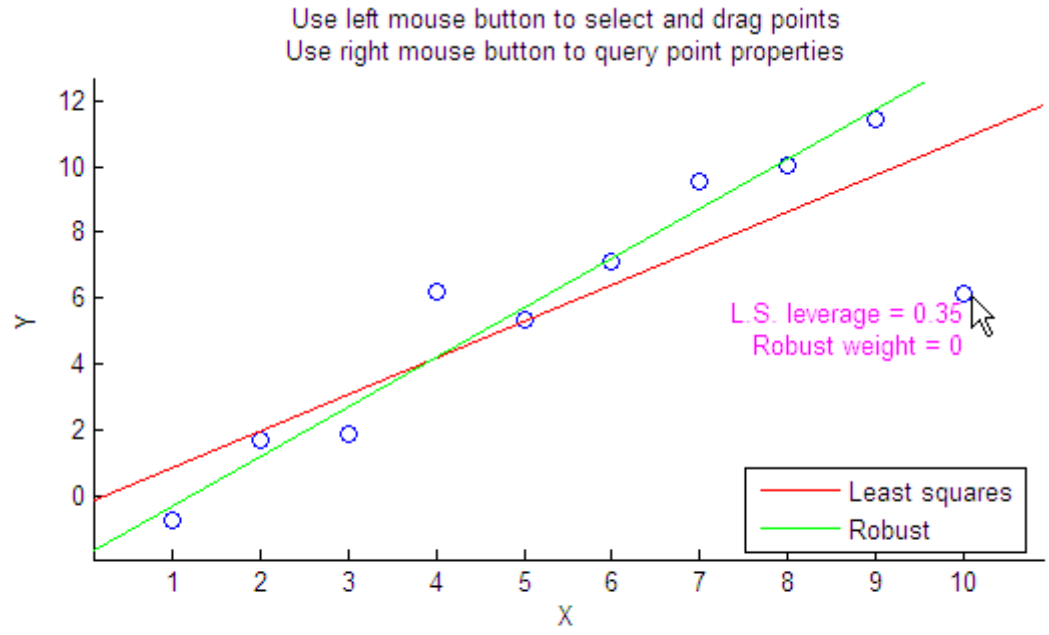
   ```
   robustdemo
   ```



Least squares:	Y = -0.188327 + 1.10351*X	RMS error = 2.21375
Robust:	Y = -1.77278 + 1.50415*X	RMS error = 1.43663

The resulting figure shows a scatter plot with two fitted lines. The red line is the fit using ordinary least-squares regression. The green line is the fit using robust regression. At the bottom of the figure are the equations for the fitted lines, together with the estimated root mean squared errors for each fit.

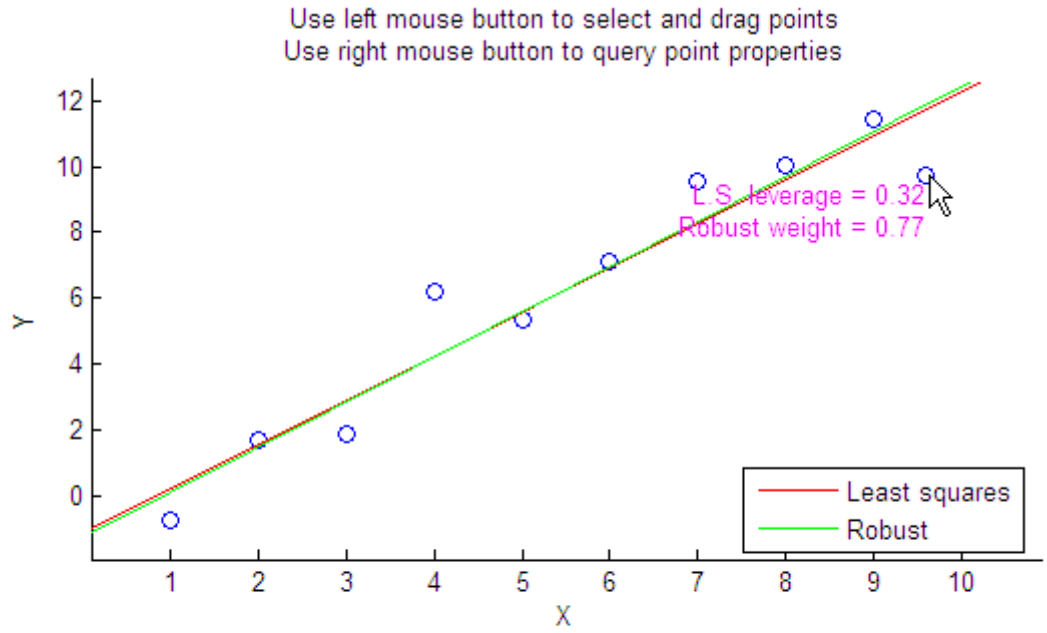
2 View leverages and robust weights. Right-click on any data point to see its least-squares leverage and robust weight:



Least squares:	Y = -0.188327 + 1.10351*X	RMS error = 2.21375
Robust:	Y = -1.77278 + 1.50415*X	RMS error = 1.43663

In the built-in data, the right-most point has a relatively high leverage of 0.35. The point exerts a large influence on the least-squares fit, but its small robust weight shows that it is effectively excluded from the robust fit.

3 See how changes in the data affect the fits. With the left mouse button, click and hold on any data point and drag it to a new location. When you release the mouse button, the displays update:



Least squares:	Y = -1.0661 + 1.33785*X	RMS error = 1.21477
Robust:	Y = -1.18916 + 1.36459*X	RMS error = 1.27697

Bringing the right-most data point closer to the least-squares line makes the two fitted lines nearly identical. The adjusted right-most data point has significant weight in the robust fit.

See Also

`robustfit` | `leverage`

Purpose

Robust regression

Syntax

```
b = robustfit(X,y)
b = robustfit(X,y,wfun,tune)
b = robustfit(X,y,wfun,tune,const)
[b,stats] = robustfit(...)
```

Description

`b = robustfit(X,y)` returns a p-by-1 vector `b` of coefficient estimates for a robust multilinear regression of the responses in `y` on the predictors in `X`. `X` is an n-by-p matrix of p predictors at each of n observations. `y` is an n-by-1 vector of observed responses. By default, the algorithm uses iteratively reweighted least squares with a bisquare weighting function.

Note By default, `robustfit` adds a first column of 1s to `X`, corresponding to a constant term in the model. Do not enter a column of 1s directly into `X`. You can change the default behavior of `robustfit` using the input *`const`*, below.

`robustfit` treats `NaN`s in `X` or `y` as missing values, and removes them.

`b = robustfit(X,y,wfun,tune)` specifies a weighting function *`wfun`*. `tune` is a tuning constant that is divided into the residual vector before computing weights.

The weighting function *`wfun`* can be any one of the following strings:

Weight Function	Equation	Default Tuning Constant
`'andrews'`	`w = (abs(r)<pi) .* sin(r) ./ r`	1.339
`'bisquare'` (default)	`w = (abs(r)<1) .* (1 - r.^2).^2`	4.685
`'cauchy'`	`w = 1 ./ (1 + r.^2)`	2.385

Weight Function	Equation	Default Tuning Constant
'fair'	w = 1 ./ (1 + abs(r))	1.400
'huber'	w = 1 ./ max(1, abs(r))	1.345
'logistic'	w = tanh(r) ./ r	1.205
'ols'	Ordinary least squares (no weighting function)	None
'talwar'	w = 1 * (abs(r)<1)	2.795
'welsch'	w = exp(-(r.^2))	2.985

If `tune` is unspecified, the default value in the table is used. Default tuning constants give coefficient estimates that are approximately 95% as statistically efficient as the ordinary least-squares estimates, provided the response has a normal distribution with no outliers. Decreasing the tuning constant increases the downweight assigned to large residuals; increasing the tuning constant decreases the downweight assigned to large residuals.

The value `r` in the weight functions is

```
r = resid/(tune*s*sqrt(1-h))
```

where `resid` is the vector of residuals from the previous iteration, `h` is the vector of leverage values from a least-squares fit, and `s` is an estimate of the standard deviation of the error term given by

```
s = MAD/0.6745
```

Here `MAD` is the median absolute deviation of the residuals from their median. The constant 0.6745 makes the estimate unbiased for the normal distribution. If there are p columns in `X`, the smallest p absolute deviations are excluded when computing the median.

You can write your own weight function. The function must take a vector of scaled residuals as input and produce a vector of weights as

output. In this case, *wfun* is specified using a function handle `@` (as in `@myfun`), and the input `tune` is required.

`b = robustfit(X,y,`*`wfun`*`,tune,`*`const`*`)` controls whether or not the model will include a constant term. *`const`* is `'on'` to include the constant term (the default), or `'off'` to omit it. When *`const`* is `'on'`, `robustfit` adds a first column of 1s to `X`. When *`const`* is `'off'`, `robustfit` does not alter `X`.

`[b,stats] = robustfit(...)` returns the structure `stats`, whose fields contain diagnostic statistics from the regression. The fields of `stats` are:

- `ols_s` — Sigma estimate (RMSE) from ordinary least squares
- `robust_s` — Robust estimate of sigma
- `mad_s` — Estimate of sigma computed using the median absolute deviation of the residuals from their median; used for scaling residuals during iterative fitting
- `s` — Final estimate of sigma, the larger of `robust_s` and a weighted average of `ols_s` and `robust_s`
- `resid` — Residual
- `rstud` — Studentized residual (see `regress` for more information)
- `se` — Standard error of coefficient estimates
- `covb` — Estimated covariance matrix for coefficient estimates
- `coeffcorr` — Estimated correlation of coefficient estimates
- `t` — Ratio of `b` to `se`
- `p` — p-values for `t`
- `w` — Vector of weights for robust fit
- `R` — R factor in QR decomposition of `X`
- `dfe` — Degrees of freedom for error
- `h` — Vector of leverage values for least-squares fit

The `robustfit` function estimates the variance-covariance matrix of the coefficient estimates using `inv(X'*X)*stats.s^2`. Standard errors and correlations are derived from this estimate.

Examples

Generate data with the trend `y = 10-2*x`, then change one value to simulate an outlier:

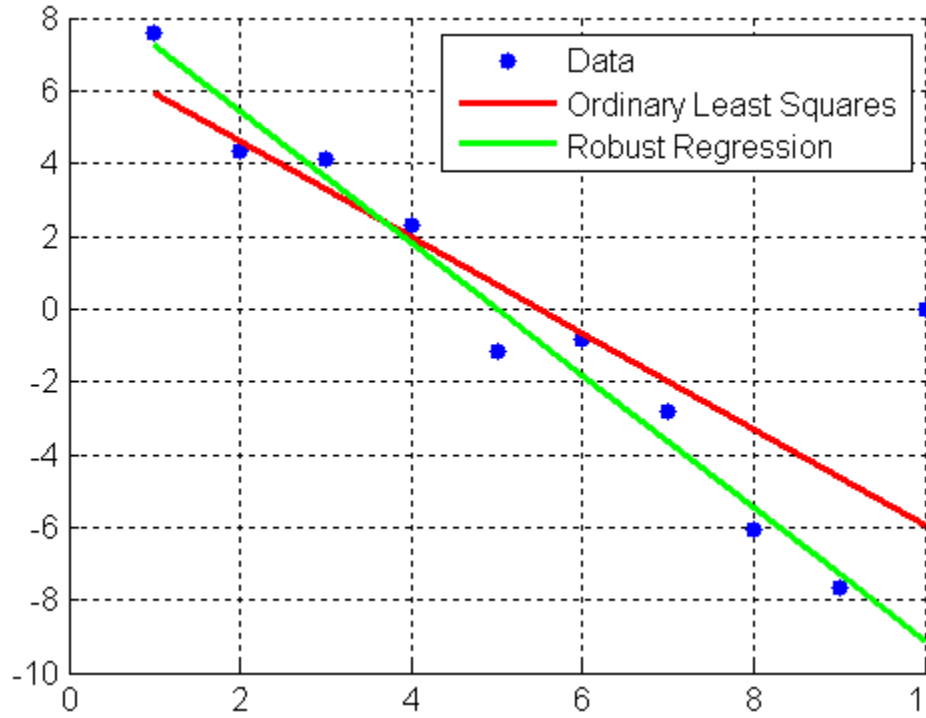
```
x = (1:10)';
y = 10 - 2*x + randn(10,1);
y(10) = 0;
```

Use both ordinary least squares and robust regression to estimate a straight-line fit:

```
bls = regress(y,[ones(10,1) x])
bls =
  7.2481
 -1.3208

brob = robustfit(x,y)
brob =
  9.1063
 -1.8231
```

A scatter plot of the data together with the fits shows that the robust fit is less influenced by the outlier than the least-squares fit:

```
scatter(x,y,'filled'); grid on; hold on
plot(x,bls(1)+bls(2)*x,'r','LineWidth',2);
plot(x,brob(1)+brob(2)*x,'g','LineWidth',2)
legend('Data','Ordinary Least Squares','Robust Regression')
```



References

[1] DuMouchel, W. H., and F. L. O'Brien. "Integrating a Robust Option into a Multiple Regression Computing Environment." *Computer Science and Statistics*: *Proceedings of the 21st Symposium on the Interface*. Alexandria, VA: American Statistical Association, 1989.

[2] Holland, P. W., and R. E. Welsch. "Robust Regression Using Iteratively Reweighted Least-Squares." *Communications in Statistics: Theory and Methods*, *A6*, 1977, pp. 813–827.

[3] Huber, P. J. *Robust Statistics*. Hoboken, NJ: John Wiley & Sons, Inc., 1981.

[4] Street, J. O., R. J. Carroll, and D. Ruppert. "A Note on Computing Robust Regression Estimates via Iteratively Reweighted Least Squares." *The American Statistician*. Vol. 42, 1988, pp. 152–154.

See Also

`regress` | `robustdemo`

Purpose

Rotate categorical matrix 90 degrees

Syntax

```
B = rot90(A)
B = rot90(A,k)
```

Description

`B = rot90(A)` returns the 90 degree counterclockwise rotation of the 2-D categorical matrix `A`.

`B = rot90(A,k)` returns the `k`*90 degree rotation of `A`, `k = +-1,+-2,...`.

See Also

`flipdim` | `fliplr` | `flipud`

Purpose

Rotate factor loadings

Syntax

```
B = rotatefactors(A)
B = rotatefactors(A,'Method','orthomax','Coeff',gamma)
B = rotatefactors(A,'Method','procrustes','Target',target)
B = rotatefactors(A,'Method','pattern','Target',target)
B = rotatefactors(A,'Method','promax')
[B,T] = rotatefactors(A,...)
```

Description

`B = rotatefactors(A)` rotates the d-by-m loadings matrix `A` to maximize the varimax criterion, and returns the result in `B`. Rows of `A` and `B` correspond to variables and columns correspond to factors, for example, the (i, j)th element of `A` is the coefficient for the i th variable on the j th factor. The matrix `A` usually contains principal component coefficients created with `princomp` or `pcacov`, or factor loadings estimated with `factoran`.

`B = rotatefactors(A,'Method','orthomax','Coeff',gamma)` rotates `A` to maximize the orthomax criterion with the coefficient `gamma`, i.e., `B` is the orthogonal rotation of `A` that maximizes

```
sum(D*sum(B.^4,1) - GAMMA*sum(B.^2,1).^2)
```

The default value of 1 for `gamma` corresponds to varimax rotation. Other possibilities include `gamma` = 0, $m/2$, and $d(m - 1)/(d + m - 2)$, corresponding to quartimax, equamax, and parsimax. You can also supply the strings `'varimax'`, `'quartimax'`, `'equamax'`, or `'parsimax'` for the `'method'` parameter and omit the `'Coeff'` parameter.

If `'Method'` is `'orthomax'`, `'varimax'`, `'quartimax'`, `'equamax'`, or `'parsimax'`, then additional parameters are

- `'Normalize'` — Flag indicating whether the loadings matrix should be row-normalized for rotation. If `'on'` (the default), rows of `A` are normalized prior to rotation to have unit Euclidean norm, and unnormalized after rotation. If `'off'`, the raw loadings are rotated and returned.

- `'Reltol'` — Relative convergence tolerance in the iterative algorithm used to find `T`. The default is `sqrt(eps)`.
- `'Maxit'` — Iteration limit in the iterative algorithm used to find `T`. The default is `250`.

`B = rotatefactors(A,'Method','procrustes','Target',target)` performs an oblique procrustes rotation of `A` to the *d*-by-*m* target loadings matrix `target`.

`B = rotatefactors(A,'Method','pattern','Target',target)` performs an oblique rotation of the loadings matrix `A` to the *d*-by-*m* target pattern matrix `target`, and returns the result in `B`. `target` defines the "restricted" elements of `B`, i.e., elements of `B` corresponding to zero elements of `target` are constrained to have small magnitude, while elements of `B` corresponding to nonzero elements of `target` are allowed to take on any magnitude.

If `'Method'` is `'procrustes'` or `'pattern'`, an additional parameter is `'Type'`, the type of rotation. If `'Type'` is `'orthogonal'`, the rotation is orthogonal, and the factors remain uncorrelated. If `'Type'` is `'oblique'` (the default), the rotation is oblique, and the rotated factors might be correlated.

When `'Method'` is `'pattern'`, there are restrictions on `target`. If `A` has *m* columns, then for orthogonal rotation, the *j*th column of `target` must contain at least *m* - *j* zeros. For oblique rotation, each column of `target` must contain at least *m* - 1 zeros.

`B = rotatefactors(A,'Method','promax')` rotates A to maximize the promax criterion, equivalent to an oblique Procrustes rotation with a target created by an orthomax rotation. Use the four orthomax parameters to control the orthomax rotation used internally by promax.

An additional parameter for 'promax' is `'Power'`, the exponent for creating promax target matrix. `'Power'` must be `1` or greater. The default is `4`.

`[B,T] = rotatefactors(A,...)` returns the rotation matrix `T` used to create `B`, that is, `B = A*T`. `inv(T'*T)` is the correlation matrix of the

rotated factors. For orthogonal rotation, this is the identity matrix, while for oblique rotation, it has unit diagonal elements but nonzero off-diagonal elements.

Examples

```
X = randn(100,10);

% Default (normalized varimax) rotation:
% first three principle components.
LPC = princomp(X);
[L1,T] = rotatefactors(LPC(:,1:3));

% Equamax rotation:
% first three principle components.
[L2,T] = rotatefactors(LPC(:,1:3),...
                       'method','equamax');

% Promax rotation:
% first three factors.
LFA = factoran(X,3,'Rotate','none');
[L3,T] = rotatefactors(LFA(:,1:3),...
                       'method','promax',...
                       'power',2);

% Pattern rotation:
% first three factors.
Tgt = [1 1 1 1 1 0 1 0 1 1; ...
       0 0 0 1 1 1 0 0 0 0; ...
       1 0 0 1 0 1 1 1 1 0]';
[L4,T] = rotatefactors(LFA(:,1:3),...
                       'method','pattern',...
                       'target',Tgt);
inv(T'*T) % Correlation matrix of the rotated factors
```

References

[1] Harman, H. H. *Modern Factor Analysis*. 3rd ed. Chicago: University of Chicago Press, 1976.

[2] Lawley, D. N., and A. E. Maxwell. *Factor Analysis as a Statistical Method.* 2nd ed. New York: American Elsevier Publishing, 1971.

See Also

`biplot` | `factoran` | `princomp` | `pcacov` | `procrustes`

rowexch

Purpose

Row exchange

Syntax

```
dRE = rowexch(nfactors,nruns)
[dRE,X] = rowexch(nfactors,nruns)
[dRE,X] = rowexch(nfactors,nruns,model)
[dRE,X] = rowexch(...,param1,val1,param2,val2,...)
```

Description

`dRE = rowexch(nfactors,nruns)` uses a row-exchange algorithm to generate a *D*-optimal design `dRE` with `nruns` runs (the rows of `dRE`) for a linear additive model with `nfactors` factors (the columns of `dRE`). The model includes a constant term.

`[dRE,X] = rowexch(nfactors,nruns)` also returns the associated design matrix `X`, whose columns are the model terms evaluated at each treatment (row) of `dRE`.

`[dRE,X] = rowexch(nfactors,nruns,model)` uses the linear regression model specified in `model`. `model` is one of the following strings:

- `'linear'` — Constant and linear terms. This is the default.
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms
- `'purequadratic'` — Constant, linear, and squared terms

The order of the columns of `X` for a full quadratic model with n terms is:

1. The constant term
2. The linear terms in order 1, 2, ..., n
3. The interaction terms in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n–1, n)
4. The squared terms in order 1, 2, ..., n

Other models use a subset of these terms, in the same order.

Alternatively, *model* can be a matrix specifying polynomial terms of arbitrary order. In this case, *model* should have one column for each factor and one row for each term in the model. The entries in any row of *model* are powers for the factors in the columns. For example, if a model has factors X1, X2, and X3, then a row [0 1 2] in *model* specifies the term (X1.^0).*(X2.^1).*(X3.^2). A row of all zeros in *model* specifies a constant term, which can be omitted.

[dRE,X] = rowexch(...,*param1*,*val1*,*param2*,*val2*,...) specifies additional parameter/value pairs for the design. Valid parameters and their values are listed in the following table.

Parameter	Value
'bounds'	Lower and upper bounds for each factor, specified as a 2-by-nfactors matrix. Alternatively, this value can be a cell array containing nfactors elements, each element specifying the vector of allowable values for the corresponding factor.
'categorical'	Indices of categorical predictors.
'display'	Either 'on' or 'off' to control display of the iteration counter. The default is 'on'.
'excludefun'	Handle to a function that excludes undesirable runs. If the function is *f*, it must support the syntax $b = f(S)$, where S is a matrix of treatments with nfactors columns and b is a vector of Boolean values with the same number of rows as S. $b(i)$ is true if the ith row S should be excluded.
'init'	Initial design as an nruns-by-nfactors matrix. The default is a randomly selected set of points.
'levels'	Vector of number of levels for each factor.
'maxiter'	Maximum number of iterations. The default is 10.

Parameter	Value
`options`	A structure that specifies whether to run in parallel, and specifies the random stream or streams. Create the `options` structure with `statset`. Option fields: • `UseParallel` — Set to `'always'` to compute in parallel. Default is `'never'`. • `UseSubstreams` — Set to `'always'` to compute in parallel in a reproducible fashion. Default is `'never'`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. • `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `rowexch` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case - You have an open MATLAB pool - `UseParallel` is `'always'` - `UseSubstreams` is `'never'` In that case, use a cell array the same size as the MATLAB pool. For more information on using parallel computing, see Chapter 17, “Parallel Statistics”.
`'tries'`	Number of times to try to generate a design from a new starting point. The algorithm uses random points for each try, except possibly the first. The default is `1`.

Algorithms

Both `cordexch` and `rowexch` use iterative search algorithms. They operate by incrementally changing an initial design matrix X to increase $D = |X^TX|$ at each step. In both algorithms, there is randomness

built into the selection of the initial design and into the choice of the incremental changes. As a result, both algorithms may return locally, but not globally, *D*-optimal designs. Run each algorithm multiple times and select the best result for your final design. Both functions have a `'tries'` parameter that automates this repetition and comparison.

At each step, the row-exchange algorithm exchanges an entire row of *X* with a row from a design matrix *C* evaluated at a candidate set of feasible treatments. The `rowexch` function automatically generates a *C* appropriate for a specified model, operating in two steps by calling the `candgen` and `candexch` functions in sequence. Provide your own *C* by calling `candexch` directly. In either case, if *C* is large, its static presence in memory can affect computation.

Examples

Suppose you want a design to estimate the parameters in the following three-factor, seven-term interaction model:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_{12} x_1 x_2 + \beta_{13} x_1 x_3 + \beta_{23} x_2 x_3 + \varepsilon$$

Use `rowexch` to generate a *D*-optimal design with seven runs:

```
nfactors = 3;
nruns = 7;
[dRE,X] = rowexch(nfactors,nruns,'interaction','tries',10)
dRE =
    -1    -1     1
     1    -1     1
     1    -1    -1
     1     1     1
    -1    -1    -1
    -1     1    -1
    -1     1     1
X =
     1    -1    -1     1     1    -1    -1
     1     1    -1     1    -1     1    -1
     1     1    -1    -1    -1    -1     1
     1     1     1     1     1     1     1
     1    -1    -1    -1     1     1     1
```

```
     1     -1      1     -1     -1      1     -1
     1     -1      1      1     -1     -1      1
```

Columns of the design matrix `X` are the model terms evaluated at each row of the design `dRE`. The terms appear in order from left to right: constant term, linear terms (1, 2, 3), interaction terms (12, 13, 23). Use `X` to fit the model, as described in "Linear Regression" on page 9-3, to response data measured at the design points in `dRE`.

See Also

`candgen` | `candexch` | `cordexch`

Purpose

Interactive response surface demonstration

Syntax

```
rsmdemo
```

Description

`rsmdemo` opens a group of three graphical user interfaces for interactively investigating response surface methodology (RSM), nonlinear fitting, and the design of experiments.

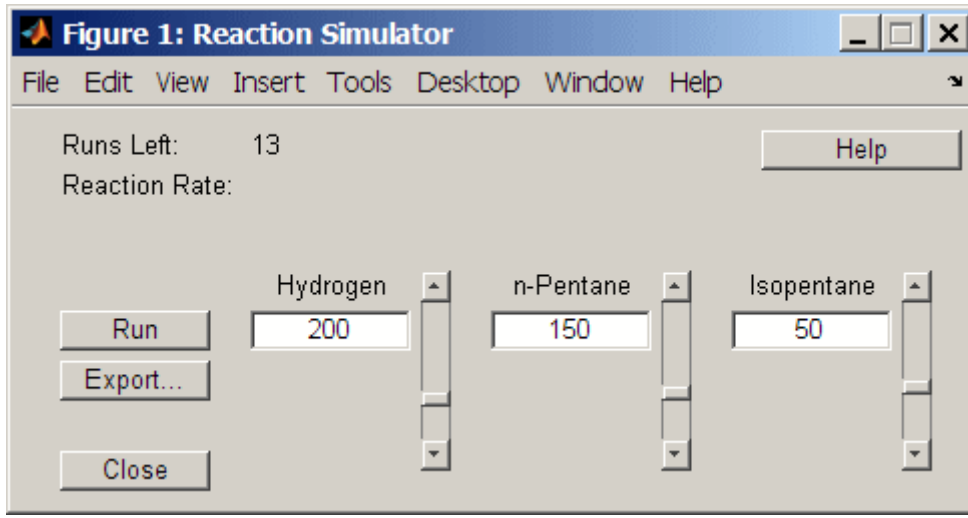
The interfaces allow you to collect and model data from a simulated chemical reaction. Experimental predictors are concentrations of three reactants (hydrogen, *n*-Pentane, and isopentane) and the response is the reaction rate. The reaction rate is simulated by a Hougen-Watson model (Bates and Watts, [2], pp. 271–272):

$$rate = \frac{\beta_1 x_2 - x_3 / \beta_5}{1 + \beta_2 x_1 + \beta_3 x_2 + \beta_4 x_3}$$

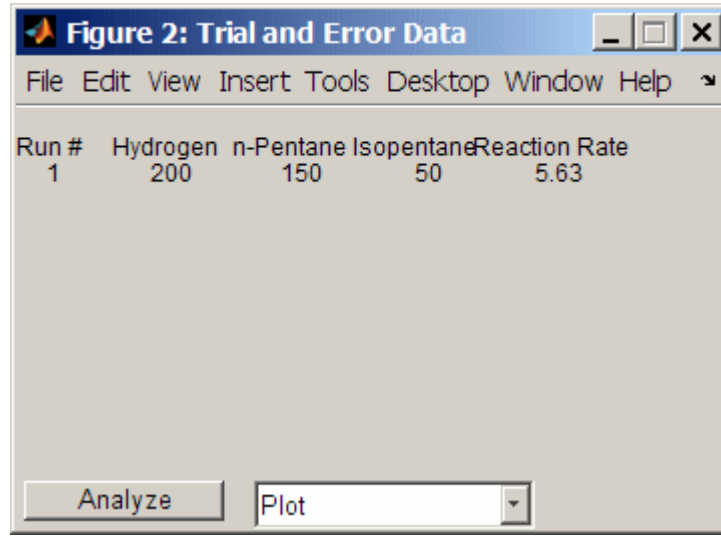
where *rate* is the reaction rate, x_1, x_2, and x_3 are the concentrations of hydrogen, *n*-pentane, and isopentane, respectively, and β_1, β_2, ... , β_5 are fixed parameters. Random errors are used to perturb the reaction rate for each combination of reactants.

Collect data using one of two methods:

1. Manually set reactant concentrations in the **Reaction Simulator** interface by editing the text boxes or by adjusting the associated sliders.

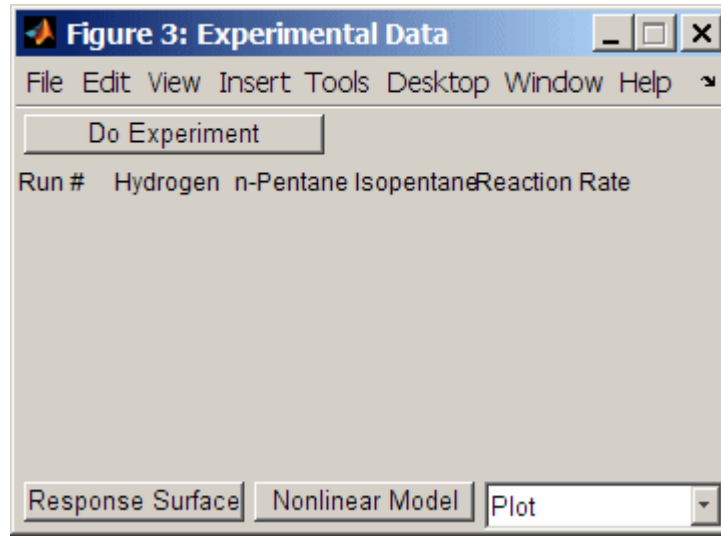


When you click **Run**, the concentrations and simulated reaction rate are recorded on the **Trial and Error Data** interface.

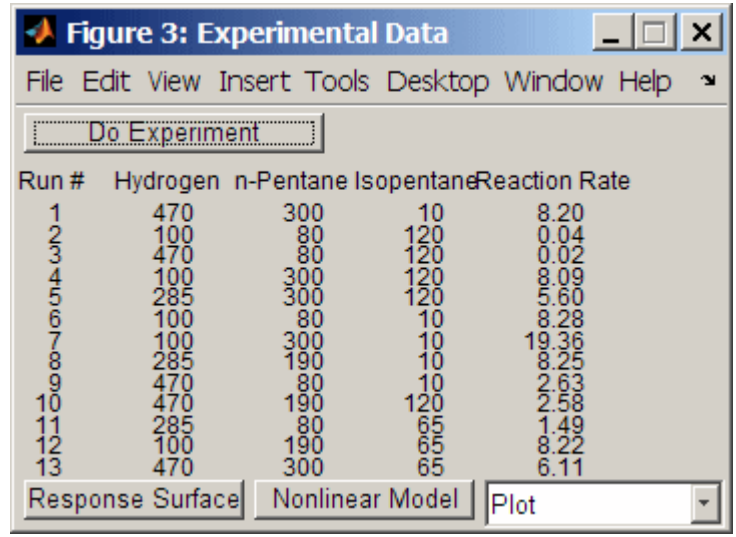


You are allowed up to 13 independent experimental runs for data collection.

2 Use a designed experiment to set reactant concentrations in the **Experimental Data** interface by clicking the **Do Experiment** button.



A 13-run *D*-optimal design for a full quadratic model is generated by the `cordexch` function, and the concentrations and simulated reaction rates are recorded on the same interface.



Once data is collected, scatter plots of reaction rates vs. individual predictors are generated by selecting one of the following from the **Plot** pop-up menu below the recorded data:

- **Hydrogen vs. Rate**
- **n-Pentane vs. Rate**
- **Isopentane vs. Rate**

Fit a response surface model to the data by clicking the **Analyze** button below the trial-and-error data or the **Response Surface** button below the experimental data. Both buttons load the data into the Response Surface Tool `rstool`. By default, trial-and-error data is fit with a linear additive model and experimental data is fit with a full quadratic model, but the models can be adjusted in the Response Surface Tool.

For experimental data, you have the additional option of fitting a Hougen-Watson model. Click the **Nonlinear Model** button to load the data and the model in `hougen` into the Nonlinear Fitting Tool `nlintool`.

See Also

hougen | cordexch | rstool | nlintool

Purpose

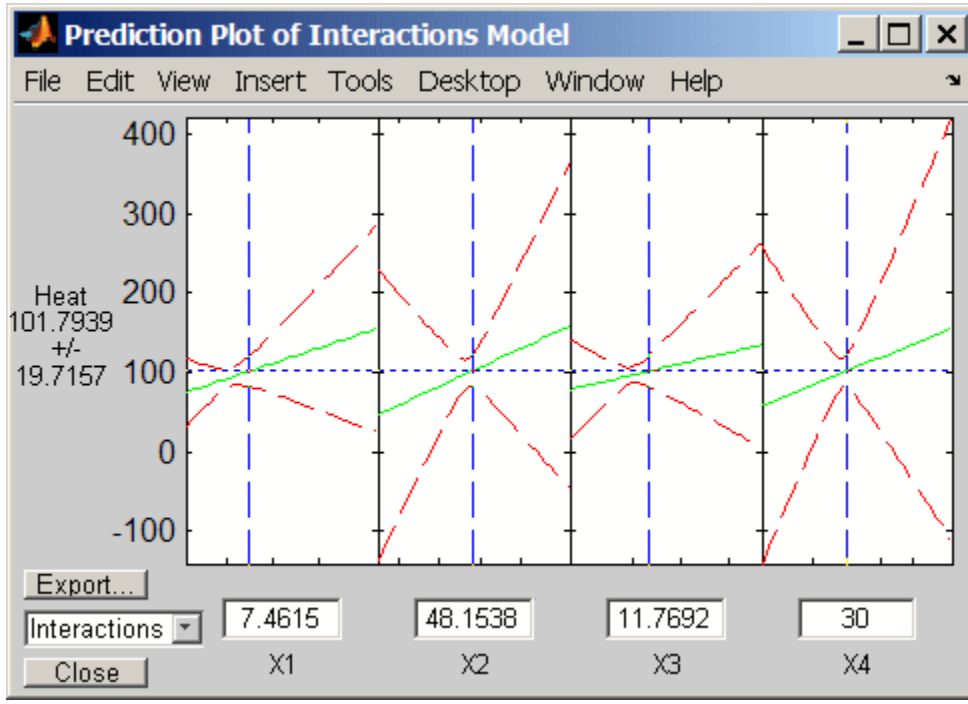
Interactive response surface modeling

Syntax

```
rstool
rstool(X,Y,model)
rstool(x,y,model,alpha)
rstool(x,y,model,alpha,xname,yname)
```

Description

`rstool` opens a graphical user interface for interactively investigating one-dimensional contours of multidimensional response surface models.



By default, the interface opens with the data from `hald.mat` and a fitted response surface with constant, linear, and interaction terms.

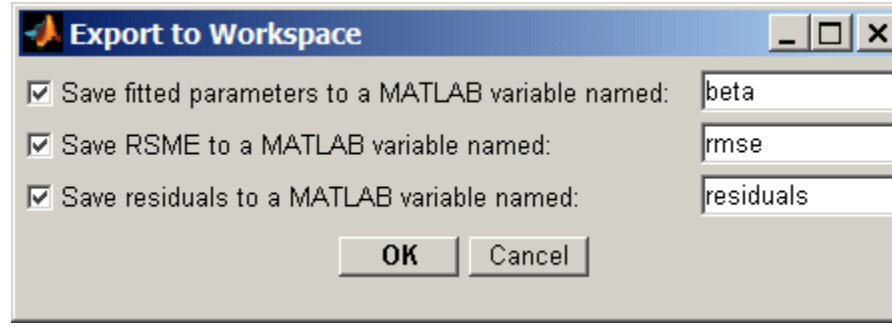
A sequence of plots is displayed, each showing a contour of the response surface against a single predictor, with all other predictors held fixed.

`rstool` plots a 95% simultaneous confidence band for the fitted response surface as two red curves. Predictor values are displayed in the text boxes on the horizontal axis and are marked by vertical dashed blue lines in the plots. Predictor values are changed by editing the text boxes or by dragging the dashed blue lines. When you change the value of a predictor, all plots update to show the new point in predictor space.

The pop-up menu at the lower left of the interface allows you to choose among the following models:

- `Linear` — Constant and linear terms (the default)
- `Pure Quadratic` — Constant, linear, and squared terms
- `Interactions` — Constant, linear, and interaction terms
- `Full Quadratic` — Constant, linear, interaction, and squared terms

Click **Export** to open the following dialog box:



The dialog allows you to save information about the fit to MATLAB workspace variables with valid names.

`rstool(X,Y,`*`model`*`)` opens the interface with the predictor data in `X`, the response data in `Y`, and the fitted model *`model`*. Distinct predictor variables should appear in different columns of `X`. `Y` can be a vector, corresponding to a single response, or a matrix, with columns corresponding to multiple responses. `Y` must have as many elements (or rows, if it is a matrix) as `X` has rows.

The optional input *model* can be any one of the following strings:

- 'linear' — Constant and linear terms (the default)
- 'purequadratic' — Constant, linear, and squared terms
- 'interaction' — Constant, linear, and interaction terms
- 'quadratic' — Constant, linear, interaction, and squared terms

To specify a polynomial model of arbitrary order, or a model without a constant term, use a matrix for *model* as described in x2fx.

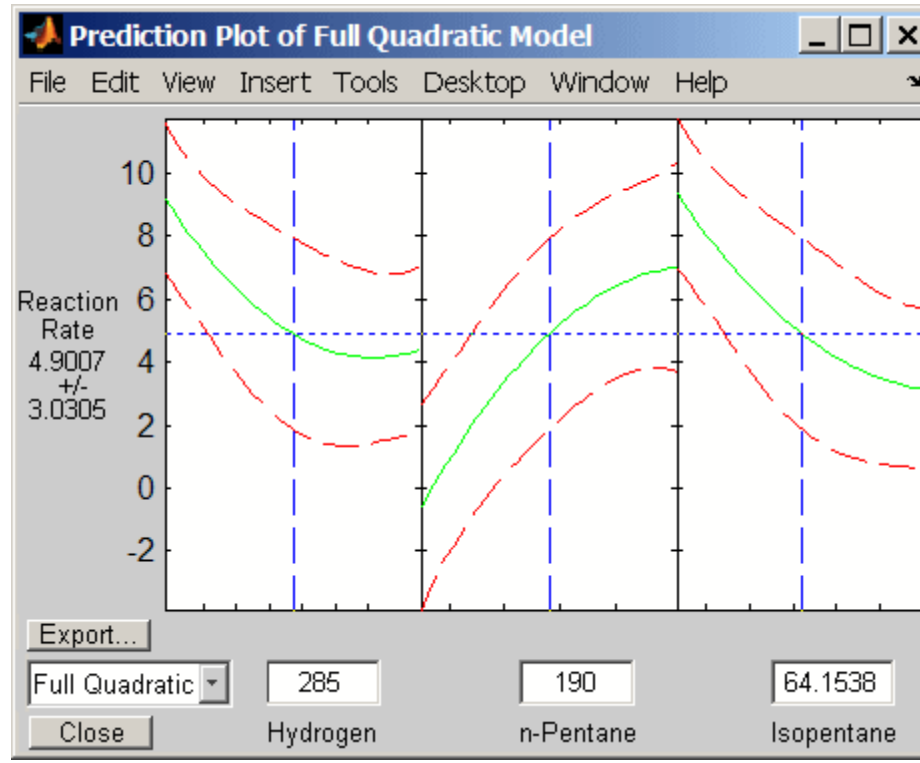
rstool(x,y,*model*,alpha) uses 100(1-alpha)% global confidence intervals for new observations in the plots.

rstool(x,y,*model*,alpha,xname,yname) labels the axes using the strings in xname and yname. To label each subplot differently, xname and yname can be cell arrays of strings.

Examples

The following uses rstool to visualize a quadratic response surface model of the 3-D chemical reaction data in reaction.mat:

```
load reaction
alpha = 0.01; % Significance level
rstool(reactants,rate,'quadratic',alpha,xn,yn)
```



The `rstool` interface is used by `rsmdemo` to visualize the results of simulated experiments with data like that in `reaction.mat`. As described in "Response Surface Designs" on page 15-9, `rsmdemo` uses a response surface model to generate simulated data at combinations of predictors specified by either the user or by a designed experiment.

See Also

`x2fx` | `rsmdemo` | `nlintool`

Purpose

Run test for randomness

Syntax

```
h = runstest(x)
h = runstest(x,v)
h = runstest(x,'ud')
h = runstest(...,param1,val1,param2,val2,...)
[h,p] = runstest(...)
[h,p,stats] = runstest(...)
```

Description

`h = runstest(x)` performs a runs test on the sequence of observations in the vector `x`. This is a test of the null hypothesis that the values in `x` come in random order, against the alternative that they do not. The test is based on the number of runs of consecutive values above or below the mean of `x`. Too few runs indicate a tendency for high and low values to cluster. Too many runs indicate a tendency for high and low values to alternate. The test returns the logical value `h = 1` if it rejects the null hypothesis at the 5% significance level, and `h = 0` if it cannot. The test treats `NaN` values in `x` as missing values, and ignores them.

`runstest` uses a test statistic which is approximately normally distributed when the null hypothesis is true. It is the difference between the number of runs and its mean, divided by its standard deviation.

`h = runstest(x,v)` performs the test using runs above or below the value `v`. Values exactly equal to `v` are discarded. The default value of `v` is the mean of `x`.

`h = runstest(x,'ud')` performs a test for the number of runs up or down. This also tests the hypothesis that the values in `x` come in random order. Too few runs indicate a trend. Too many runs indicate an oscillation. Values exactly equal to the preceding value are discarded.

`h = runstest(...,param1,val1,param2,val2,...)` specifies additional parameters and their values. Valid parameter/value pairs are the following:

- `'alpha'` — A scalar giving the significance level of the test

- `'method'` — Either `'exact'` to compute the *p* value using an exact algorithm, or `'approximate'` to use a normal approximation. The default is `'exact'`, except for runs up/down when the length of is 51 or more. The `'exact'` method is not available for runs up/down when the length of `x` is over 50.
- `'tail'` — Performs the test against one of the following alternative hypotheses:
  - `'both'` — two-tailed test (sequence is not random)
  - `'right'` — right-tailed test (like values separate for runs above/below, direction alternates for runs up/down)
  - `'left'` — left-tailed test (like values cluster for runs above/below, values trend for runs up/down)

`[h,p] = runstest(...)` returns the *p* value of the test. The output `p` is computed from either the test statistic or the exact distribution of the number of runs, depending on the value of the `'method'` parameter.

`[h,p,stats] = runstest(...)` returns a structure `stats` with the following fields:

- `nruns` — The number of runs
- `n1` — The number of values above `v`
- `n0` — The number of values below `v`
- `z` — The test statistic

Examples

```
x = randn(40,1);
[h,p] = runstest(x,median(x))
h =
     0
p =
    0.6286
```

See Also

`signrank` | `signtest`

TreeBagger.SampleWithReplacement property

Purpose

Flag to sample with replacement

Description

The `SampleWithReplacement` property is a logical flag specifying if data are sampled for each decision tree with replacement. True if `TreeBagger` samples data with replacement and false otherwise. True by default.

Purpose

Sample size and power of test

Syntax

```
n = sampsizepwr(testtype,p0,p1)
n = sampsizepwr(testtype,p0,p1,power)
power = sampsizepwr(testtype,p0,p1,[],n)
p1 = sampsizepwr(testtype,p0,[],power,n)
[...] = sampsizepwr(...,n,param1,val1,param2,val2,...)
```

Description

`n = sampsizepwr(testtype,p0,p1)` returns the sample size `n` required for a two-sided test of the specified type to have a power (probability of rejecting the null hypothesis when the alternative hypothesis is true) of 0.90 when the significance level (probability of rejecting the null hypothesis when the null hypothesis is true) is 0.05. `p0` specifies parameter values under the null hypothesis. `p1` specifies the single parameter value being tested under the alternative hypothesis.

The following values are available for *testtype*:

- `'z'` — *z*-test for normally distributed data with known standard deviation. `p0` is a two-element vector `[mu0 sigma0]` of the mean and standard deviation, respectively, under the null hypothesis. `p1` is the value of the mean under the alternative hypothesis.
- `'t'` — *t*-test for normally distributed data with unknown standard deviation. `p0` is a two-element vector `[mu0 sigma0]` of the mean and standard deviation, respectively, under the null hypothesis. `p1` is the value of the mean under the alternative hypothesis.
- `'var'` — Chi-square test of variance for normally distributed data. `p0` is the variance under the null hypothesis. `p1` is the variance under the alternative hypothesis.
- `'p'` — Test of the *p* parameter (success probability) for a binomial distribution. `p0` is the value of *p* under the null hypothesis. `p1` is the value of *p* under the alternative hypothesis.

  The `'p'` test is a discrete test for which increasing the sample size does not always increase the power. For `n` values larger than 200,

there may be values smaller than the returned `n` value that also produce the desired size and power.

`n = sampsizepwr(`*`testtype`*`,p0,p1,power)` returns the sample size `n` such that the power is `power` for the parameter value `p1`.

`power = sampsizepwr(`*`testtype`*`,p0,p1,[],n)` returns the power achieved for a sample size of `n` when the true parameter value is `p1`.

`p1 = sampsizepwr(`*`testtype`*`,p0,[],power,n)` returns the parameter value detectable with the specified sample size `n` and power `power`.

When computing `p1` for the `'p'` test, if no alternative can be rejected for a given null hypothesis and significance level, the function displays a warning message and returns `NaN`.

`[...] = sampsizepwr(...,n,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` specifies one or more of the following name/value pairs:

- `'alpha'` — Significance level of the test (default 0.05)
- `'tail'` — The type of test is one of the following:
  - `'both'` — Two-sided test for an alternative not equal to `p0`
  - `'right'` — One-sided test for an alternative larger than `p0`
  - `'left'` — One-sided test for an alternative smaller than `p0`

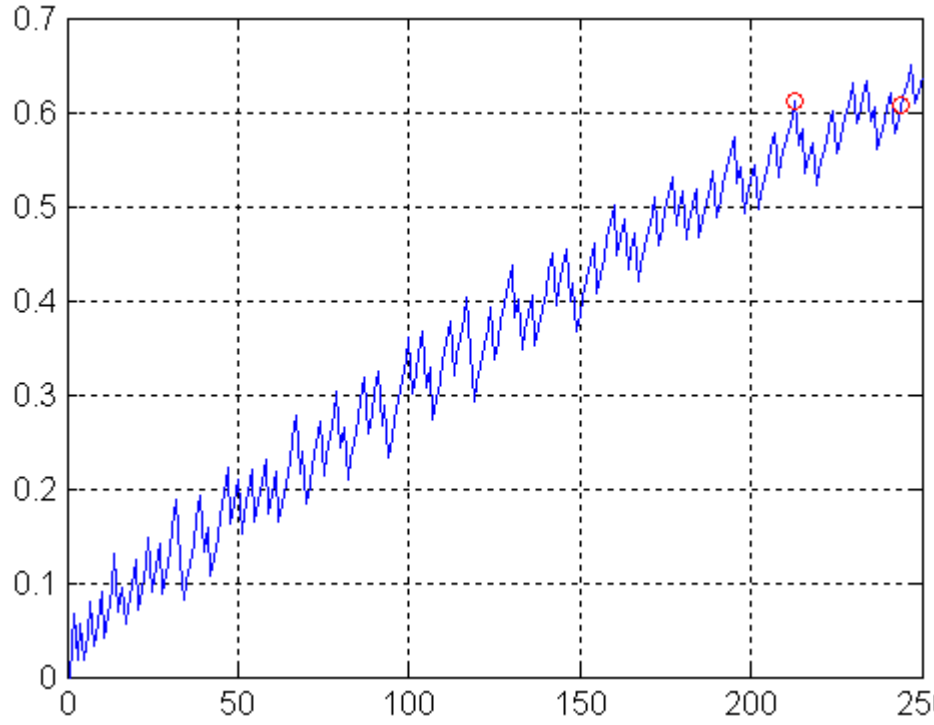
Examples

Compute the mean closest to 100 that can be determined to be significantly different from 100 using a *t*-test with a sample size of 60 and a power of 0.8.

```
mu1 = sampsizepwr('t',[100 10],[],0.8,60)
mu1 =
  103.6770
```

Compute the sample size n required to distinguish $p = 0.26$ from $p = 0.6$ with a binomial test. The result is approximate, so make a plot to see if any smaller n values also have the required power of 0.5.

```
napprox = sampsizepwr('p',0.2,0.26,0.6)
Warning: Values N>200 are approximate.  Plotting the power as a function
of N may reveal lower N values that have the required power.
napprox =
   244

nn = 1:250;
pwr = sampsizepwr('p',0.2,0.26,[],nn);
nexact = min(nn(pwr>=0.6))
nexact =
   213

plot(nn,pwr,'b-',[napprox nexact],pwr([napprox nexact]),'ro');
grid on
```



See Also vartest | ttest | ztest | binocdf

Purpose

Scatter plot with marginal histograms

Syntax

```
scatterhist(x,y)
h = scatterhist(...)
scatterhist(...,'param1',val1,'param2',val2,...)
```

Description

`scatterhist(x,y)` creates a 2-D scatterplot of the data in the vectors `x` and `y`, and puts a univariate histogram on the horizontal and vertical axes of the plot. `x` and `y` must be the same length.

The function is useful for viewing properties of random samples produced by functions such as `copularnd`, `mvnrnd`, `lhsdesign`.

`h = scatterhist(...)` returns a vector of three axes handles for the scatterplot, the histogram along the horizontal axis, and the histogram along the vertical axis, respectively.

`scatterhist(...,'param1',val1,'param2',val2,...)` specifies additional parameter name/values pairs to control how the plot is made. Valid parameters are the following:

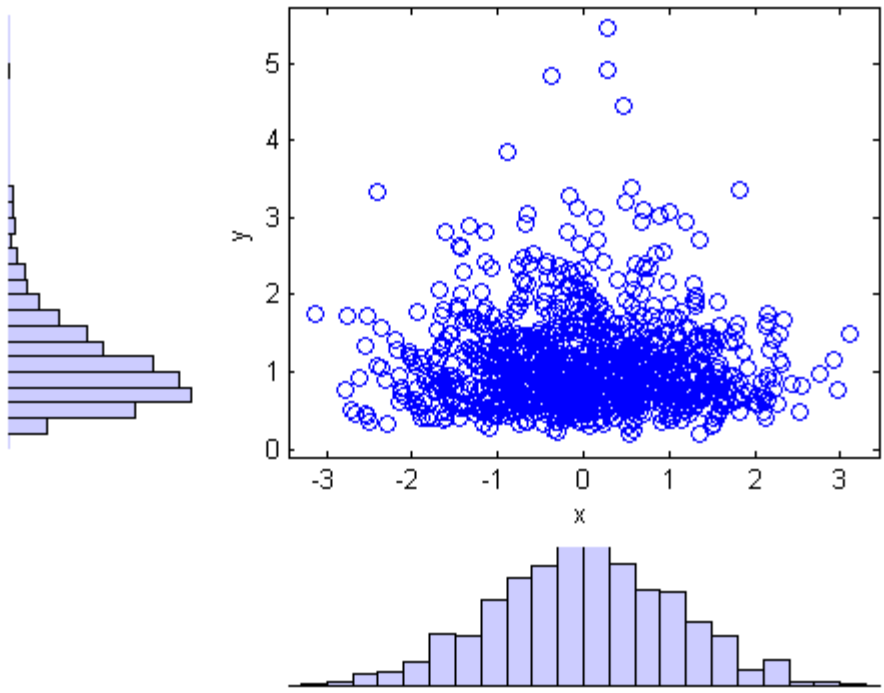
- `'NBins'` — A scalar or a two-element vector specifying the number of bins for the `X` and `Y` histograms. The default is to compute the number of bins using Scott's rule based on the sample standard deviation.
- `'Location'` — A string controlling the location of the marginal histograms within the figure. `'SouthWest'` (the default) plots the histograms below and to the left of the scatterplot, `'SouthEast'` plots them below and to the right, `'NorthEast'` above and to the right, and `'NorthWest'` above and to the left.
- `'Direction'` — A string controlling the directation of the marginal histograms in the figure. `'in'` (the default) plots the histograms with bars directed in towards the scatterplot, `'out'` plots the histograms with bars directed out away from the scatterplot.

Examples

Example 1

Independent normal and lognormal random samples:

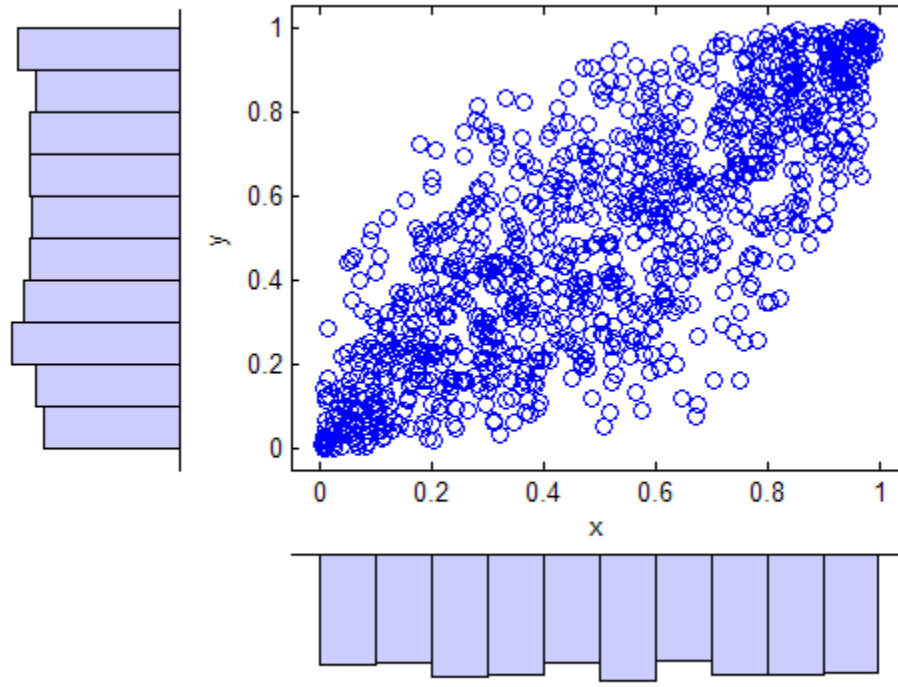
```
x = randn(1000,1);
y = exp(.5*randn(1000,1));
scatterhist(x,y)
```



Example 2

Marginal uniform samples that are not independent:

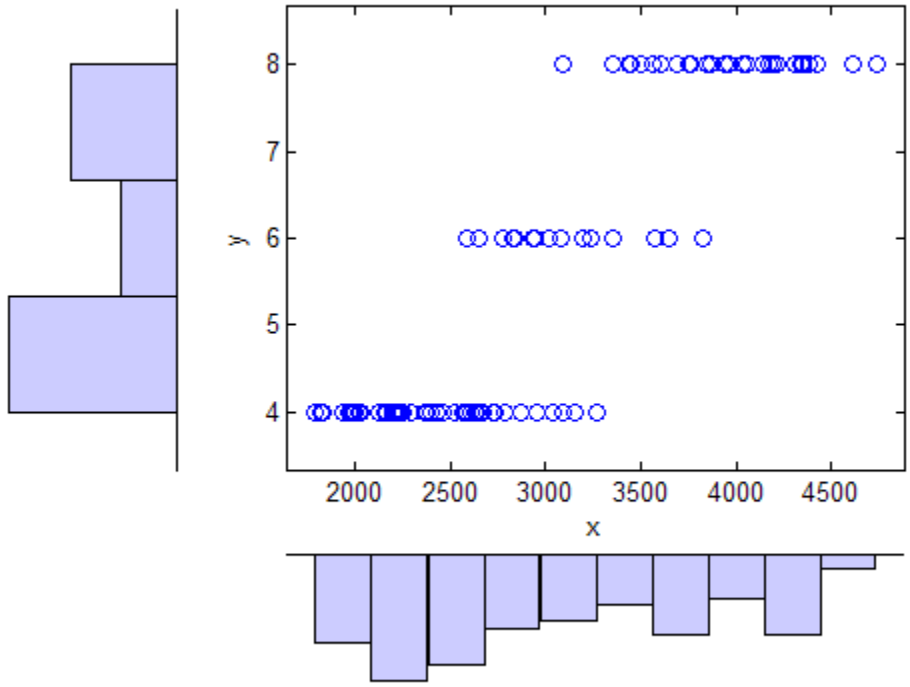
```
u = copularnd('Gaussian',.8,1000);
scatterhist(u(:,1),u(:,2),'Direction','out')
```



Example 3

Mixed discrete and continuous data:

```
load('carsmall');
scatterhist(Weight,Cylinders,'NBins',[10 3],'Direction','out')
```



See Also `scatter` | `hist`

Purpose

Scramble quasi-random point set

Syntax

```
ps = scramble(p,type)
ps = scramble(p,'clear')
ps = scramble(p)
```

Description

`ps = scramble(p,type)` returns a scrambled copy `ps` of the point set `p` of the `qrandset` class, created using the scramble type specified in the string *`type`*. Point sets from different subclasses of `qrandset` support different scramble types, as indicated in the following table.

Subclass	Scramble Types
`haltonset`	`'RR2'` — A permutation of the radical inverse coefficients derived by applying a reverse-radix operation to all of the possible coefficient values. The scramble is described in [1].
`sobolset`	`'MatousekAffineOwen'` — A random linear scramble combined with a random digital shift. The scramble is described in [2].

`ps = scramble(p,'clear')` removes all scramble settings from `p` and returns the result in `ps`.

`ps = scramble(p)` removes all scramble settings from `p` and then adds them back in the order they were originally applied. This typically results in a different point set because of the randomness of the scrambling algorithms.

Examples

Use `haltonset` to generate a 3-D Halton point set, skip the first 1000 values, and then retain every 101st point:

```
p = haltonset(3,'Skip',1e3,'Leap',1e2)
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
```

```
                Leap : 100
    ScrambleMethod : none
```

Use `scramble` to apply reverse-radix scrambling:

```
p = scramble(p,'RR2')
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
                Skip : 1000
                Leap : 100
    ScrambleMethod : RR2
```

Use `net` to generate the first four points:

```
X0 = net(p,4)
X0 =
    0.0928    0.6950    0.0029
    0.6958    0.2958    0.8269
    0.3013    0.6497    0.4141
    0.9087    0.7883    0.2166
```

Use parenthesis indexing to generate every third point, up to the 11th point:

```
X = p(1:3:11,:)
X =
    0.0928    0.6950    0.0029
    0.9087    0.7883    0.2166
    0.3843    0.9840    0.9878
    0.6831    0.7357    0.7923
```

References

[1] Kocis, L., and W. J. Whiten. "Computational Investigations of Low-Discrepancy Sequences." *ACM Transactions on Mathematical Software*. Vol. 23, No. 2, 1997, pp. 266–294.

[2] Matousek, J. "On the L2-Discrepancy for Anchored Boxes." *Journal of Complexity*. Vol. 14, No. 4, 1998, pp. 527–556.

See Also

`haltonset` | `sobolset`

qrandset.ScrambleMethod property

Purpose

Settings that control scrambling

Description

The `ScrambleMethod` property contains a structure that defines which scrambles to apply to the sequence. The structure consists of two fields:

- `Type`: A string containing the name of the scramble.
- `Options`: A cell array of parameter values for the scramble.

Different point sets support different scramble types as outlined in the help for each point set class. An error occurs if you set an invalid scramble type for a given point set.

The `ScrambleMethod` property also accepts an empty matrix as a value. This will clear all scrambling and set the property to contain a `(0x0)` structure.

The `scramble` method provides an alternative, easier way to set scrambles.

Examples

Apply a random linear scramble combined with a random digital shift to a `sobolset` point set class:

```
P = sobolset(5);
P = scramble(P, 'MatousekAffineOwen');
P.ScrambleMethod
```

See Also

`sobolset | scramble`

Purpose

Segments containing values

Syntax

```
S = segment(obj,X,P)
```

Description

`S = segment(obj,X,P)` returns an array `S` of integers indicating which segment of the piecewise distribution object `obj` contains each value of `X` or, alternatively, `P`. One of `X` and `P` must be empty (`[]`). If `X` is nonempty, `S` is determined by comparing `X` with the quantile boundary values defined for `obj`. If `P` is nonempty, `S` is determined by comparing `P` with the probability boundary values.

Examples

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);

pvals = 0:0.2:1;
s = segment(obj,[],pvals)
s =
     1     2     2     2     2     3
```

See Also

`paretotails` | `boundary` | `nsegments`

sequentialfs

Purpose

Sequential feature selection

Syntax

```
inmodel = sequentialfs(fun,X,y)
inmodel = sequentialfs(fun,X,Y,Z,...)
[inmodel,history] = sequentialfs(fun,X,...)
[] = sequentialfs(...,param1,val1,param2,val2,...)
```

Description

`inmodel = sequentialfs(fun,X,y)` selects a subset of features from the data matrix `X` that best predict the data in `y` by sequentially selecting features until there is no improvement in prediction. Rows of `X` correspond to observations; columns correspond to variables or features. `y` is a column vector of response values or class labels for each observation in `X`. `X` and `y` must have the same number of rows. `fun` is a function handle to a function that defines the criterion used to select features and to determine when to stop. The output `inmodel` is a logical vector indicating which features are finally chosen.

Starting from an empty feature set, `sequentialfs` creates candidate feature subsets by sequentially adding each of the features not yet selected. For each candidate feature subset, `sequentialfs` performs 10-fold cross-validation by repeatedly calling `fun` with different training subsets of `X` and `y`, `XTRAIN` and `ytrain`, and test subsets of `X` and `y`, `XTEST` and `ytest`, as follows:

```
criterion = fun(XTRAIN,ytrain,XTEST,ytest)
```

`XTRAIN` and `ytrain` contain the same subset of rows of `X` and `Y`, while `XTEST` and `ytest` contain the complementary subset of rows. `XTRAIN` and `XTEST` contain the data taken from the columns of `X` that correspond to the current candidate feature set.

Each time it is called, `fun` must return a scalar value `criterion`. Typically, `fun` uses `XTRAIN` and `ytrain` to train or fit a model, then predicts values for `XTEST` using that model, and finally returns some measure of distance, or *loss*, of those predicted values from `ytest`. In the cross-validation calculation for a given candidate feature set, `sequentialfs` sums the values returned by `fun` and divides that sum

by the total number of test observations. It then uses that mean value to evaluate each candidate feature subset.

Typical loss measures include sum of squared errors for regression models (`sequentialfs` computes the mean-squared error in this case), and the number of misclassified observations for classification models (`sequentialfs` computes the misclassification rate in this case).

Note `sequentialfs` divides the sum of the values returned by `fun` across all test sets by the total number of test observations. Accordingly, `fun` should not divide its output value by the number of test observations.

After computing the mean `criterion` values for each candidate feature subset, `sequentialfs` chooses the candidate feature subset that minimizes the mean criterion value. This process continues until adding more features does not decrease the criterion.

`inmodel = sequentialfs(fun,X,Y,Z,...)` allows any number of input variables `X`, `Y`, `Z`, ... `sequentialfs` chooses features (columns) only from `X`, but otherwise imposes no interpretation on `X`, `Y`, `Z`, ... All data inputs, whether column vectors or matrices, must have the same number of rows. `sequentialfs` calls `fun` with training and test subsets of `X`, `Y`, `Z`, ... as follows:

```
criterion = fun(XTRAIN,YTRAIN,ZTRAIN,...,
                XTEST,YTEST,ZTEST,...)
```

`sequentialfs` creates `XTRAIN`, `YTRAIN`, `ZTRAIN`, ... , `XTEST`, `YTEST`, `ZTEST`, ... by selecting subsets of the rows of `X`, `Y`, `Z`, ... `fun` must return a scalar value `criterion`, but may compute that value in any way. Elements of the logical vector `inmodel` correspond to columns of `X` and indicate which features are finally chosen.

`[inmodel,history] = sequentialfs(fun,X,...)` returns information on which feature is chosen at each step. `history` is a scalar structure with the following fields:

- `Crit` — A vector containing the criterion values computed at each step.
- `In` — A logical matrix in which row `i` indicates the features selected at step `i`.

`[] = sequentialfs(...,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs from the following table.

Parameter	Value
`'cv'`	The validation method used to compute the criterion for each candidate feature subset. • When the value is a positive integer `k`, `sequentialfs` uses `k`-fold cross-validation without stratification. • When the value is an object of the `cvpartition` class, other forms of cross-validation can be specified. • When the value is `'resubstitution'`, the original data are passed to `fun` as both the training and test data to compute the criterion. • When the value is `'none'`, `sequentialfs` calls `fun` as `criterion = fun(X,Y,Z,...)`, without separating test and training sets. The default value is `10`, that is, 10-fold cross-validation without stratification. So-called *wrapper methods* use a function `fun` that implements a learning algorithm. These methods usually apply cross-validation to select features. So-called *filter methods* use a function

Parameter	Value
	`fun` that measures characteristics of the data (such as correlation) to select features.
`'mcreps'`	A positive integer indicating the number of Monte-Carlo repetitions for cross-validation. The default value is `1`. The value must be `1` if the value of `'cv'` is `'resubstitution'` or `'none'`.
`'direction'`	The direction of the sequential search. The default is `'forward'`. A value of `'backward'` specifies an initial candidate set including all features and an algorithm that removes features sequentially until the criterion increases.
`'keepin'`	A logical vector or a vector of column numbers specifying features that must be included. The default is empty.
`'keepout'`	A logical vector or a vector of column numbers specifying features that must be excluded. The default is empty.
`'nfeatures'`	The number of features at which `sequentialfs` should stop. `inmodel` includes exactly this many features. The default value is empty, indicating that `sequentialfs` should stop when a local minimum of the criterion is found. A nonempty value overrides values of `'MaxIter'` and `'TolFun'` in `'options'`.
`'nullmodel'`	A logical value, indicating whether or not the null model (containing no features from `X`) should be included in feature selection and in the `history` output. The default is `false`.

Parameter	Value
'options'	Options structure for the iterative sequential search algorithm, as created by statset. sequentialfs uses the following statset parameters: • Display — Amount of information displayed by the algorithm. The default is 'off'. • MaxIter — Maximum number of iterations allowed. The default is Inf. • TolFun — Termination tolerance for the objective function value. The default is 1e-6 if 'direction' is 'forward'; 0 if 'direction' is 'backward'. • TolTypeFun — Use absolute or relative objective function tolerances. The default is 'rel'. • UseParallel — Set to 'always' to compute in parallel. Default is 'never'. • UseSubstreams — Set to 'always' to compute in parallel in a reproducible fashion. Default is 'never'. To compute reproducibly, set Streams to a type allowing substreams: 'mlfg6331_64' or 'mrg32k3a'. • Streams — A RandStream object or cell array consisting of one such object. If you do not specify Streams, sequentialfs uses the default stream. For more information on using parallel computing, see Chapter 17, "Parallel Statistics".

Examples

Perform sequential feature selection for classification of noisy features:

```
load fisheriris;
X = randn(150,10);
X(:,[1 3 5 7 ])= meas;
y = species;

c = cvpartition(y,'k',10);
opts = statset('display','iter');
fun = @(XT,yT,Xt,yt)...
      (sum(~strcmp(yt,classify(Xt,XT,yT,'quadratic'))));

[fs,history] = sequentialfs(fun,X,y,'cv',c,'options',opts)

Start forward sequential feature selection:
Initial columns included: none
Columns that can not be included: none
Step 1, added column 7, criterion value 0.04
Step 2, added column 5, criterion value 0.0266667
Final columns included:  5 7

fs =
     0  0  0  0  1  0  1  0  0  0
history =
      In: [2x10 logical]
    Crit: [0.0400 0.0267]

history.In
ans =
     0  0  0  0  0  0  1  0  0  0
     0  0  0  0  1  0  1  0  0  0
```

See Also

`crossval` | `cvpartition` | `stepwisefit` | `statset`

Tutorials

- "Example: Sequential Feature Selection" on page 10-24

How To

- "Sequential Feature Selection" on page 10-23

Purpose

Set and display properties

Syntax

```
set(A)
set(A,PropertyName)
A = set(A,PropertyName,PropertyValue,...)
B = set(A,PropertyName,value)
```

Description

`set(A)` displays all properties of the dataset array `A` and their possible values.

`set(A,PropertyName)` displays possible values for the property specified by the string *`PropertyName`*.

`A = set(A,PropertyName,PropertyValue,...)` sets property name/value pairs.

`B = set(A,PropertyName,value)` returns a dataset array `B` that is a copy of `A`, but with the property `'PropertyName'` set to the value `value`.

Note Using `set(A,'PropertyName',value)` without assigning to a variable does not modify A's properties. Use `A = set(A,'PropertyName',value)` to modify `A`.

Examples

Create a dataset array from Fisher's iris data and add a description:

```
load fisheriris
NumObs = size(meas,1);
NameObs = strcat({'Obs'},num2str((1:NumObs)','%-d'));
iris = dataset({nominal(species),'species'},...
               {meas,'SL','SW','PL','PW'},...
               'ObsNames',NameObs);
iris = set(iris,'Description','Fisher''s Iris Data');
get(iris)
   Description: 'Fisher's Iris Data'
   Units: {}
   DimNames: {'Observations' 'Variables'}
```

```
    UserData: []
    ObsNames: {150x1 cell}
    VarNames: {'species' 'SL' 'SW' 'PL' 'PW'}
```

See Also

get | summary

CompactTreeBagger.SetDefaultYfit

Purpose

Set default value for `predict`

Syntax

```
B = SetDefaultYfit(B,Yfit)
```

Description

`B = SetDefaultYfit(B,Yfit)` sets the default prediction for ensemble `B` to `Yfit`. The default prediction must be a character variable for classification or a numeric scalar for regression. This setting controls what predicted value `CompactTreeBagger` returns when no prediction is possible, for example when the `predict` method needs to predict for an observation which has only false values in the matrix supplied through `'useifort'` argument.

See Also

`predict` | `TreeBagger.DefaultYfit`

Purpose

Set difference for categorical arrays

Syntax

```
C = setdiff(A,B)
[C,I] = setdiff(A,B)
```

Description

`C = setdiff(A,B)` when `A` and `B` are categorical arrays returns a categorical vector `C` containing the values in `A` that are not in `B`. The result `C` is sorted. The set of categorical levels for `C` is the sorted union of the sets of levels of the inputs, as determined by their labels.

`[C,I] = setdiff(A,B)` also returns index vectors I such that `C = A(I)`.

See Also

`intersect` | `ismember` | `setxor` | `union` | `unique`

categorical.setlabels

Purpose

Label levels

Syntax

```
A = setlabels(A,labels)
A = setlabels(A,labels,levels)
```

Description

`A = setlabels(A,labels)` labels the levels in the categorical array `A` using the cell array of strings or 2-D character matrix `labels`. Labels are assigned in the order given in `labels`.

`A = setlabels(A,labels,levels)` labels only the levels specified in the cell array of strings or 2-D character matrix `levels`.

Examples

Example 1

Relabel the species in Fisher's iris data using new categories:

```
load fisheriris
species = nominal(species);
species = mergelevels(...
          species,{'setosa','virginica'},'parent');
species = setlabels(species,'hybrid','versicolor');
getlabels(species)
ans =
    'hybrid'    'parent'
```

Example 2

1. Load patient data from the CSV file `hospital.dat` and store the information in a dataset array with observation names given by the first column in the data (patient identification):

   ```
   patients = dataset('file','hospital.dat',...
                      'delimiter',',',...
                      'ReadObsNames',true);
   ```

2. Make the {0,1}-valued variable `smoke` nominal, and change the labels to `'No'` and `'Yes'`:

   ```
   patients.smoke = nominal(patients.smoke,{'No','Yes'});
   ```

3 Add new levels to `smoke` as placeholders for more detailed histories of smokers:

```
patients.smoke = addlevels(patients.smoke,...
                 {'0-5 Years','5-10 Years','LongTerm'});
```

4 Assuming the nonsmokers have never smoked, relabel the `'No'` level:

```
patients.smoke = setlabels(patients.smoke,'Never','No');
```

5 Drop the undifferentiated `'Yes'` level from `smoke`:

```
patients.smoke = droplevels(patients.smoke,'Yes');

Warning: OLDLEVELS contains categorical levels that
were present in A, caused some array elements to have
undefined levels.
```

Note that smokers now have an undefined level.

6 Set each smoker to one of the new levels, by observation name:

```
patients.smoke('YPL-320') = '5-10 Years';
```

See Also

`getlabels`

categorical.setxor

Purpose

Set exclusive-or for categorical arrays

Syntax

```
C = setxor(A,B)
[C,IA,IB] = setxor(A,B)
```

Description

`C = setxor(A,B)` when `A` and `B` are categorical arrays returns a categorical vector `C` containing the values not in the intersection of `A` and `B`. The result `C` is sorted. The set of categorical levels for `C` is the sorted union of the sets of levels of the inputs, as determined by their labels.

`[C,IA,IB] = setxor(A,B)` also returns index vectors `IA` and `IB` such that `C` is a sorted combination of the elements `A(IA)` and `B(IB)`.

See Also

`intersect` | `ismember` | `setdiff` | `union` | `unique`

Purpose

`true` if all covariance matrices are restricted to be the same

Description

Logical `true` if all the covariance matrices are restricted to be the same (pooled estimate); logical `false` otherwise.

categorical.shiftdim

Purpose

Shift dimensions of categorical array

Syntax

```
B = shiftdim(A,n)
[B,nshifts] = shiftdim(A)
```

Description

`B = shiftdim(A,n)` shifts the dimensions of the categorical array `A` by `N`. When `n` is positive, `shiftdim` shifts the dimensions to the left and wraps the `n` leading dimensions to the end. When `n` is negative, `shiftdim` shifts the dimensions to the right and pads with singletons.

`[B,nshifts] = shiftdim(A)` returns the array `B` with the same number of elements as `A` but with any leading singleton dimensions removed. `nshifts` returns the number of dimensions that are removed. If `A` is a scalar, `shiftdim` has no effect.

See Also

`circshift` | `reshape` | `squeeze`

Purpose

Prune ensemble

Syntax

```
cmp = shrink(ens)
cmp = shrink(ens,Name,Value)
```

Description

`cmp = shrink(ens)` returns a compact shrunken version of `ens`, a regularized ensemble. `cmp` retains only learners with weights above a threshold.

`cmp = shrink(ens,Name,Value)` returns an ensemble with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`lambda`

Vector of nonnegative regularization parameter values for lasso. If `ens.Regularization` is nonempty (populate it with `regularize`), `shrink` regularizes `ens` using `lambda`. If `ens` contains a `Regularization` structure, you cannot pass `lambda`.

Default: `[]`

`threshold`

Lower cutoff on weights for weak learners, a numeric nonnegative scalar. `shrink` creates `cmp` from those learners with weights above `threshold`.

Default: `0`

`weightcolumn`

Column index of `ens.Regularization.TrainedWeights`, a positive integer. `shrink` creates `cmp` with learner weights from this column.

Default: `1`

Output Arguments

`cmp`

A regression ensemble of class `CompactRegressionEnsemble`. Use `cmp` for making predictions exactly as you use `ens`, with the `predict` method.

Examples

Shrink a 300-member bagged regression ensemble using `0.1` for the parameter `lambda`, and view the number of members of the resulting ensemble:

```
X = rand(2000,20);
Y = repmat(-1,2000,1);
Y(sum(X(:,1:5),2)>2.5) = 1;
bag = fitensemble(X,Y,'Bag',300,'Tree','type','regression');
cmp = shrink(bag,'lambda',0.1);
cmp.NTrained

ans =
    83
```

See Also

`regularize` | `cvshrink` | `predict`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Input array of covariances

Description

Input array of covariances `SIGMA`.

signrank

Purpose

Wilcoxon signed rank test

Syntax

```
p = signrank(x)
p = signrank(x,m)
p = signrank(x,y)
[p,h] = signrank(...)
[p,h] = signrank(...,'alpha',alpha)
[p,h] = signrank(...,'method',method)
[p,h,stats] = signrank(...)
```

Description

`p = signrank(x)` performs a two-sided signed rank test of the null hypothesis that data in the vector `x` comes from a continuous, symmetric distribution with zero median, against the alternative that the distribution does not have zero median. The *p* value of the test is returned in `p`.

`p = signrank(x,m)` performs a two-sided signed rank test of the null hypothesis that data in the vectors `x` and `y` are independent samples from a continuous, symmetric distribution with median `m`, against the alternative that the distribution does not have median `m`. `m` must be a scalar.

`p = signrank(x,y)` performs a paired, two-sided signed rank test of the null hypothesis that data in the vector `x-y` come from a continuous, symmetric distribution with zero median, against the alternative that the distribution does not have zero median. `x` and `y` must have equal lengths. Note that a hypothesis of zero median for `x-y` is not equivalent to a hypothesis of equal median for `x` and `y`.

`[p,h] = signrank(...)` returns the result of the test in `h`. `h = 1` indicates a rejection of the null hypothesis at the 5% significance level. `h = 0` indicates a failure to reject the null hypothesis at the 5% significance level.

`[p,h] = signrank(...,'alpha',alpha)` performs the test at the (100*`alpha`)% significance level. The default, when unspecified, is `alpha = 0.05`.

`[p,h] = signrank(...,'method',method)` computes the *p* value using either an exact algorithm, when *method* is `'exact'`, or a normal approximation, when *method* is `'approximate'`. The default, when unspecified, is the exact method for small samples and the approximate method for large samples.

`[p,h,stats] = signrank(...)` returns the structure `stats` with the following fields:

- `signedrank` — Value of the signed rank test statistic
- `zval` — Value of the *z*-statistic (computed only for large samples)

Examples

Test the hypothesis of zero median for the difference between two paired samples.

```
before = lognrnd(2,.25,10,1);
after = before+trnd(2,10,1);
[p,h] = signrank(before,after)
p =
   0.5566
h =
   0
```

The sampling distribution of the difference between `before` and `after` is symmetric with zero median. At the default 5% significance level, the test fails to reject to the null hypothesis of zero median in the difference.

References

[1] Gibbons, J. D. *Nonparametric Statistical Inference*. New York: Marcel Dekker, 1985.

[2] Hollander, M., and D. A. Wolfe. *Nonparametric Statistical Methods*. Hoboken, NJ: John Wiley & Sons, Inc., 1999.

See Also

`ranksum` | `ttest` | `ztest`

signtest

Purpose

Sign test

Syntax

```
p = signtest(x)
p = signtest(x,m)
p = signtest(x,y)
[p,h] = signtest(...)
[p,h] = signtest(...,'alpha',alpha)
[p,h] = signtest(...,'method',method)
[p,h,stats] = signtest(...)
```

Description

`p = signtest(x)` performs a two-sided sign test of the null hypothesis that data in the vector `x` come from a continuous distribution with zero median, against the alternative that the distribution does not have zero median. The *p* value of the test is returned in `p`

`p = signtest(x,m)` performs a two-sided sign test of the null hypothesis that data in the vector `x` come from a continuous distribution with median `m`, against the alternative that the distribution does not have median `m`. `m` must be a scalar.

`p = signtest(x,y)` performs a paired, two-sided sign test of the null hypothesis that data in the vector `x-y` come from a continuous distribution with zero median, against the alternative that the distribution does not have zero median. `x` and `y` must be the same length. Note that a hypothesis of zero median for `x-y` is not equivalent to a hypothesis of equal median for `x` and `y`.

`[p,h] = signtest(...)` returns the result of the test in `h`. `h = 1` indicates a rejection of the null hypothesis at the 5% significance level. `h = 0` indicates a failure to reject the null hypothesis at the 5% significance level.

`[p,h] = signtest(...,'alpha',alpha)` performs the test at the (100*`alpha`)% significance level. The default, when unspecified, is `alpha = 0.05`.

`[p,h] = signtest(...,'method',method)` computes the *p* value using either an exact algorithm, when *`method`* is `'exact'`, or a normal approximation, when `method` is `'approximate'`. The default, when

unspecified, is the exact method for small samples and the approximate method for large samples.

`[p,h,stats] = signtest(...)` returns the structure `stats` with the following fields:

- `sign` — Value of the sign test statistic
- `zval` — Value of the *z*-statistic (computed only for large samples)

Examples

Test the hypothesis of zero median for the difference between two paired samples.

```
before = lognrnd(2,.25,10,1);
after = before + (lognrnd(0,.5,10,1) - 1);
[p,h] = signtest(before,after)
p =
   0.3438
h =
   0
```

The sampling distribution of the difference between `before` and `after` is symmetric with zero median. At the default 5% significance level, the test fails to reject to the null hypothesis of zero median in the difference.

References

[1] Gibbons, J. D. *Nonparametric Statistical Inference*. New York: Marcel Dekker, 1985.

[2] Hollander, M., and D. A. Wolfe. *Nonparametric Statistical Methods*. Hoboken, NJ: John Wiley & Sons, Inc., 1999.

See Also

`ranksum` | `signrank` | `ttest` | `ztest`

Purpose

Silhouette plot

Syntax

```
silhouette(X,clust)
s = silhouette(X,clust)
[s,h] = silhouette(X,clust)
[...] = silhouette(X,clust,metric)
[...] = silhouette(X,clust,distfun,p1,p2,...)
```

Description

`silhouette(X,clust)` plots cluster silhouettes for the *n*-by-*p* data matrix `X`, with clusters defined by `clust`. Rows of `X` correspond to points, columns correspond to coordinates. `clust` can be a categorical variable, numeric vector, character matrix, or cell array of strings containing a cluster name for each point. (See "Grouped Data" on page 2-34.) `silhouette` treats `NaN`s or empty strings in `clust` as missing values, and ignores the corresponding rows of `X`. By default, `silhouette` uses the squared Euclidean distance between points in `X`.

`s = silhouette(X,clust)` returns the silhouette values in the *n*-by-1 vector `s`, but does not plot the cluster silhouettes.

`[s,h] = silhouette(X,clust)` plots the silhouettes, and returns the silhouette values in the *n*-by-1 vector `s`, and the figure handle in `h`.

`[...] = silhouette(X,clust,metric)` plots the silhouettes using the inter-point distance function specified in *`metric`*. Choices for *`metric`* are given in the following table.

Metric	Description
`'Euclidean'`	Euclidean distance
`'sqEuclidean'`	Squared Euclidean distance (default)
`'cityblock'`	Sum of absolute differences
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors)
`'correlation'`	One minus the sample correlation between points (treated as sequences of values)

Metric	Description
'Hamming'	Percentage of coordinates that differ
'Jaccard'	Percentage of nonzero coordinates that differ
Vector	A numeric distance matrix in upper triangular vector form, such as is created by pdist. X is not used in this case, and can safely be set to [].

For more information on each metric, see "Distance Metrics" on page 13-9.

`[...] = silhouette(X,clust,distfun,p1,p2,...)` accepts a function handle `distfun` to a metric of the form

```
d = distfun(X0,X,p1,p2,...)
```

where `X0` is a `1`-by-`p` point, `X` is an `n`-by-`p` matrix of points, and `p1,p2,...` are optional additional arguments. The function `distfun` returns an `n`-by-`1` vector `d` of distances between `X0` and each point (row) in `X`. The arguments `p1`, `p2,...` are passed directly to the function `distfun`.

Tips

The silhouette value for each point is a measure of how similar that point is to points in its own cluster compared to points in other clusters, and ranges from -1 to +1. It is defined as

```
S(i) = (min(b(i,:),2) - a(i)) ./ max(a(i),min(b(i,:)))
```

where `a(i)` is the average distance from the `i`th point to the other points in its cluster, and `b(i,k)` is the average distance from the `i`th point to points in another cluster `k`.

Examples

```
X = [randn(10,2)+ones(10,2);
randn(10,2)-ones(10,2)];
cidx = kmeans(X,2,'distance','sqeuclid');
s = silhouette(X,cidx,'sqeuclid');
```

References

[1] Kaufman L., and P. J. Rousseeuw. *Finding Groups in Data: An Introduction to Cluster Analysis*. Hoboken, NJ: John Wiley & Sons, Inc., 1990.

See Also

`dendrogram` | `kmeans` | `linkage` | `pdist`

How To

- "Grouped Data" on page 2-34

Purpose

Convert categorical array to single array

Syntax

```
B = single(A)
```

Description

`B = single(A)` converts the categorical array `A` to a single array. Each element of `B` contains the internal categorical level code for the corresponding element of `A`.

See Also

`double`

dataset.single

Purpose

Convert dataset variables to single array

Syntax

```
B = single(A)
B = single(A,vars)
```

Description

`B = single(A)` returns the contents of the dataset `A`, converted to one single array. The classes of the variables in the dataset must support the conversion.

`B = single(A,vars)` returns the contents of the dataset variables specified by `vars`. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

See Also

`dataset` | `double` | `replacedata`

Purpose

Size of categorical array

Syntax

```
d = size(A)
[m,n] = size(A)
[m1,m2,m3,...,mn] = size(A)
m = size(A,dim)
```

Description

`d = size(A)` returns the two-element row vector `d = [m,n]` containing the number of rows and columns in the matrix for an `m`-by-`n` categorical matrix `A`. For `n`-D categorical arrays, `size(A)` returns a 1-by-`n` vector of dimension lengths. Trailing singleton dimensions are ignored.

`[m,n] = size(A)` for a categorical matrix `A`, returns the number of rows and columns in `A` as separate output variables.

`[m1,m2,m3,...,mn] = size(A)`, for `n>1`, returns the sizes of the first `n` dimensions of the categorical array `A`. If the number of output arguments `n` does not equal `ndims(A)`, then for:

`n > ndims(A)`	`size` returns ones in the "extra" variables, i.e., outputs `ndims(A)+1` through `n`.
`n < ndims(A)`	`mn` contains the product of the sizes of dimensions `n` through `ndims(A)`.

`m = size(A,dim)` returns the length of the dimension specified by the scalar `dim`. For example, `size(A,1)` returns the number of rows. If `dim > ndims(A)`, `m` will be 1.

See Also

`length` | `ndims` | `numel`

dataset.size

Purpose

Size of dataset array

Syntax

```
D = SIZE(A)
[NOBS,NVARS] = SIZE(A)
[M1,M2,M3,...,MN] = SIZE(A)
M = size(A,dim)
```

Description

`D = SIZE(A)` returns the two-element row vector `D = [NOBS,NVARS]` containing the number of observations and number of variables in the dataset `A`. A dataset array always has two dimensions.

`[NOBS,NVARS] = SIZE(A)` returns the numbers of observations and variables in the dataset `A` as separate output variables.

`[M1,M2,M3,...,MN] = SIZE(A)`, for `N > 2`, returns `M1 = NOBS`, `M2 = NVARS`, and `M3,..,MN = 1`.

`M = size(A,dim)` returns the length of the dimension specified by the scalar `dim`:

- `M = size(A,1)` returns `NOBS`
- `M = size(A,2)` returns `NVARS`
- `M = size(A,k)` returns `1` for `k > 2`

See Also

`length` | `ndims` | `numel`

Purpose

Number of dimensions in matrix

Syntax

```
d = size(p)
[m,n] = size(p)
m = size(p,dim)
```

Description

`d = size(p)` returns the two-element row vector `d = [m,n]` containing the number of points in the point set and the number of dimensions the points are in, for the point set `p`. These correspond to the number of rows and columns in the matrix that would be produced by the expression `p(:,:)`.

`[m,n] = size(p)` returns the number of points and dimensions for `p` as separate output variables.

`m = size(p,dim)` returns the length of the dimension specified by the scalar `dim`. For example, `size(p,1)` returns the number of rows (points in the point set). If `dim` is greater than 2, `m` will be 1.

Examples

The commands

```
P = sobolset(12);
d = size(P)
```

return

```
d = [9.0072e+015 12]
```

The command

```
[m,n] = size(P)
```

returns

```
m = 9.0072e+015
n = 12
```

The command

```
m2 = size(P, 2)
```

returns

```
m2 = 12
```

See Also

length | ndims | qrandset

Purpose

Slice sampler

Syntax

```
rnd = slicesample(initial,nsamples,'pdf',pdf)
rnd = slicesample(initial,nsamples,'logpdf',logpdf)
[rnd,neval] = slicesample(initial,...)
[rnd,neval] = slicesample(initial,...,Name,Value)
```

Description

`rnd = slicesample(initial,nsamples,'pdf',pdf)` generates `nsamples` random samples using the slice sampling method (see "Algorithms" on page 20-1777). `pdf` gives the target probability density function (pdf). `initial` is a row vector or scalar containing the initial value of the random sample sequences.

`rnd = slicesample(initial,nsamples,'logpdf',logpdf)` generates samples using the logarithm of the pdf.

`[rnd,neval] = slicesample(initial,...)` returns the average number of function evaluations that occurred in the slice sampling.

`[rnd,neval] = slicesample(initial,...,Name,Value)` generates random samples with additional options specified by one or more `Name,Value` pair arguments.

Tips

- There are no definitive suggestions for choosing appropriate values for `burnin`, `thin`, or `width`. Choose starting values of `burnin` and `thin`, and increase them, if necessary, to give the requisite independence and marginal distributions. See Neal [1] for details of the effect of adjusting `width`.

Input Arguments

`initial`

Initial point, a scalar or row vector. Set `initial` so `pdf(initial)` is a strictly positive scalar. `length(initial)` is the number of dimensions of each sample.

`nsamples`

Positive integer, the number of samples that `slicesample` generates.

`pdf`

Handle to a function that generates the probability density function, specified with `@`. `pdf` can be unnormalized, meaning it need not integrate to `1`.

`logpdf`

Handle to a function that generates the logarithm of the probability density function, specified with `@`. `logpdf` can be the logarithm of an unnormalized pdf.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`burnin`

Nonnegative integer, the number of samples to generate and discard before generating the samples to return. The slice sampling algorithm is a Markov chain whose stationary distribution is proportional to that of the `pdf` argument. Set `burnin` to a high enough value that you believe the Markov chain approximately reaches stationarity after `burnin` samples.

Default: `0`

`thin`

Positive integer, where `slicesample` discards every `thin - 1` samples and returns the next. The slice sampling algorithm is a Markov chain, so the samples are serially correlated. To reduce the serial correlation, choose a larger value of `thin`.

Default: `1`

`width`

Width of the interval around the current sample, a scalar or vector of positive values. `slicesample` begins with this interval and searches for an appropriate region containing the points of `pdf` that evaluate to a large enough value.

- If `width` is a scalar and the samples have multiple dimensions, `slicesample` uses `width` for each dimension.
- If `width` is a vector, it should have the same length as `initial`.

Default: `10`

Output Arguments

`rnd`

`nsamples`-by-`length(initial)` matrix, where each row is one sample.

`neval`

Scalar, the mean number of function evaluations per sample. `neval` includes the `burnin` and `thin` evaluations, not just the evaluations of samples returned in `rnd`. Therefore the total number of function evaluations is

```
neval*(nsamples*thin + burnin).
```

Examples

Generate random samples from a multimodal density using `slicesample`.

1 Define a function proportional to a multimodal density:

```
f = @(x) exp(-x.^2/2).*(1 + (sin(3*x)).^2).*...
    (1 + (cos(5*x).^2));
area = quad(f,-5,5);
```

2 Generate 2000 samples from the density, using a burn-in period of 1000, and keeping one in five samples:

```
N = 2000;
```

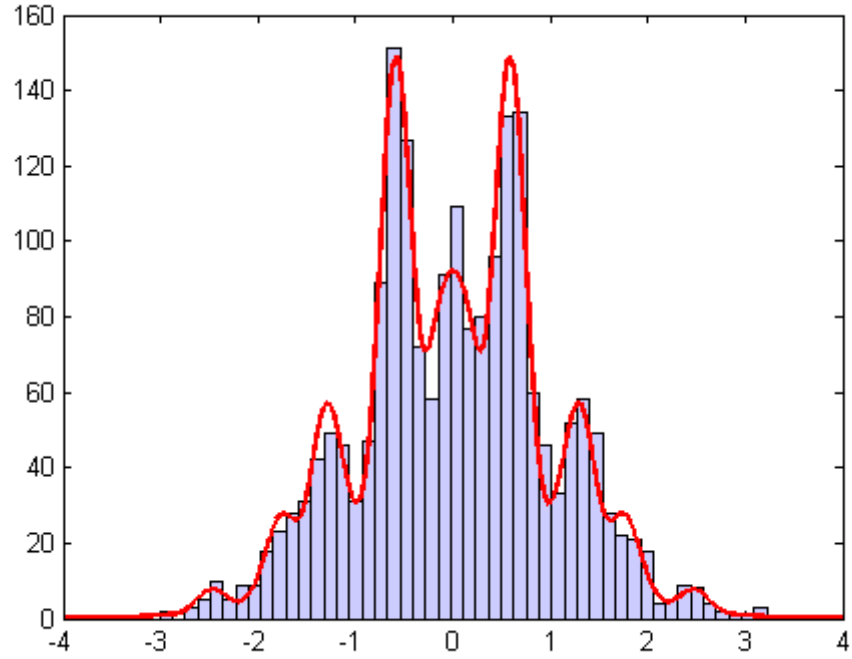
```
x = slicesample(1,N,'pdf',f,'thin',5,'burnin',1000);
```

3 Plot a histogram of the sample:

```
[binheight,bincenter] = hist(x,50);
h = bar(bincenter,binheight,'hist');
set(h,'facecolor',[0.8 .8 1]);
```

4 Scale the density to have the same area as the histogram, and superimpose it on the histogram:

```
hold on
xd = get(gca,'XLim');
xgrid = linspace(xd(1),xd(2),1000);
binwidth = (bincenter(2)-bincenter(1));
y = (N*binwidth/area) * f(xgrid);
plot(xgrid,y,'r','LineWidth',2)
hold off
```



The samples seem to fit the theoretical distribution well, so the `burnin` value seems adequate.

Algorithms

At each point in the sequence of random samples, `slicesample` selects the next point by "slicing" the density to form a neighborhood around the previous point where the density is above some value. Consequently, the sample points are not independent. Nearby points in the sequence tend to be closer together than they would be from a sample of independent values. For many purposes, the entire set of points can be used as a sample from the target distribution. However, when this type of serial correlation is a problem, the `burnin` and `thin` parameters can help reduce that correlation.

`slicesample` uses the slice sampling algorithm of Neal [1]. For numerical stability, it converts a `pdf` function into a `logpdf` function. The algorithm to resize the support region for each level, called "stepping-out" and "stepping-in," was suggested by Neal.

References

[1] Neal, Radford M. *Slice Sampling*. Ann. Stat. Vol. 31, No. 3, pp. 705–767, 2003. Available at Project Euclid.

See Also

`mhsample` | `rand` | `randsample`

Purpose

Skewness

Syntax

```
y = skewness(X)
y = skewness(X,flag)
```

Description

`y = skewness(X)` returns the sample skewness of `X`. For vectors, `skewness(x)` is the skewness of the elements of `x`. For matrices, `skewness(X)` is a row vector containing the sample skewness of each column. For N-dimensional arrays, `skewness` operates along the first nonsingleton dimension of `X`.

`y = skewness(X,flag)` specifies whether to correct for bias (`flag = 0`) or not (`flag = 1`, the default). When `X` represents a sample from a population, the skewness of `X` is biased; that is, it will tend to differ from the population skewness by a systematic amount that depends on the size of the sample. You can set `flag = 0` to correct for this systematic bias.

`skewness(X,flag,dim)` takes the skewness along dimension `dim` of `X`.

`skewness` treats `NaN`s as missing values and removes them.

Algorithms

Skewness is a measure of the asymmetry of the data around the sample mean. If skewness is negative, the data are spread out more to the left of the mean than to the right. If skewness is positive, the data are spread out more to the right. The skewness of the normal distribution (or any perfectly symmetric distribution) is zero.

The skewness of a distribution is defined as

$$s = \frac{E(x-\mu)^3}{\sigma^3}$$

where μ is the mean of x, σ is the standard deviation of x, and $E(t)$ represents the expected value of the quantity t. `skewness` computes a sample version of this population value.

When you set `flag` to 1, the following equation applies:

$$s_1 = \frac{\frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^3}{\left(\sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^2}\right)^3}$$

When you set `flag` to 0, the following equation applies:

$$s_0 = \frac{\sqrt{n(n-1)}}{n-2} s_1$$

This bias-corrected formula requires that `X` contain at least three elements.

Examples

```
X = randn([5 4])
X =
  1.1650  1.6961 -1.4462 -0.3600
  0.6268  0.0591 -0.7012 -0.1356
  0.0751  1.7971  1.2460 -1.3493
  0.3516  0.2641 -0.6390 -1.2704
 -0.6965  0.8717  0.5774  0.9846

y = skewness(X)
y =
  -0.2933  0.0482  0.2735  0.4641
```

See Also

`kurtosis` | `mean` | `moment` | `std` | `var`

Purpose

Number of initial points to omit from sequence

Description

The `Skip` property of a point set contains a positive integer which specifies the number of initial points in the sequence to omit from the point set. The default `Skip` value is 0.

Initial points of a sequence sometimes exhibit undesirable properties, for example the first point is often `(0,0,0,...)` and this may "unbalance" the sequence since its counterpart, `(1,1,1,...)`, never appears. Another common reason is that initial points often exhibit correlations among different dimensions which disappear later in the sequence.

Examples

Examine the difference between skipping and not skipping points:

```
% No skipping produces the standard Sobol sequence.
P = sobolset(5);
P(1:3,:)

% Skip the first point of the sequence.  The point set now
% starts at the second point of the basic Sobol sequence.
P.Skip = 1;
P(1:3,:)
```

See Also

`Leap` | `net` | `qrandset` | `subsref`

sobolset

Superclasses

qrandset

Purpose

Sobol quasi-random point sets

Description

`sobolset` is a quasi-random point set class that produces points from the Sobol sequence. The Sobol sequence is a base-2 digital sequence that fills space in a highly uniform manner.

Construction

sobolset	Construct Sobol quasi-random point set

Methods

Inherited Methods

Methods in the following table are inherited from `qrandset`.

disp	Display qrandset object
end	Last index in indexing expression for point set
length	Length of point set
ndims	Number of dimensions in matrix
net	Generate quasi-random point set
scramble	Scramble quasi-random point set
size	Number of dimensions in matrix
subsref	Subscripted reference for qrandset

Properties

PointOrder	Point generation method

Inherited Properties

Properties in the following table are inherited from `qrandset`.

Dimensions	Number of dimensions
Leap	Interval between points
ScrambleMethod	Settings that control scrambling
Skip	Number of initial points to omit from sequence
Type	Name of sequence on which point set `P` is based

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

References

[1] Bratley, P., and B. L. Fox, "ALGORITHM 659 Implementing Sobol's Quasirandom Sequence Generator," ACM Transactions on Mathematical Software, Vol. 14, No. 1, pp. 88-100, 1988.

[2] Joe, S., and F. Y. Kuo, "Remark on Algorithm 659: Implementing Sobol's Quasirandom Sequence Generator," ACM Transactions on Mathematical Software, Vol. 29, No. 1, pp. 49-57, 2003.

[3] Hong, H. S., and F. J. Hickernell, "ALGORITHM 823: Implementing Scrambled Digital Sequences," ACM Transactions on Mathematical Software, Vol. 29, No. 2, pp. 95-109, 2003.

[4] Matousek, J., "On the L2-discrepancy for anchored boxes," Journal of Complexity, Vol. 14, pp. 527-556, 1998.

See Also

`haltonset`

How To

- "Quasi-Random Point Sets" on page 6-16

sobolset

Purpose

Construct Sobol quasi-random point set

Syntax

```
p = sobolset(d)
p = sobolset(d,prop1,val1,prop2,val2,...)
```

Description

`p = sobolset(d)` constructs a `d`-dimensional point set `p` of the `sobolset` class, with default property settings.

`p = sobolset(d,prop1,val1,prop2,val2,...)` specifies property name/value pairs used to construct `p`.

The object `p` returned by `sobolset` encapsulates properties of a specified quasi-random sequence. The point set is finite, with a length determined by the `Skip` and `Leap` properties and by limits on the size of point set indices (maximum value of 2^{53}). Values of the point set are not generated and stored in memory until you access `p` using `net` or parenthesis indexing.

Examples

Generate a 3-D Sobol point set, skip the first 1000 values, and then retain every 101st point:

```
p = sobolset(3,'Skip',1e3,'Leap',1e2)
p =
    Sobol point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none
        PointOrder : standard
```

Use `scramble` to apply a random linear scramble combined with a random digital shift:

```
p = scramble(p,'MatousekAffineOwen')
p =
    Sobol point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
```

```
              Leap : 100
     ScrambleMethod : MatousekAffineOwen
         PointOrder : standard
```

Use `net` to generate the first four points:

```
X0 = net(p,4)
X0 =
    0.7601    0.5919    0.9529
    0.1795    0.0856    0.0491
    0.5488    0.0785    0.8483
    0.3882    0.8771    0.8755
```

Use parenthesis indexing to generate every third point, up to the 11th point:

```
X = p(1:3:11,:)
X =
    0.7601    0.5919    0.9529
    0.3882    0.8771    0.8755
    0.6905    0.4951    0.8464
    0.1955    0.5679    0.3192
```

References

[1] Bratley, P., and B. L. Fox. "Algorithm 659 Implementing Sobol's Quasirandom Sequence Generator." *ACM Transactions on Mathematical Software*. Vol. 14, No. 1, 1988, pp. 88–100.

[2] Joe, S., and F. Y. Kuo. "Remark on Algorithm 659: Implementing Sobol's Quasirandom Sequence Generator." *ACM Transactions on Mathematical Software*. Vol. 29, No. 1, 2003, pp. 49–57.

[3] Hong, H. S., and F. J. Hickernell. "Algorithm 823: Implementing Scrambled Digital Sequences." *ACM Transactions on Mathematical Software*. Vol. 29, No. 2, 2003, pp. 95–109.

[4] Matousek, J. "On the L2-Discrepancy for Anchored Boxes." *Journal of Complexity*. Vol. 14, No. 4, 1998, pp. 527–556.

See Also

haltonset | net | scramble

Purpose

Sort elements of ordinal array

Syntax

```
B = sort(A)
B = sort(A,dim)
B = sort(A,dim,mode)
[B,I] = sort(A,...)
```

Description

`B = sort(A)`, when `A` is an ordinal vector, sorts the elements of `A` in ascending order. For ordinal matrices, `sort(A)` sorts each column of `A` in ascending order. For *N*-D ordinal arrays, `sort(A)` sorts the along the first nonsingleton dimension of `A`. `B` is an ordinal array with the same levels as `A`.

`B = sort(A,dim)` sorts `A` along dimension `dim`.

`B = sort(A,dim,mode)` sorts `A` in the order specified by `mode`. `mode` is `'ascend'` for ascending order, or `'descend'` for descending order.

`[B,I] = sort(A,...)` also returns an index matrix `I`. If `A` is a vector, then `B = A(I)`. If `A` is an *m*-by-*n* matrix and `dim` is `1`, then `B(:,j) = A(I(:,j),j)` for `j = 1:n`.

Elements with undefined levels are sorted to the end.

Examples

Sort the columns of an ordinal array in ascending order:

```
A = ordinal([6 2 5; 2 4 1; 3 2 4],...
            {'lo','med','hi'},[],[0 2 4 6])
A =
     hi       med      hi
     med      hi       lo
     med      med      hi

B = sort(A)
B =
     med      med      lo
     med      med      hi
     hi       hi       hi
```

See Also

sortrows

Purpose

Sort rows of dataset array

Syntax

```
B = sortrows(A)
B = sortrows(A,vars)
B = sortrows(A,'obsnames')
B = sortrows(A,vars,mode)
[B,idx] = sortrows(A)
```

Description

`B = sortrows(A)` returns a copy of the dataset array `A`, with the observations sorted in ascending order by all of the variables in `A`. The observations in `B` are sorted first by the first variable, next by the second variable, and so on. The variables in `A` must be scalar valued (i.e., column vectors) and be from a class for which a `sort` method exists.

`B = sortrows(A,vars)` sorts the observations in `A` by the variables specified by `vars`. `vars` is a positive integer, a vector of positive integers, variable names, a cell array containing one or more variable names, or a logical vector.

`B = sortrows(A,'obsnames')` sorts the observations in `A` by observation name.

`B = sortrows(A,vars,mode)` sorts in the direction specified by *`mode`*. *`mode`* is `'ascend'` (the default) or `'descend'`. Use `[]` for `vars` to sort using all variables.

`[B,idx] = sortrows(A)` also returns an index vector `idx` such that `B = A(idx,:)`.

Examples

Sort the data in `hospital.mat` by age and then by last name:

```
load hospital
hospital(1:5,1:3)
ans =
            LastName       Sex       Age
 YPL-320    'SMITH'        Male      38
 GLI-532    'JOHNSON'      Male      43
 PNI-258    'WILLIAMS'     Female    38
 MIJ-579    'JONES'        Female    40
```

```
 XLK-030    'BROWN'        Female    49

hospital = sortrows(hospital,{'Age','LastName'});
hospital(1:5,1:3)
ans =
            LastName       Sex       Age
 REV-997    'ALEXANDER'    Male      25
 FZR-250    'HALL'         Male      25
 LIM-480    'HILL'         Female    25
 XUE-826    'JACKSON'      Male      25
 SCQ-914    'JAMES'        Male      25
```

See Also

sortrows

Purpose

Sort rows

Syntax

```
B = sortrows(A)
B = sortrows(A,col)
[B,I] = sortrows(A)
[B,I] = sortrows(A,col)
```

Description

`B = sortrows(A)` sorts the rows of the 2-D ordinal matrix `A` in ascending order, as a group. `B` is an ordinal array with the same levels as `A`.

`B = sortrows(A,col)` sorts `A` based on the columns specified in the vector `col`. If an element of `col` is positive, the corresponding column in `A` is sorted in ascending order; if an element of `col` is negative, the corresponding column in `A` is sorted in descending order.

`[B,I] = sortrows(A)` and `[B,I] = sortrows(A,col)` also returns an index matrix `I` such that `B = A(I,:)`.

Elements with undefined levels are sorted to the end.

Examples

Sort the rows of an ordinal array in ascending order for the first column, and then in descending order for the second column:

```
A = ordinal([6 2 5; 2 4 1; 3 2 4],...
            {'lo','med','hi'},[],[0 2 4 6])
A =
     hi       med      hi
     med      hi       lo
     med      med      hi

B = sortrows(A,[1 -2])
B =
     med      hi       lo
     med      med      hi
     hi       med      hi
```

See Also

`sort` | `sortrows`

squareform

Purpose

Format distance matrix

Syntax

```
Z = squareform(y)
y = squareform(Z)
Z = squareform(y,'tovector')
Y = squareform(Z,'tomatrix')
```

Description

`Z = squareform(y)`, where `y` is a vector as created by the `pdist` function, converts `y` into a square, symmetric format `Z`, in which `Z(i,j)` denotes the distance between the `i`th and `j`th objects in the original data.

`y = squareform(Z)`, where `Z` is a square, symmetric matrix with zeros along the diagonal, creates a vector `y` containing the `Z` elements below the diagonal. `y` has the same format as the output from the `pdist` function.

`Z = squareform(y,'tovector')` forces `squareform` to treat `y` as a vector.

`Y = squareform(Z,'tomatrix')` forces `squareform` to treat `Z` as a matrix.

The last two formats are useful if the input has a single element, so that it is ambiguous whether the input is a vector or square matrix.

Examples

```
y = 1:6
y =
   1   2   3   4   5   6

X = [0 1 2 3; 1 0 4 5; 2 4 0 6; 3 5 6 0]
X =
   0   1   2   3
   1   0   4   5
   2   4   0   6
   3   5   6   0
```

Then `squareform(y) = X` and `squareform(X) = y`.

See Also

pdist

categorical.squeeze

Purpose

Squeeze singleton dimensions from categorical array

Syntax

```
B = squeeze(A)
```

Description

`B = squeeze(A)` returns an array `B` with the same elements as the categorical array `A` but with all the singleton dimensions removed. A singleton is a dimension such that `size(A,dim)=1`. 2-D arrays are unaffected by `squeeze` so that row vectors remain rows.

See Also

`shiftdim`

Purpose

Stack data from multiple variables into single variable

Syntax

```
tall = stack(wide,datavars)
[tall,iwide] = stack(wide,datavars)
tall = stack(wide,datavars,Parameter,value)
```

Description

`tall = stack(wide,datavars)` converts a wide-format dataset array into a tall-format array, by stacking multiple variables in `wide` into a single variable in `tall`. In general, `tall` contains fewer variables but more observations than `wide`.

`datavars` specifies a group of `m` data variables in `wide`. `stack` creates a single data variable in `tall` by interleaving their values, and if `wide` has `n` observations, then `tall` has `m`-by-`n` observations. In other words, `stack` takes the `m` data values from each observation in `wide` and stacks them up to create `m` observations in `tall`. `datavars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. `stack` also creates a grouping variable in `tall` to indicate which of the `m` data variables in `wide` each observation in `tall` corresponds to.

`stack` assigns values for the "per-variable properties (e.g., `Units` and `VarDescription`) for the new data variable in `tall` from the corresponding property values for the first variable listed in `datavars`.

`stack` copies the remaining variables from `wide` to `tall` without stacking, by replicating each of their values `m` times. These variables are typically grouping variables. Because their values are constant across each group of `m` observations in `tall`, they identify which observation in `wide` an observation in `tall` came from.

`[tall,iwide] = stack(wide,datavars)` returns an index vector `iwide` indicating the correspondence between observations in `tall` and those in `wide`. `stack` creates `tall(j,:)` using `wide(iwide(j),datavarss)`.

For more information on grouping variables, see “Grouping Variables” on page 2-34.

Input Arguments

`tall = stack(wide,datavars,`*`Parameter`*`,`*`value`*`)` uses the following parameter name/value pairs to control how `stack` converts variables in `wide` to variables in `tall`:

`'ConstVars'`	Variables in `wide` to copy to `tall` without stacking. `ConstVars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. The default is all variables in `wide` not specified in `datavars`.
`'NewDataVarName'`	A name for the data variable to be created in `tall`. The default is a concatenation of the names of the `m` variables that are stacked up.
`'IndVarName'`	A name for the grouping variable to create in `tall` to indicate the source of each value in the new data variable. The default is based on the `'NewDataVarName'` parameter.

You can also specify multiple groups of data variables in `wide`, each of which becomes a variable in `tall`. All groups must contain the same number of variables. Use a cell array to contain multiple parameter values for `datavars`, and a cell array of strings to contain multiple `'NewDataVarName'`.

Examples

Convert a wide format data set to tall format, and then back to a different wide format:

```
load flu

% FLU has a 'Date' variable, and 10 variables for estimated
% influenza rates (in 9 different regions, estimated from
```

```
% Google searches, plus a nationwide extimate from the
% CDC). Combine those 10 variables into a "tall" array that
% has a single data variable, 'FluRate', and an indicator
% variable, 'Region', that says which region each estimate
% is from.
[flu2,iflu] = stack(flu, 2:11, 'NewDataVarName','FluRate', ...
    'IndVarName','Region')

% The second observation in FLU is for 10/16/2005.  Find the
% observations in FLU2 that correspond to that date.
flu(2,:)
flu2(iflu==2,:)

% Use the 'Date' variable from that tall array to split
% 'FluRate' into 52 separate variables, each containing the
% estimated influenza rates for each unique date.  The new
% "wide" array has one observation for each region.  In
% effect, this is the original array FLU "on its side".
dateNames = cellstr(datestr(flu.Date,'mmm_DD_YYYY'));
[flu3,iflu2] = unstack(flu2, 'FluRate', 'Date', ...
    'NewDataVarNames',dateNames)

% Since observations in FLU3 represent regions, IFLU2
% indicates the first occurrence in FLU2 of each region.
flu2(iflu2,:)
```

See Also

dataset.unstack | dataset.join | dataset.grpstats

How To

- “Grouping Variables” on page 2-34

qrandstream.State property

Purpose

Current state of the stream

Description

The `State` property of a quasi-random stream contains the index into the associated point set of the next point to draw in the stream. Getting and resetting the `State` property allows you to return a stream to a previous state. The initial value of `State` is `1`.

Examples

```
Q = qrandstream('sobol', 5);
s = Q.State;
u1 = qrand(Q, 10)
Q.State = s;
u2 = qrand(Q, 10) % contains exactly the same values as u1
```

See Also

`qrand`

Purpose

Access values in statistics options structure

Syntax

```
val = statget(options,param)
val = statget(options,param,default)
```

Description

`val = statget(options,param)` returns the value of the parameter specified by the string `param` in the statistics options structure `options`. If the parameter is undefined in `options`, `statget` returns `[]`. You need to type only enough leading characters to define the parameter name uniquely. `statget` ignores case for parameter names. For available `options`, see Inputs.

`val = statget(options,param,default)` returns `default` if the specified parameter is undefined in the optimization options structure `options`.

Input Arguments

`DerivStep`

Relative difference used in finite difference derivative calculations. A positive scalar, or a vector of positive scalars the same size as the vector of parameters estimated by the Statistics Toolbox function using the options structure.

`Display`

Amount of information displayed by the algorithm.

- `'off'` — Displays no information.
- `'final'` — Displays the final output.
- `'iter'` — Displays iterative output to the command window for some functions; otherwise displays the final output.

`FunValCheck`

Check for invalid values, such as `NaN` or `Inf`, from the objective function.

- `'off'`

- 'on'

GradObj

Flags whether the objective function returns a gradient vector as a second output.

- 'off'
- 'on'

Jacobian

Flags whether the objective function returns a Jacobian as a second output.

- 'off'
- 'on'

MaxFunEvals

Maximum number of objective function evaluations allowed. Positive integer.

MaxIter

Maximum number of iterations allowed. Positive integer.

OutputFcn

The solver calls all output functions after each iteration.

- Function handle specified using @
- a cell array with function handles
- an empty array (default)

Robust

Invoke robust fitting option.

- 'off'
- 'on'

Streams

A single instance of the RandStream class, or a cell array of RandStream instances. The Streams option is accepted by some functions to govern what stream(s) to use in generating random numbers within the function. If 'UseSubstreams' is 'always', the Streams value must be a scalar, or must be empty. If 'UseParallel' is 'always' and 'UseSubstreams' is 'never', then the Streams argument must either be empty, or its length must match the number of processors used in the computation: equal to the *matlabpool* size if a *matlabpool* is open, a scalar otherwise. For more information on parallel computing, see Chapter 17, "Parallel Statistics".

TolBnd

Parameter bound tolerance. Positive scalar.

TolFun

Termination tolerance for the objective function value. Positive scalar.

TolTypeFun

Use TolFun for absolute or relative objective function tolerances.

- 'abs'
- 'rel'

TolTypeX

Use TolX for absolute or relative parameter tolerances.

- 'abs'
- 'rel'

`TolX`

Termination tolerance for the parameters. Positive scalar.

`Tune`

The tuning constant used in robust fitting to normalize the residuals before applying the weight function. The default value depends upon the weight function. This parameter is necessary if you specify the weight function as a function handle. Positive scalar.

`UseParallel`

Flag indicating whether eligible functions should use capabilities of the Parallel Computing Toolbox (PCT), if the capabilities are available. That is, if the PCT is installed, and a PCT matlabpool is in effect. Valid values are `'never'` (the default), for serial computation, and `'always'`, for parallel computation. For more information on parallel computing, see Chapter 17, "Parallel Statistics".

`UseSubstreams`

Flag indicating whether the random number generator in eligible functions should use `Substream` property of the `RandStream` class. `'never'` (default) or `'always'`. `'always'`, high level iterations within the function will set the `Substream` property to the value of the iteration. This behavior helps to generate reproducible random number streams in parallel and/or serial mode computation. For more information on parallel computing, see Chapter 17, "Parallel Statistics".

`WgtFun`

A weight function for robust fitting. Valid only when `Robust` is `'on'`. Can also be a function handle that accepts a normalized residual as input and returns the robust weights as output.

- `'bisquare'`
- `'andrews'`

- 'cauchy'
- 'fair'
- 'huber'
- 'logistic'
- 'talwar'
- 'welsch'

Examples

This statement returns the value of the Display statistics options parameter from the structure called my_options.

```
val = statget(my_options,'Display')
```

Return the value of the Display statistics options parameter from the structure called my_options (as in the previous example). If the Display parameter is undefined, statget returns the value 'final'.

```
optnew = statget(my_options,'Display','final');
```

See Also

statset

statset

Purpose

Create statistics options structure

Syntax

```
statset
statset(statfun)
options = statset(...)
options = statset(fieldname1,val1,fieldname2,val2,...)
options = statset(oldopts,fieldname1,val1,fieldname2,val2,
   ...)
options = statset(oldopts,newopts)
```

Description

`statset` with no input arguments and no output arguments displays all fields of a statistics options structure and their possible values.

`statset(statfun)` displays fields and default values used by the Statistics Toolbox function `statfun`. Specify `statfun` using a string name or a function handle.

`options = statset(...)` creates a statistics options structure `options`. With no input arguments, all fields of the options structure are an empty array (`[]`). With a specified `statfun`, function-specific fields are default values and the remaining fields are `[]`. Function-specific fields set to `[]` indicate that the function is to use its default value for that parameter. For available `options`, see Inputs.

`options = statset(fieldname1,val1,fieldname2,val2,...)` creates an options structure in which the named fields have the specified values. Any unspecified values are `[]`. Use strings for field names. For fields that are string-valued, you must input the complete string for the value. If you provide an invalid string for a value, `statset` uses the default.

`options = statset(oldopts,fieldname1,val1,fieldname2,val2,...)` creates a copy of `oldopts` with the named parameters changed to the specified values.

`options = statset(oldopts,newopts)` combines an existing options structure, `oldopts`, with a new options structure, `newopts`. Any

parameters in `newopts` with nonempty values overwrite corresponding parameters in `oldopts`.

Input Arguments

`DerivStep`

Relative difference used in finite difference derivative calculations. A positive scalar, or a vector of positive scalars the same size as the vector of parameters estimated by the Statistics Toolbox function using the options structure.

`Display`

Amount of information displayed by the algorithm.

- `'off'` — Displays no information.
- `'final'` — Displays the final output.
- `'iter'` — Displays iterative output to the command window for some functions; otherwise displays the final output.

`FunValCheck`

Check for invalid values, such as `NaN` or `Inf`, from the objective function.

- `'off'`
- `'on'`

`GradObj`

Flags whether the objective function returns a gradient vector as a second output.

- `'off'`
- `'on'`

`Jacobian`

Flags whether the objective function returns a Jacobian as a second output.

- `'off'`
- `'on'`

`MaxFunEvals`

Maximum number of objective function evaluations allowed. Positive integer.

`MaxIter`

Maximum number of iterations allowed. Positive integer.

`OutputFcn`

The solver calls all output functions after each iteration.

- Function handle specified using @
- a cell array with function handles
- an empty array (default)

`Robust`

Invoke robust fitting option.

- `'off'`
- `'on'`

`Streams`

A single instance of the `RandStream` class, or a cell array of `RandStream` instances. The Streams option is accepted by some functions to govern what stream(s) to use in generating random numbers within the function. If `'UseSubstreams'` is `'always'`, the Streams value must be a scalar, or must be empty. If `'UseParallel'` is `'always'` and `'UseSubstreams'` is `'never'`,

then the Streams argument must either be empty, or its length must match the number of processors used in the computation: equal to the *matlabpool* size if a *matlabpool* is open, a scalar otherwise. For more information on parallel computing, see Chapter 17, "Parallel Statistics".

`TolBnd`

Parameter bound tolerance. Positive scalar.

`TolFun`

Termination tolerance for the objective function value. Positive scalar.

`TolTypeFun`

Use `TolFun` for absolute or relative objective function tolerances.

- `'abs'`
- `'rel'`

`TolTypeX`

Use `TolX` for absolute or relative parameter tolerances.

- `'abs'`
- `'rel'`

`TolX`

Termination tolerance for the parameters. Positive scalar.

`Tune`

The tuning constant used in robust fitting to normalize the residuals before applying the weight function. The default value depends upon the weight function. This parameter is necessary if you specify the weight function as a function handle. Positive scalar.

`UseParallel`

Flag indicating whether eligible functions should use capabilities of the Parallel Computing Toolbox (PCT), if the capabilities are available. That is, if the PCT is installed, and a PCT matlabpool is in effect. Valid values are `'never'` (the default), for serial computation, and `'always'`, for parallel computation. For more information on parallel computing, see Chapter 17, "Parallel Statistics".

`UseSubstreams`

Flag indicating whether the random number generator in eligible functions should use `Substream` property of the `RandStream` class. `'never'` (default) or `'always'`. `'always'`, high level iterations within the function will set the `Substream` property to the value of the iteration. This behavior helps to generate reproducible random number streams in parallel and/or serial mode computation. For more information on parallel computing, see Chapter 17, "Parallel Statistics".

`WgtFun`

A weight function for robust fitting. Valid only when `Robust` is `'on'`. Can also be a function handle that accepts a normalized residual as input and returns the robust weights as output.

- `'bisquare'`
- `'andrews'`
- `'cauchy'`
- `'fair'`
- `'huber'`
- `'logistic'`
- `'talwar'`
- `'welsch'`

Examples

Suppose you want to change the default parameter values for the function `evfit`, which fits an extreme value distribution to data. The defaults parameter values are:

```
statset('evfit')
ans =
        Display: 'off'
    MaxFunEvals: []
        MaxIter: []
         TolBnd: []
         TolFun: []
           TolX: 1.0000e-006
        GradObj: []
      DerivStep: []
    FunValCheck: []
         Robust: []
         WgtFun: []
           Tune: []
```

The only parameters that `evfit` uses are `Display` and `TolX`. To create an options structure with the value of `TolX` set to `1e-8`, enter:

```
options = statset('TolX',1e-8)
% Pass options to evfit:
mu = 1;
sigma = 1;
data = evrnd(mu,sigma,1,100);

paramhat = evfit(data,[],[],[],options)
```

See Also

`statget`

ProbDistUnivParam.std

Purpose

Return standard deviation of ProbDistUnivParam object

Syntax

```
S = std(PD)
```

Description

`S = std(PD)` returns `S`, the standard deviation of the ProbDistUnivParam object `PD`.

Input Arguments

`PD`	An object of the class `ProbDistUnivParam`.

Output Arguments

`S`	The standard deviation of the ProbDistUnivParam object `PD`.

See Also

`std`

Purpose

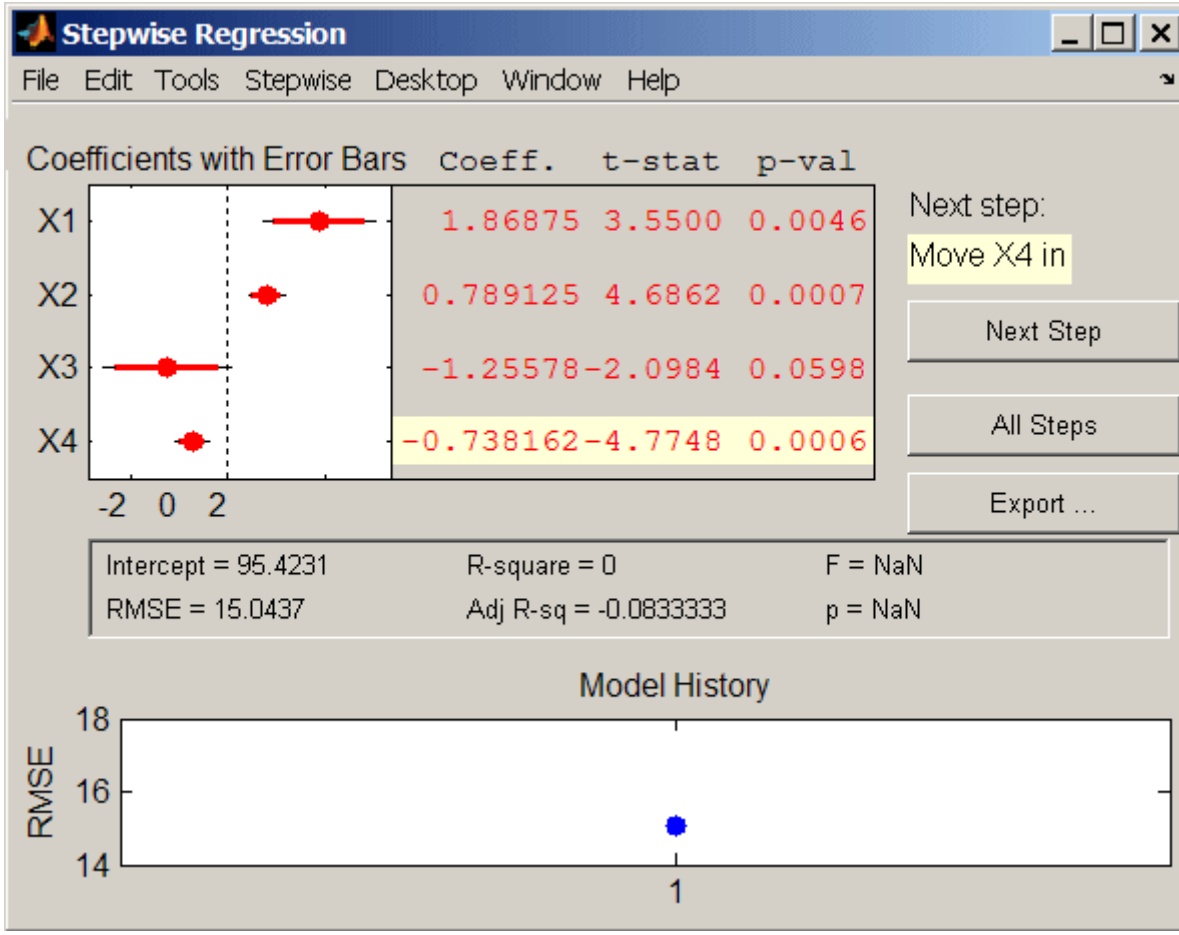
Interactive stepwise regression

Syntax

```
stepwise
stepwise(X,y)
stepwise(X,y,inmodel,penter,premove)
```

Description

`stepwise` uses the sample data in `hald.mat` to display a graphical user interface for performing stepwise regression of the response values in `heat` on the predictive terms in `ingredients`.



The upper left of the interface displays estimates of the coefficients for all potential terms, with horizontal bars indicating 90% (colored) and 95% (grey) confidence intervals. The red color indicates that, initially, the terms are not in the model. Values displayed in the table are those that would result if the terms were added to the model.

The middle portion of the interface displays summary statistics for the entire model. These statistics are updated with each step.

The lower portion of the interface, **Model History**, displays the RMSE for the model. The plot tracks the RMSE from step to step, so you can compare the optimality of different models. Hover over the blue dots in the history to see which terms were in the model at a particular step. Click on a blue dot in the history to open a copy of the interface initialized with the terms in the model at that step.

Initial models, as well as entrance/exit tolerances for the p-values of F-statistics, are specified using additional input arguments to `stepwise`. Defaults are an initial model with no terms, an entrance tolerance of 0.05, and an exit tolerance of 0.10.

To center and scale the input data (compute z-scores) to improve conditioning of the underlying least-squares problem, select `Scale Inputs` from the **Stepwise** menu.

You proceed through a stepwise regression in one of two ways:

1. Click **Next Step** to select the recommended next step. The recommended next step either adds the most significant term or removes the least significant term. When the regression reaches a local minimum of RMSE, the recommended next step is "Move no terms." You can perform all of the recommended steps at once by clicking **All Steps**.

2. Click a line in the plot or in the table to toggle the state of the corresponding term. Clicking a red line, corresponding to a term not currently in the model, adds the term to the model and changes the line to blue. Clicking a blue line, corresponding to a term currently in the model, removes the term from the model and changes the line to red.

To call `addedvarplot` and produce an added variable plot from the `stepwise` interface, select **Added Variable Plot** from the **Stepwise** menu. A list of terms is displayed. Select the term you want to add, and then click **OK**.

Click **Export** to display a dialog box that allows you to select information from the interface to save to the MATLAB workspace.

Check the information you want to export and, optionally, change the names of the workspace variables to be created. Click **OK** to export the information.

`stepwise(X,y)` displays the interface using the p predictive terms in the n-by-p matrix `X` and the response values in the n-by-1 vector `y`. Distinct predictive terms should appear in different columns of `X`.

Note `stepwise` automatically includes a constant term in all models. Do not enter a column of 1s directly into `X`.

`stepwise` treats `NaN` values in either `X` or `y` as missing values, and ignores them.

`stepwise(X,y,inmodel,penter,premove)` additionally specifies the initial model (`inmodel`) and the entrance (`penter`) and exit (`premove`) tolerances for the p-values of F-statistics. `inmodel` is either a logical vector with length equal to the number of columns of `X`, or a vector of indices, with values ranging from 1 to the number of columns in `X`. The value of `penter` must be less than or equal to the value of `premove`.

Algorithms

Stepwise regression is a systematic method for adding and removing terms from a multilinear model based on their statistical significance in a regression. The method begins with an initial model and then compares the explanatory power of incrementally larger and smaller models. At each step, the p value of an F-statistic is computed to test models with and without a potential term. If a term is not currently in the model, the null hypothesis is that the term would have a zero coefficient if added to the model. If there is sufficient evidence to reject the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model. The method proceeds as follows:

1. Fit the initial model.

2. If any terms not in the model have *p*-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest *p* value and repeat this step; otherwise, go to step 3.

3. If any terms in the model have *p*-values greater than an exit tolerance (that is, if it is unlikely that the hypothesis of a zero coefficient can be rejected), remove the one with the largest *p* value and go to step 2; otherwise, end.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method may build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but may not be globally optimal.

See Also

`addedvarplot` | `regress` | `stepwisefit`

How To

- "Stepwise Regression" on page 9-19

stepwisefit

Purpose

Stepwise regression

Syntax

```
b = stepwisefit(X,y)
[b,se,pval,inmodel,stats,nextstep,history] = stepwisefit(...)
[...] = stepwisefit(X,y,param1,val1,param2,val2,...)
```

Description

`b = stepwisefit(X,y)` uses a stepwise method to perform a multilinear regression of the response values in the n-by-1 vector `y` on the p predictive terms in the n-by-p matrix `X`. Distinct predictive terms should appear in different columns of `X`. `b` is a p-by-1 vector of estimated coefficients for all of the terms in `X`. The value in `b` for a term not included in the final model is the coefficient estimate that would result from adding the term to the model.

Note `stepwisefit` automatically includes a constant term in all models. Do not enter a column of 1s directly into `X`.

`stepwisefit` treats `NaN` values in either `X` or `y` as missing values, and ignores them.

`[b,se,pval,inmodel,stats,nextstep,history] = stepwisefit(...)` returns the following additional information:

- `se` — A vector of standard errors for `b`
- `pval` — A vector of p-values for testing whether elements of `b` are 0
- `inmodel` — A logical vector, with length equal to the number of columns in `X`, specifying which terms are in the final model
- `stats` — A structure of additional statistics with the following fields. All statistics pertain to the final model except where noted.
  - `source` — The string `'stepwisefit'`
  - `dfe` — Degrees of freedom for error
  - `df0` — Degrees of freedom for the regression

  - `SStotal` — Total sum of squares of the response
  - `SSresid` — Sum of squares of the residuals
  - `fstat` — *F*-statistic for testing the final model vs. no model (mean only)
  - `pval` — *p* value of the *F*-statistic
  - `rmse` — Root mean square error
  - `xr` — Residuals for predictors not in the final model, after removing the part of them explained by predictors in the model
  - `yr` — Residuals for the response using predictors in the final model
  - `B` — Coefficients for terms in final model, with values for a term not in the model set to the value that would be obtained by adding that term to the model
  - `SE` — Standard errors for coefficient estimates
  - `TSTAT` — *t* statistics for coefficient estimates
  - `PVAL` — *p*-values for coefficient estimates
  - `intercept` — Estimated intercept
  - `wasnan` — Indicates which rows in the data contained `NaN` values
- `nextstep` — The recommended next step—either the index of the next term to move in or out of the model, or `0` if no further steps are recommended
- `history` — A structure containing information on steps taken, with the following fields:
  - `rmse` — Root mean square errors for the model at each step
  - `df0` — Degrees of freedom for the regression at each step
  - `in` — Logical array indicating which predictors are in the model at each step

`[...] = stepwisefit(X,y,param1,val1,param2,val2,...)` specifies one or more of the name/value pairs described in the following table.

Parameter	Value
`'inmodel'`	A logical vector specifying terms to include in the initial fit. The default is to specify no terms.
`'penter'`	The maximum p value for a term to be added. The default is `0.05`.
`'premove'`	The minimum p value for a term to be removed. The default is the maximum of the value of `'penter'` and `0.10`.
`'display'`	`'on'` displays information about each step in the command window. This is the default. `'off'` omits the display.
`'maxiter'`	The maximum number of steps in the regression. The default is `Inf`.
`'keep'`	A logical vector specifying terms to keep in their initial state. The default is to specify no terms.
`'scale'`	`'on'` centers and scales each column of `X` (computes z-scores) before fitting. `'off'` does not scale the terms. This is the default.

Algorithms

Stepwise regression is a systematic method for adding and removing terms from a multilinear model based on their statistical significance in a regression. The method begins with an initial model and then compares the explanatory power of incrementally larger and smaller models. At each step, the p value of an F-statistic is computed to test models with and without a potential term. If a term is not currently in the model, the null hypothesis is that the term would have a zero coefficient if added to the model. If there is sufficient evidence to reject

the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model. The method proceeds as follows:

1. Fit the initial model.
2. If any terms not in the model have p-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest p value and repeat this step; otherwise, go to step 3.
3. If any terms in the model have p-values greater than an exit tolerance (that is, if it is unlikely that the hypothesis of a zero coefficient can be rejected), remove the one with the largest p value and go to step 2; otherwise, end.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method may build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but may not be globally optimal.

Examples

Load the data in `hald.mat`, which contains observations of the heat of reaction of various cement mixtures:

```
load hald
whos
  Name          Size    Bytes   Class   Attributes

  Description   22x58   2552    char
  hald          13x5     520    double
  heat          13x1     104    double
  ingredients   13x4     416    double
```

The response (heat) depends on the quantities of the four predictors (the columns of ingredients).

Use stepwisefit to carry out the stepwise regression algorithm, beginning with no terms in the model and using entrance/exit tolerances of 0.05/0.10 on the *p*-values:

```
stepwisefit(ingredients,heat,...
            'penter',0.05,'premove',0.10);
Initial columns included:  none
Step 1, added column 4, p=0.000576232
Step 2, added column 1, p=1.10528e-006
Final columns included:  1 4
    'Coeff'      'Std.Err.'    'Status'    'P'
    [ 1.4400]    [  0.1384]    'In'        [1.1053e-006]
    [ 0.4161]    [  0.1856]    'Out'       [     0.0517]
    [-0.4100]    [  0.1992]    'Out'       [     0.0697]
    [-0.6140]    [  0.0486]    'In'        [1.8149e-007]
```

stepwisefit automatically includes an intercept term in the model, so you do not add it explicitly to ingredients as you would for regress. For terms not in the model, coefficient estimates and their standard errors are those that result if the term is added.

The inmodel parameter is used to specify terms in an initial model:

```
initialModel = ...
           [false true false false]; % Force in 2nd term
stepwisefit(ingredients,heat,...
            'inmodel',initialModel,...
            'penter',.05,'premove',0.10);
Initial columns included:  2
Step 1, added column 1, p=2.69221e-007
Final columns included:  1 2
    'Coeff'      'Std.Err.'    'Status'    'P'
    [ 1.4683]    [  0.1213]    'In'        [2.6922e-007]
    [ 0.6623]    [  0.0459]    'In'        [5.0290e-008]
    [ 0.2500]    [  0.1847]    'Out'       [     0.2089]
```

```
    [-0.2365]    [  0.1733]    'Out'       [     0.2054]
```

The preceding two models, built from different initial models, use different subsets of the predictive terms. Terms 2 and 4, swapped in the two models, are highly correlated:

```
term2 = ingredients(:,2);
term4 = ingredients(:,4);
R = corrcoef(term2,term4)
R =
    1.0000   -0.9730
   -0.9730    1.0000
```

To compare the models, use the `stats` output of `stepwisefit`:

```
[betahat1,se1,pval1,inmodel1,stats1] = ...
          stepwisefit(ingredients,heat,...
          'penter',.05,'premove',0.10,...
          'display','off');
[betahat2,se2,pval2,inmodel2,stats2] = ...
          stepwisefit(ingredients,heat,...
                      'inmodel',initialModel,...
                      'penter',.05,'premove',0.10,...
                      'display','off');
RMSE1 = stats1.rmse
RMSE1 =
    2.7343
RMSE2 = stats2.rmse
RMSE2 =
    2.4063
```

The second model has a lower Root Mean Square Error (RMSE).

References

[1] Draper, N. R., and H. Smith. *Applied Regression Analysis*. Hoboken, NJ: Wiley-Interscience, 1998. pp. 307–312.

See Also

`stepwise` | `addedvarplot` | `regress`

categorical.subsasgn

Purpose

Subscripted assignment for categorical array

Syntax

```
A = subsasgn(A,S,B)
```

Description

`A = subsasgn(A,S,B)` is called for the syntax `A(i)=B`. `S` is a structure array with the fields:

`type`	String containing `'()'` specifying the subscript type. Only parenthesis subscripting is allowed.
`subs`	Cell array or string containing the actual subscripts.

See Also

`categorical` | `subsref`

Purpose

Subscripted reference for `classregtree` object

Syntax

Description

Subscript assignment is not allowed for a `classregtree` object.

See Also

`classregtree`

dataset.subsasgn

Purpose

Subscripted assignment to dataset array

Description

`A = subsasgn(A,S,B)` is called for the syntax `A(i,j)=B`, `A{i,j}=B`, or `A.var=B` when `A` is a dataset array. `S` is a structure array with the fields:

`type`	String containing `'()'`, `'{}'`, or `'.'` specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

`A(i,j) = B` assigns the contents of the dataset array `B` to a subset of the observations and variables in the dataset array `A`. `i` and `j` are one of the following types:

- positive integers
- vectors of positive integers
- observation/variable names
- cell arrays containing one or more observation/variable names
- logical vectors

The assignment does not use observation names, variable names, or any other properties of `B` to modify properties of `A`; however properties of `A` are extended with default values if the assignment expands the number of observations or variables in `A`. Elements of `B` are assigned into `A` by position, not by matching names.

`A{i,j} = B` assigns the value `B` into an element of the dataset array `A`. `i` and `J` are positive integers, or logical vectors. Cell indexing cannot assign into multiple dataset elements, that is, the subscripts `i` and `j` must each refer to only a single observation or variable. `B` is cast to the type of the target variable if necessary. If the dataset element already exists, `A{i,j}` may also be followed by further subscripting as supported by the variable.

For dataset variables that are cell arrays, assignments such as `A{1,'CellVar'} = B` assign into the contents of the target dataset element in the same way that `{}`-indexing of an ordinary cell array does.

For dataset variables that are `n`-D arrays, i.e., each observation is a matrix or array, an assignment such as `A{1,'ArrayVar'} = B` assigns into the second and following dimensions of the target dataset element, i.e., the assignment adds a leading singleton dimension to `B` to account for the observation dimension of the dataset variable.

`A.var = B` or `A.(varname) = B` assigns `B` to a dataset variable. `var` is a variable name literal, or `varname` is a character variable containing a variable name. If the dataset variable already exists, the assignment completely replaces that variable. To assign into an element of the variable, `A.var` or `A.(varname)` may be followed by further subscripting as supported by the variable. In particular, `A.var(obsnames,...) = B` and `A.var{obsnames,...} = B` (when supported by `var`) provide assignment into a dataset variable using observation names.

`A.properties.propertyname = P` assigns to a dataset property. `propertyname` is one of the following:

- `'ObsNames'`
- `'VarNames'`
- `'Description'`
- `'Units'`
- `'DimNames'`
- `'UserData'`
- `'VarDescription'`

To assign into an element of the property, `A.properties.propertyname` may also be followed by further subscripting as supported by the property.

You cannot assign multiple values into dataset variables or properties using assignments such as `[A.CellVar{1:2}] = B`,

`[A.StructVar(1:2).field] = B`, or `[A.Properties.ObsNames{1:2}] = B`. Use multiple assignments of the form `A.CellVar{1} = B` instead.

Similarly, if a dataset variable is a cell array with multiple columns or is an n-D cell array, then the contents of that variable for a single observation consists of multiple cells, and you cannot assign to all of them using the syntax `A{1,'CellVar'} = B`. Use multiple assignments of the form `[A.CellVar{1,1}] = B` instead.

See Also

`dataset | set | subsref`

Purpose

Subscripted reference for Gaussian mixture distribution object

Description

Subscript assignment is not allowed for `gmdistribution` objects.

See Also

`gmdistribution`

NaiveBayes.subsasgn

Purpose

Subscripted reference for `NaiveBayes` object

Description

Subscript assignment is not allowed for a `NaiveBayes` object.

Purpose

Subscript index for categorical array

Syntax

```
I = subsindex(A)
```

Description

`I = subsindex(A)` is called for the syntax `'X(A)'` when `A` is a categorical array and `X` is one of the built-in types (most commonly `'double'`). `subsindex` returns the internal categorical level codes of `A` converted to zero-based integer indices. `subsindex` is invoked separately on all the subscripts in an expression such as `X(A,B)`.

Examples

```
load fisheriris
a = ordinal(species,[],unique(species));
colmeans = grpstats(meas,a,@mean);
residuals = meas - colmeans(a,:);
```

See Also

`categorical` | `double`

classregtree.subsref

Purpose

Subscripted reference for `classregtree` object

Syntax

```
B = subsref(T,S)
```

Description

`B = subsref(T,S)` is called for the syntax `T(X)` when `T` is a `classregtree` object. `S` is a structure array with the fields:

`type`	String containing `'()'`, `'{}'`, or `'.'` specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

`[...]=T(...)` invokes the `eval` method for the tree `T`.

See Also

`classregtree` | `eval`

Purpose

Subscripted reference for categorical array

Syntax

```
A = subsref(A,S,B)
```

Description

`A = subsref(A,S,B)` is called for the syntax `A(I)=B`. `S` is a structure array with the fields:

`type`	String containing `'()'` specifying the subscript type. Only parenthesis subscripting is allowed.
`subs`	Cell array or string containing the actual subscripts.

See Also

`categorical` | `subsasgn`

dataset.subsref

Purpose

Subscripted reference for dataset array

Syntax

```
B = subsref(A,S)
```

Description

`B = subsref(A,S)` is called for the syntax `A(i,j)`, `A{i,j}`, or `A.var` when `A` is a dataset array. `S` is a structure array with the fields:

`type`	String containing `'()'`, `'{}'`, or `'.'` specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

`B = A(i,j)` returns a dataset array that contains a subset of the observations and variables in the dataset array `A`. `i` and `j` are one of the following types:

- positive integers
- vectors of positive integers
- observation/variable names
- cell arrays containing one or more observation/variable names
- logical vectors

`B` contains the same property values as `A`, subsetted for observations or variables where appropriate.

`B = A{i,j}` returns an element of a dataset variable. `i` and `j` are positive integers, or logical vectors. Cell indexing cannot return multiple dataset elements, that is, the subscripts `i` and `j` must each refer to only a single observation or variable. `A{i,j}` may also be followed by further subscripting as supported by the variable.

For dataset variables that are cell arrays, expressions such as `A{1,'CellVar'}` return the contents of the referenced dataset element in the same way that `{}`-indexing on an ordinary cell array does. If the dataset variable is a single column of cells, the contents of a single cell

is returned. If the dataset variable has multiple columns or is n-D, multiple outputs containing the contents of multiple cells are returned.

For dataset variables that are n-D arrays, i.e., each observation is a matrix or an array, expressions such as `A{1,'ArrayVar'}` return `A.ArrayVar(1,:,...)` with the leading singleton dimension squeezed out.

`B = A.var` or `A.(varname)` returns a dataset variable. `var` is a variable name literal, or `varname` is a character variable containing a variable name. `A.var` or `A.(varname)` may also be followed by further subscripting as supported by the variable. In particular, `A.var(obsnames,...)` and `A.var{obsnames,...}` (when supported by `var`) provide subscripting into a dataset variable using observation names.

`P = A.Properties.propertyname` returns a dataset property. `propertyname` is one of the following:

- `'ObsNames'`
- `'VarNames'`
- `'Description'`
- `'Units'`
- `'DimNames'`
- `'UserData'`
- `'VarDescription'`

`A.properties.propertyname` may also be followed by further subscripting as supported by the property.

Limitations

Subscripting expressions such as `A.CellVar{1:2}`, `A.StructVar(1:2).field`, or `A.Properties.ObsNames{1:2}` are valid, but result in `subsref` returning multiple outputs in the form of a comma-separated list. If you explicitly assign to output

arguments on the left-hand side of an assignment, for example, `[cellval1,cellval2] = A.CellVar{1:2}`, those variables will receive the corresponding values. However, if there are no output arguments, only the first output in the comma-separated list is returned.

Similarly, if a dataset variable is a cell array with multiple columns or is an n-D cell array, then subscripting expressions such as `A{1,'CellVar'}` result in `subsref` returning the contents of multiple cells. You should explicitly assign to output arguments on the left-hand side of an assignment, for example, `[cellval1,cellval2] = A{1,'CellVar'}`.

See Also

`dataset | set | subsasgn`

Purpose

Subscripted reference for Gaussian mixture distribution object

Syntax

```
B = subsref(T,S)
```

Description

`B = subsref(T,S)` is called for the syntax `T(X)` when `T` is a `gmdistribution` object. `S` is a structure array with the following fields:

`type`	String containing `'()'`, `'{}'`, or `'.'` specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

See Also

`gmdistribution`

NaiveBayes.subsref

Purpose

Subscripted reference for `NaiveBayes` object

Syntax

```
b = subsref(nb,s)
```

Description

`b = subsref(nb,s)` is called for the syntax `nb(s)` when `nb` is a `NaiveBayes` object. `S` is a structure array with the fields:

`type`	string containing '()', '{}', or '.' specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

Purpose

Subscripted reference for qrandset

Syntax

```
x = p(i,j)
x = subsref(p,s)
```

Description

`x = p(i,j)` returns a matrix that contains a subset of the points from the point set `p`. The indices in `i` select points from the set and the indices in `j` select columns from those points. `i` and `j` are vector of positive integers or logical vectors. A colon used as a subscript, as in `p(i,:)`, indicates the entire row (or column).

`x = subsref(p,s)` is called for the syntax `p(i)`, `p{i}`, or `p.i`. `s` is a structure array with the fields:

`type`	string containing '()', '{}', or '.' specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

Examples

Command	Returns
`p = sobolset(5);`	The fifth point
`x = p(1:10,:)`	All columns of the first 10 points
`x = p(end,1)`	The first column of the last point
`x = p([1,4,5], :)`	Points 1, 4, and 5

See Also

`qrandset`

categorical.summary

Purpose

Summary statistics for categorical array

Syntax

```
summary(A)
C = summary(A)
[C,labels] = summary(A)
```

Description

`summary(A)` displays the number of elements in the categorical array `A` equal to each of the possible levels in `A`. If `A` contains any undefined elements, the output also includes the number of undefined elements.

`C = summary(A)` returns counts of the number of elements in the categorical array `A` equal to each of the possible levels in `A`. If `A` is a matrix or *N*-dimensional array, `C` is a matrix or array with rows corresponding to the levels of `A`. If `A` contains any undefined elements, `C` contains one more row than the number of levels of `A`, with the number of undefined elements in `c(end)` or `c(end,:)`.

`[C,labels] = summary(A)` also returns the list of categorical level labels corresponding to the counts in `C`.

Examples

Count the number of patients in each age group in the data in `hospital.mat`:

```
load hospital
edges = 0:10:100;
labels = strcat(num2str((0:10:90)','%d'),{'s'});
AgeGroup = ordinal(hospital.Age,labels,[],edges);
[c,labels] = summary(AgeGroup);

Table = dataset({labels,'AgeGroup'},{c,'Count'});
Table(3:6,:)
ans =
    AgeGroup     Count
    '20s'        15
    '30s'        41
    '40s'        42
    '50s'         2
```

See Also

`islevel` | `ismember` | `levelcounts`

dataset.summary

Purpose

Print summary of dataset array

Syntax

```
summary(A)
s = summary(A)
```

Description

`summary(A)` prints a summary of a dataset array and the variables that it contains.

`s = summary(A)` returns a scalar structure `s` that contains a summary of the dataset `A` and the variables that `A` contains. For more information on the fields in `s`, see Outputs.

Summary information depends on the type of the variables in the data set:

- For numerical variables, `summary` computes a five-number summary of the data, giving the minimum, the first quartile, the median, the third quartile, and the maximum.
- For logical variables, `summary` counts the number of `true`s and `false`s in the data.
- For categorical variables, `summary` counts the number of data at each level.

Output Arguments

The following list describes the fields in the structure `s`:

- `Description` — A character array containing the dataset description.
- `Variables` — A structure array with one element for each dataset variable in A. Each element has the following fields:
  - `Name` — A character string containing the name of the variable.
  - `Description` — A character string containing the variable's description.
  - `Units` — A character string containing the variable's units.
  - `Size` — A numeric vector containing the size of the variable.

- `Class` — A character string containing the class of the variable.
- `Data` — A scalar structure containing the following fields.

  For numeric variables:

  - `Probabilities` — A numeric vector containing the probabilities [0.0 .25 .50 .75 1.0] and NaN (if any are present in the corresponding dataset variable).
  - `Quantiles` — A numeric vector containing the values that correspond to 'Probabilities' for the corresponding dataset variable, and a count of NaNs (if any are present).

  For logical variables:

  - `Values` — The logical vector [true false].
  - `Counts` — A numeric vector of counts for each logical value.

  For categorical variables:

  - `Levels` — A cell array containing the labels for each level of the corresponding dataset variable.
  - `Counts` — A numeric vector of counts for each level.

  `'Data'` is empty if variable is not numeric, categorical, or logical. If a dataset variable has more than one column, then the corresponding `'Quantiles'` or `'Counts'` field is a matrix or an array.

Examples

Summarize Fisher's iris data:

```
load fisheriris
species = nominal(species);
data = dataset(species,meas);
summary(data)
species: [150x1 nominal]
  setosa   versicolor   virginica
      50           50          50
```

```
meas: [150x4 double]
  min       4.3000         2         1    0.1000
  1st Q     5.1000    2.8000    1.6000    0.3000
  median    5.8000         3    4.3500    1.3000
  3rd Q     6.4000    3.3000    5.1000    1.8000
  max       7.9000    4.4000    6.9000    2.5000
```

Summarize the data in `hospital.mat`:

```
load hospital
summary(hospital)

Dataset array created from the data file hospital.dat.

The first column of the file ("id") is used for observation
names.  Other columns ("sex" and "smoke") have been
converted from their original coded values into categorical
and logical variables.  Two sets of columns ("sys" and
"dia", "trial1" through "trial4") have been combined into
single variables with multivariate observations.  Column
headers have been replaced with more descriptive variable
names.  Units have been added where appropriate.


LastName: [100x1 cell string]
Sex: [100x1 nominal]
     Female      Male
         53        47

Age: [100x1 double, Units = Yrs]
     min      1st Q      median      3rd Q      max
      25         32          39         44       50

Weight: [100x1 double, Units = Lbs]
     min      1st Q         median        3rd Q        max
     111      130.5000      142.5000      180.5000     202
```

```
Smoker: [100x1 logical]
     true      false
       34         66

BloodPressure: [100x2 double, Units = mm Hg]
Systolic/Diastolic
     min              109           68
     1st Q       117.5000      77.5000
     median           122      81.5000
     3rd Q       127.5000           89
     max              138           99

Trials: [100x1 cell, Units = Counts]
From zero to four measurement trials performed
```

See Also

get | set | grpstats

ProbDist.Support property

Purpose

Read-only structure containing information about support of ProbDist object

Description

`Support` is a read-only property of the `ProbDist` class. `Support` is a structure containing information about the support of a ProbDist object. It includes the following fields:

- `range`
- `closedbound`
- `iscontinuous`

Values

The values for the three fields in the structure are:

- `range` — A two-element vector `[L, U]`, such that all of the probability is contained from `L` to `U`.
- `closedbound` — A two-element logical vector indicating whether the corresponding range endpoint is included. Possible values for each endpoint are `1` (`true`) or `0` (`false`).
- `iscontinuous` — A logical value indicates if the distribution takes values on the entire interval from `L` to `U` (true), or if it takes only integer values within this range (false). Possible values are `1` (`true`) or `0` (`false`).

Use this information to view and compare information about the support of distributions.

Purpose

Interactive contour plot

Syntax

```
surfht(Z)
surfht(x,y,Z)
```

Description

`surfht(Z)` is an interactive contour plot of the matrix `Z` treating the values in `Z` as height above the plane. The *x*-values are the column indices of `Z` while the *y*-values are the row indices of `Z`.

`surfht(x,y,Z)` where `x` and `y` are vectors specify the *x* and *y*-axes on the contour plot. The length of `x` must match the number of columns in `Z`, and the length of `y` must match the number of rows in `Z`.

There are vertical and horizontal reference lines on the plot whose intersection defines the current *x* value and *y* value. You can drag these dotted white reference lines and watch the interpolated *z* value (at the top of the plot) update simultaneously. Alternatively, you can get a specific interpolated *z* value by typing the *x* value and *y* value into editable text fields on the *x*-axis and *y*-axis respectively.

classregtree.surrcutcategories

Purpose

Categories used for surrogate splits in decision tree

Syntax

```
C = surrcutcategories(T)
C = surrcutcategories(T,J)
```

Description

`C = surrcutcategories(T)` returns an n-element cell array `C` of the categories used for surrogate splits in the decision tree `T`, where n is the number of nodes in the tree. For each node `K`, `C{K}` is a cell array. The length of `C{K}` is equal to the number of surrogate predictors found at this node. Every element of `C{K}` is either an empty string for a continuous surrogate predictor or a two-element cell array with categories for a categorical surrogate predictor. The first element of this two-element cell array lists categories assigned to the left child by this surrogate split and the second element of this two-element cell array lists categories assigned to the right child by this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables returned by `surrcutvar`. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, `C` contains an empty cell.

`C = surrcutcategories(T,J)` takes an array `J` of node numbers and returns the categories for the specified nodes.

See Also

`classregtree` | `surrcutvar` | `cutcategories` | `surrcuttype` | `surrcutpoint`

Purpose

Numeric cutpoint assignments used for surrogate splits in decision tree

Syntax

```
V = surrcutflip(T)
V = surrcutflip(T,J)
```

Description

`V = surrcutflip(T)` returns an n-element cell array `V` of the numeric cut assignments used for surrogate splits in the decision tree `T`, where n is the number of nodes in the tree. For each node `K`, `V{K}` is a numeric vector. The length of `V{K}` is equal to the number of surrogate predictors found at this node. Every element of `V{K}` is either zero for a categorical surrogate predictor or a numeric cut assignment for a continuous surrogate predictor. The numeric cut assignment can be either -1 or +1. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and the cut assignment for this surrogate split is +1, or if $Z>=C$ and the cut assignment for this surrogate split is -1. Similarly, the right child is chosen if $Z>=C$ and the cut assignment for this surrogate split is +1, or if $Z<C$ and the cut assignment for this surrogate split is -1. The order of the surrogate split variables at each node is matched to the order of variables returned by `surrcutvar`. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, `V` contains an empty array.

`V = surrcutflip(T,J)` takes an array `J` of node numbers and returns the cutpoint assignments for the specified nodes.

See Also

`classregtree` | `surrcutvar` | `surrcutcategories` | `surrcuttype` | `surrcutpoint` | `cutpoint`

classregtree.surrcutpoint

Purpose

Cutpoints used for surrogate splits in decision tree

Syntax

```
V = surrcutpoint(T)
V = surrcutpoint(T,J)
```

Description

`V = surrcutpoint(T)` returns an n-element cell array `V` of the numeric values used for surrogate splits in the decision tree `T`, where n is the number of nodes in the tree. For each node `K`, `V{K}` is a numeric vector. The length of `V{K}` is equal to the number of surrogate predictors found at this node. Every element of `V{K}` is either either `NaN` for a categorical surrogate predictor or a numeric cut for a continuous surrogate predictor. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and `surrcutflip` for this surrogate split is -1. Similarly, the right child is chosen if $Z>=C$ and `surrcutflip` for this surrogate split is +1, or if $Z<C$ and `surrcutflip` for this surrogate split is -1. The order of the surrogate split variables at each node is matched to the order of variables returned by `surrcutvar`. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, `V` contains an empty cell.

`V = surrcutpoint(T,J)` takes an array `J` of node numbers and returns the cutpoint assignments for the specified nodes.

See Also

`classregtree` | `surrcutvar` | `surrcutcategories` | `surrcuttype` | `surrcutflip` | `cutpoint`

Purpose

Types of surrogate splits used at branches in decision tree

Syntax

```
C = surrcuttype(T)
C = surrcuttype(T,J)
```

Description

`C = surrcuttype(T)` returns an *n*-element cell array `C` indicating types of surrogate splits at each node in the tree `T`, where *n* is the number of nodes in the tree. For each node `K`, `C{K}` is a cell array with the types of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The order of the surrogate split variables at each node is matched to the order of variables returned by `surrcutvar`. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, `C` contains an empty cell. A surrogate split type can be either `'continuous'` if the cut is defined in the form `Z<V` for a variable `Z` and cutpoint `V` or `'categorical'` if the cut is defined by whether `Z` takes a value in a set of categories.

`C = surrcuttype(T,J)` takes an array `J` of node numbers and returns the cut types for the specified nodes.

See Also

`classregtree` | `numnodes` | `cuttype` | `surrcutvar`

classregtree.surrcutvar

Purpose

Variables used for surrogate splits in decision tree

Syntax

```
V = surrcutvar(T)
V = surrcutvar(T,J)
[V,NUM] = surrcutvar(...)
```

Description

`V = surrcutvar(T)` returns an n-element cell array `V` of the names of the variables used for surrogate splits in each node of the tree `T`, where n is the number of nodes in the tree. Every element of `V` is a cell array with the names of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, `V` contains an empty cell.

`V = surrcutvar(T,J)` takes an array `J` of node numbers and returns the cut types for the specified nodes.

`[V,NUM] = surrcutvar(...)` also returns a cell array `NUM` with indices for each variable.

See Also

`classregtree` | `numnodes` | `children` | `cutvar`

Purpose

Predictive measure of association for surrogate splits in decision tree

Syntax

```
A = surrvarassoc(T)
A = surrvarassoc(T,J)
```

Description

`A = surrvarassoc(T)` returns an n-element cell array `A` of the predictive measures of association for surrogate splits in the decision tree `T`, where n is the number of nodes in the tree. For each node `K`, `A{K}` is a numeric vector. The length of `A{K}` is equal to the number of surrogate predictors found at this node. Every element of `A{K}` gives the predictive measure of association between the optimal split and this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables returned by `surrcutvar`. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, V contains an empty cell.

`A = surrvarassoc(T,J)` takes an array `J` of node numbers and returns the predictive measure of association for the specified nodes.

See Also

`classregtree` | `surrcutcategories` | `surrcuttype` | `surrcutflip` | `surrcutpoint` | `surrcutvar`

tabulate

Purpose

Frequency table

Syntax

```
TABLE = tabulate(x)
tabulate(x)
```

Description

`TABLE = tabulate(x)` creates a frequency table of data in vector `x`. Information in `TABLE` is arranged as follows:

- 1st column — The unique values of `x`
- 2nd column — The number of instances of each value
- 3rd column — The percentage of each value

If `x` is a numeric array, `TABLE` is a numeric matrix. If the elements of `x` are nonnegative integers, `TABLE` includes 0 counts for integers between `1` and `max(x)` that do not appear in `x`.

If `x` is a categorical variable, character array, or cell array of strings, `TABLE` is a cell array. (See “Grouped Data” on page 2-34.)

`tabulate(x)` with no output arguments displays the table in the command window.

Examples

```
tabulate([1 2 4 4 3 4])
  Value  Count  Percent
  1      1      16.67%
  2      1      16.67%
  3      1      16.67%
  4      3      50.00%
```

See Also

`pareto`

How To

- “Grouped Data” on page 2-34

Purpose

Read tabular data from file

Syntax

```
[data,varnames,casenames] = tblread
[data,varnames,casenames] = tblread(filename)
[data,varnames,casenames] = tblread(filename,delimiter)
```

Description

`[data,varnames,casenames] = tblread` displays the File Open dialog box for interactive selection of a tabular data file. The file format has variable names in the first row, case names in the first column and data starting in the (2, 2) position. Outputs are:

- `data` — Numeric matrix with a value for each variable-case pair
- `varnames` — String matrix containing the variable names in the first row of the file
- `casenames` — String matrix containing the names of each case in the first column of the file

`[data,varnames,casenames] = tblread(filename)` allows command line specification of the name of a file in the current folder, or the complete path name of any file, using the string *`filename`*.

`[data,varnames,casenames] = tblread(filename,delimiter)` reads from the file using *`delimiter`* as the delimiting character. Accepted values for *`delimiter`* are:

- `' '` or `'space'`
- `'\t'` or `'tab'`
- `','` or `'comma'`
- `';'` or `'semi'`
- `'|'` or `'bar'`

The default value of *`delimiter`* is `'space'`.

Examples

```
[data,varnames,casenames] = tblread('sat.dat')
data =
  470  530
  520  480

varnames =
Male
Female

casenames =
Verbal
Quantitative
```

See Also

tblwrite | tdfread | caseread

Purpose

Write tabular data to file

Syntax

```
tblwrite(data,varnames,casenames)
tblwrite(data,varnames,casenames,filename)
tblwrite(data,varnames,casenames,filename,delimiter)
```

Description

`tblwrite(data,varnames,casenames)` displays the **File Open** dialog box for interactive specification of the tabular data output file. The file format has variable names in the first row, case names in the first column and `data` starting in the (2,2) position.

`varnames` is a string matrix containing the variable names. `casenames` is a string matrix containing the names of each case in the first column. `data` is a numeric matrix with a value for each variable-case pair.

`tblwrite(data,varnames,casenames,filename)` specifies a file in the current folder, or the complete path name of any file in the string *`filename`*.

`tblwrite(data,varnames,casenames,filename,delimiter)` writes to the file using *`delimiter`* as the delimiting character. The following table lists the accepted character values for *`delimiter`* and their equivalent string values.

Character	String
`' '`	`'space'`
`'\t'`	`'tab'`
`','`	`'comma'`
`';'`	`'semi'`
`'|'`	`'bar'`

The default value of *`delimiter`* is `'space'`.

Examples

Continuing the example from `tblread`:

```
tblwrite(data,varnames,casenames,'sattest.dat')
```

```
type sattest.dat
               Male  Female
Verbal      470  530
Quantitative  520  480
```

See Also

casewrite | tblread

Purpose

Student's t cumulative distribution function

Syntax

```
P = tcdf(X,V)
```

Description

`P = tcdf(X,V)` computes Student's t cdf at each of the values in `X` using the corresponding degrees of freedom in `V`. `X` and `V` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

The t cdf is

$$p = F(x \mid \nu) = \int_{-\infty}^{x} \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{t^2}{\nu}\right)^{\frac{\nu+1}{2}}} dt$$

The result, p, is the probability that a single observation from the t distribution with ν degrees of freedom will fall in the interval $[-\infty, x)$.

Examples

```
mu = 1; % Population mean
sigma = 2; % Population standard deviation
n = 100; % Sample size
x = normrnd(mu,sigma,n,1); % Random sample from population
xbar = mean(x); % Sample mean
s = std(x); % Sample standard deviation
t = (xbar-mu)/(s/sqrt(n)) % t-statistic
t =
    0.2489
p = 1-tcdf(t,n-1) % Probability of larger t-statistic
p =
    0.4020
```

This probability is the same as the p value returned by a t-test of the null hypothesis that the sample comes from a normal population with mean μ:

```
[h,ptest] = ttest(x,mu,0.05,'right')
h =
     0
ptest =
    0.4020
```

See Also

cdf | tpdf | tinv | tstat | trnd

How To

- “Student’s t Distribution” on page B-95

Purpose

Read tab-delimited file

Syntax

```
tdfread
tdfread(filename)
tdfread(filename,delimiter)
s = tdfread(filename,...)
```

Description

`tdfread` displays the **File Open** dialog box for interactive selection of a data file, then reads data from the file. The file should have variable names separated by tabs in the first row, and data values separated by tabs in the remaining rows. `tdfread` creates variables in the workspace, one for each column of the file. The variable names are taken from the first row of the file. If a column of the file contains only numeric data in the second and following rows, `tdfread` creates a `double` variable. Otherwise, `tdfread` creates a `char` variable. After all values are imported, `tdfread` displays information about the imported values using the format of the `tdfread` command.

`tdfread(`*`filename`*`)` allows command line specification of the name of a file in the current folder, or the complete path name of any file, using the string *`filename`*.

`tdfread(`*`filename`*`,`*`delimiter`*`)` indicates that the character specified by *`delimiter`* separates columns in the file. Accepted values for *`delimiter`* are:

- `' '` or `'space'`
- `'\t'` or `'tab'`
- `','` or `'comma'`
- `';'` or `'semi'`
- `'|'` or `'bar'`

The default delimiter is `'tab'`.

`s = tdfread(`*`filename`*`,...)` returns a scalar structure `s` whose fields each contain a variable.

Examples

The following displays the contents of the file `sat2.dat`:

```
type sat2.dat

Test,Gender,Score
Verbal,Male,470
Verbal,Female,530
Quantitative,Male,520
Quantitative,Female,480
```

The following creates the variables `Gender`, `Score`, and `Test` from the file `sat2.dat` and displays the contents of the MATLAB workspace:

```
tdfread('sat2.dat',',')

Name    Size    Bytes    Class    Attributes

Gender  4x6     48       char
Score   4x1     32       double
Test    4x12    96       char
```

See Also

`tblread` | `caseread`

Purpose

Create classification template

Syntax

```
t = ClassificationTree.template
t = ClassificationTree.template(Name,Value)
```

Description

`t = ClassificationTree.template` returns a learner template suitable to use in the `fitensemble` function.

`t = ClassificationTree.template(Name,Value)` creates a template with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`MergeLeaves`

String that specifies whether to merge leaves after the tree is grown. Values are `'on'` or `'off'`.

When `'on'`, `ClassificationTree` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, `ClassificationTree` does not merge leaves.

Default: `'off'`

`MinLeaf`

Each leaf has at least `MinLeaf` observations per tree leaf. If you supply both `MinParent` and `MinLeaf`, `ClassificationTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: Half the number of training observations for boosting, 1 for bagging

`MinParent`

Each branch node in the tree has at least `MinParent` observations. If you supply both `MinParent` and `MinLeaf`, `ClassificationTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: Number of training observations for boosting, 2 for bagging

`NVarToSample`

Number of predictors to select at random for each split. Can be a positive integer or `'all'`, which means use all available predictors.

Default: `'all'` for boosting, square root of number of predictors for bagging

`Prune`

When `'on'`, `ClassificationTree` grows the classification tree and computes the optimal sequence of pruned subtrees. When `'off'` `ClassificationTree` grows the tree without pruning.

Default: `'off'`

`PruneCriterion`

String with the pruning criterion, either `'error'` or `'impurity'`.

Default: `'error'`

`SplitCriterion`

Criterion for choosing a split. One of `'gdi'` (Gini's diversity index), `'twoing'` for the twoing rule, or `'deviance'` for maximum deviance reduction (also known as cross entropy).

Default: `'gdi'`

`Surrogate`

String describing whether to find surrogate decision splits at each branch node. This setting improves the accuracy of predictions for data with missing values. The setting also enables you to compute measures of predictive association between predictors. This setting can use much time and memory. Values are `'on'` or `'off'`.

Default: `'off'`

Output Arguments

`t`

Classification tree template suitable to use in the `fitensemble` function. In an ensemble, `t` specifies how to grow the classification trees.

Examples

Create a classification template with surrogate splits, and train an ensemble for the Fisher iris model with the template:

```
t = ClassificationTree.template('surrogate','on');
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,t);
```

See Also

`ClassificationTree` | `ClassificationTree.fit` | `fitensemble`

How To

- Chapter 13, "Nonparametric Supervised Learning"

RegressionTree.template

Purpose

Create regression template

Syntax

```
t = RegressionTree.template
t = RegressionTree.template(Name,Value)
```

Description

`t = RegressionTree.template` returns a learner template suitable to use in the `fitensemble` function.

`t = RegressionTree.template(Name,Value)` creates a template with additional options specified by one or more `Name,Value` pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

Input Arguments

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`MergeLeaves`

String that specifies whether to merge leaves after the tree is grown. Values are `'on'` or `'off'`.

When `'on'`, `RegressionTree` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, `RegressionTree` does not merge leaves.

Default: `'off'`

`MinLeaf`

Each leaf has at least `MinLeaf` observations per tree leaf. If you supply both `MinParent` and `MinLeaf`, `RegressionTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: Half the number of training observations for boosting, `5` for bagging

`MinParent`

Each branch node in the tree has at least `MinParent` observations. If you supply both `MinParent` and `MinLeaf`, `RegressionTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: Number of training observations for boosting, `10` for bagging

`NVarToSample`

Number of predictors to select at random for each split. Can be a positive integer or `'all'`, which means use all available predictors.

Default: `'all'` for boosting, one third of the number of predictors for bagging

`Prune`

When `'on'`, `RegressionTree` grows the regression tree and computes the optimal sequence of pruned subtrees. When `'off'` `RegressionTree` grows the tree without pruning.

Default: `'off'`

`Surrogate`

String describing whether to find surrogate decision splits at each branch node. This setting improves the accuracy of predictions for data with missing values. The setting also enables you to compute measures of predictive association between predictors. This setting can use much time and memory. Values are `'on'` or `'off'`.

Default: `'off'`

Output Arguments

`t`

Regression tree template suitable to use in the `fitensemble` function. In an ensemble, `t` specifies how to grow the regression trees.

Examples

Create a regression template with surrogate splits, and train an ensemble for the `carsmall` data with the template:

```
t = RegressionTree.template('surrogate','on');
load carsmall
X = [Acceleration Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',100,t);
```

See Also

`RegressionTree` | `RegressionTree.fit` | `fitensemble`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

Error rate

Syntax

```
cost = test(t,'resubstitution')
cost = test(t,'test',X,y)
cost = test(t,'crossvalidate',X,y)
[cost,secost,ntnodes,bestlevel] = test(...)
[...] = test(...,param1,val1,param2,val2,...)
```

Description

`cost = test(t,'resubstitution')` computes the cost of the tree `t` using a resubstitution method. `t` is a decision tree as created by `classregtree`. The cost of the tree is the sum over all terminal nodes of the estimated probability of a node times the cost of a node. If `t` is a classification tree, the cost of a node is the sum of the misclassification costs of the observations in that node. If `t` is a regression tree, the cost of a node is the average squared error over the observations in that node. `cost` is a vector of cost values for each subtree in the optimal pruning sequence for `t`. The resubstitution cost is based on the same sample that was used to create the original tree, so it under estimates the likely cost of applying the tree to new data.

`cost = test(t,'test',X,y)` uses the matrix of predictors `X` and the response vector `y` as a test sample, applies the decision tree `t` to that sample, and returns a vector `cost` of cost values computed for the test sample. `X` and `y` should not be the same as the learning sample, that is, the sample that was used to fit the tree `t`.

`cost = test(t,'crossvalidate',X,y)` uses 10-fold cross-validation to compute the cost vector. `X` and `y` should be the learning sample, that is, the sample that was used to fit the tree `t`. The function partitions the sample into 10 subsamples, chosen randomly but with roughly equal size. For classification trees, the subsamples also have roughly the same class proportions. For each subsample, `test` fits a tree to the remaining data and uses it to predict the subsample. It pools the information from all subsamples to compute the cost for the whole sample.

`[cost,secost,ntnodes,bestlevel] = test(...)` also returns the vector `secost` containing the standard error of each `cost` value, the vector `ntnodes` containing the number of terminal nodes for each

subtree, and the scalar `bestlevel` containing the estimated best level of pruning. A `bestlevel` of `0` means no pruning. The best level is the one that produces the smallest tree that is within one standard error of the minimum-cost subtree.

`[...] = test(...,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs for methods other than `'resubstitution'`, chosen from the following:

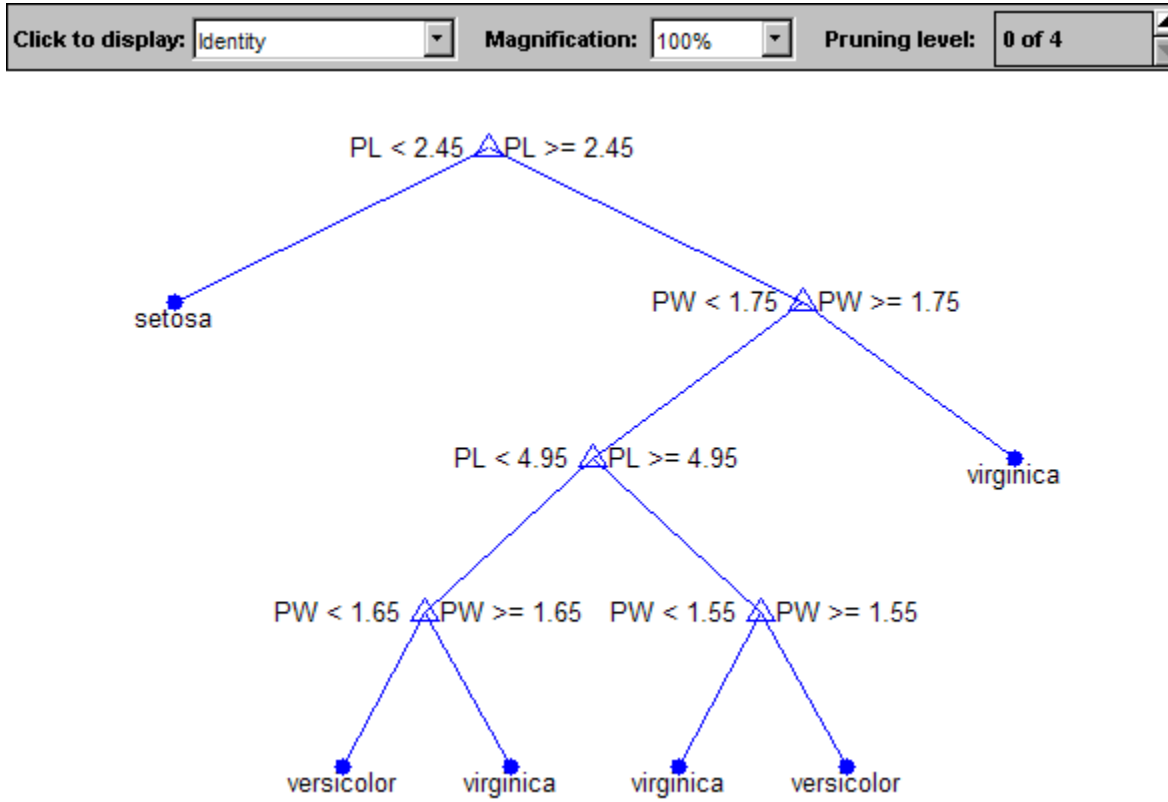
- `'weights'` — Observation weights.
- `'nsamples'` — The number of cross-validation samples (default is `10`).
- `'treesize'` — Either `'se'` (default) to choose the smallest tree whose cost is within one standard error of the minimum cost, or `'min'` to choose the minimal cost tree.

Examples

Find the best tree for Fisher's iris data using cross-validation. Start with a large tree:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'},...
                 'splitmin',5)
t =
Decision tree for classification
 1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
 2  class = setosa
 3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
 4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
 5  class = virginica
 6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
 7  if PW<1.55 then node 10 elseif PW>=1.55 then node 11 else virginica
 8  class = versicolor
 9  class = virginica
10  class = virginica
```

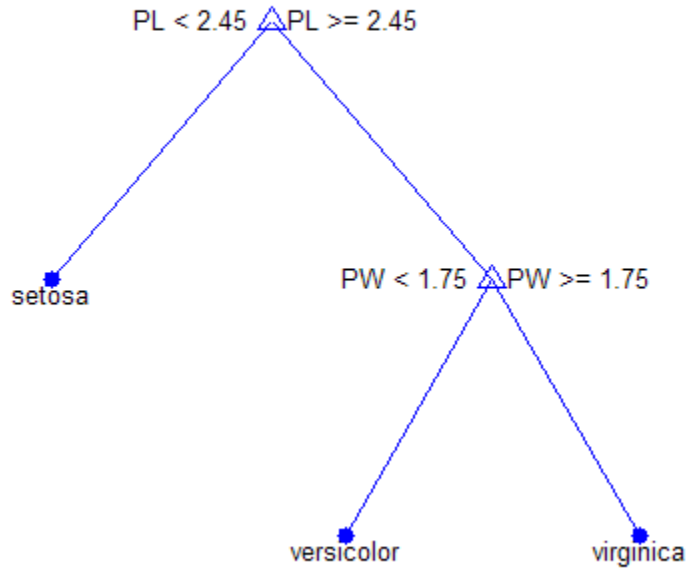
```
11  class = versicolor

view(t)
```



Find the minimum-cost tree:

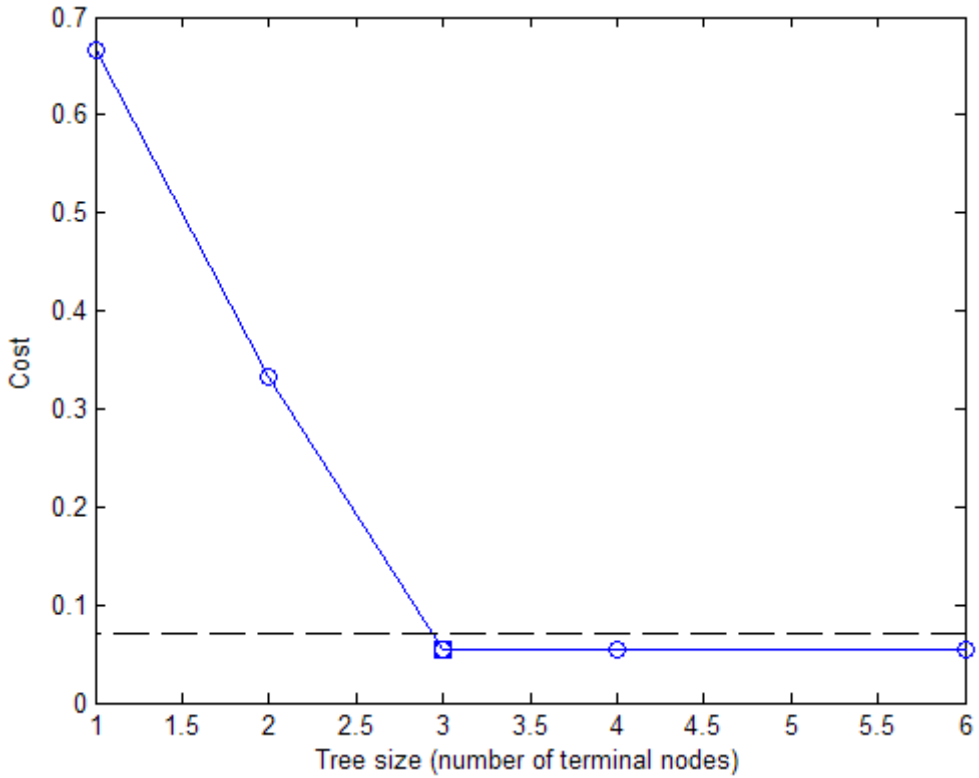
```
[c,s,n,best] = test(t,'cross',meas,species);
tmin = prune(t,'level',best)
tmin =
Decision tree for classification
```

```
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  class = versicolor
5  class = virginica

view(tmin)
```



Plot the smallest tree within one standard error of the minimum cost tree:

```
[mincost,minloc] = min(c);
plot(n,c,'b-o',...
     n(best+1),c(best+1),'bs',...
     n,(mincost+s(minloc))*ones(size(n)),'k--')
xlabel('Tree size (number of terminal nodes)')
ylabel('Cost')
```



The solid line shows the estimated cost for each tree size, the dashed line marks one standard error above the minimum, and the square marks the smallest tree under the dashed line.

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `eval` | `view` | `prune`

Purpose

Test indices for cross-validation

Syntax

```
idx = test(c)
idx = test(c,i)
```

Description

`idx = test(c)` returns the logical vector `idx` of test indices for an object `c` of the `cvpartition` class of type `'holdout'` or `'resubstitution'`.

If `c.Type` is `'holdout'`, `idx` specifies the observations in the test set.

If `c.Type` is `'resubstitution'`, `idx` specifies all observations.

`idx = test(c,i)` returns the logical vector `idx` of test indices for repetition `i` of an object `c` of the `cvpartition` class of type `'kfold'` or `'leaveout'`.

If `c.Type` is `'kfold'`, `idx` specifies the observations in the test set in fold `i`.

If `c.Type` is `'leaveout'`, `idx` specifies the observation left out at repetition `i`.

Examples

Identify the test indices in the first fold of a partition of 10 observations for 3-fold cross-validation:

```
c = cvpartition(10,'kfold',3)
c =
K-fold cross validation partition
             N: 10
   NumTestSets: 3
     TrainSize: 7  6  7
      TestSize: 3  4  3

test(c,1)
ans =
     1
     1
     0
     0
```

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

See Also

cvpartition | training

Purpose

Size of each test set

Description

Value is a vector in partitions of type `'kfold'` and `'leaveout'`. Value is a scalar in partitions of type `'holdout'` and `'resubstitution'`.

tiedrank

Purpose

Rank adjusted for ties

Syntax

```
[R,TIEADJ] = tiedrank(X)
[R,TIEADJ] = tiedrank(X,1)
[R,TIEADJ] = tiedrank(X,0,1)
```

Description

`[R,TIEADJ] = tiedrank(X)` computes the ranks of the values in the vector `X`. If any `X` values are tied, `tiedrank` computes their average rank. The return value `TIEADJ` is an adjustment for ties required by the nonparametric tests `signrank` and `ranksum`, and for the computation of Spearman's rank correlation.

`[R,TIEADJ] = tiedrank(X,1)` computes the ranks of the values in the vector `X`. `TIEADJ` is a vector of three adjustments for ties required in the computation of Kendall's tau. `tiedrank(X,0)` is the same as `tiedrank(X)`.

`[R,TIEADJ] = tiedrank(X,0,1)` computes the ranks from each end, so that the smallest and largest values get rank 1, the next smallest and largest get rank 2, etc. These ranks are used in the Ansari-Bradley test.

Examples

Counting from smallest to largest, the two 20 values are 2nd and 3rd, so they both get rank 2.5 (average of 2 and 3):

```
tiedrank([10 20 30 40 20])
ans =
    1.0000    2.5000    4.0000    5.0000    2.5000
```

See Also

`ansaribradley` | `corr` | `partialcorr` | `ranksum` | `signrank`

Purpose

Product of categorical arrays

Syntax

```
C = times(A,B)
```

Description

`C = times(A,B)` returns a categorical array each of whose elements has the level formed from the concatenation of the levels of the corresponding elements of `A` and `B`. The set of levels of `C` is the cartesian product of the sets of levels of `A` and of `B`. The syntax `A .* B` calls `C = times(A,B)`.

See Also

`categorical`

Purpose

Student's *t* inverse cumulative distribution function

Syntax

```
X = tinv(P,V)
```

Description

`X = tinv(P,V)` computes the inverse of Student's *t* cdf using the degrees of freedom in `V` for the corresponding probabilities in `P`. `P` and `V` can be vectors, matrices, or multidimensional arrays that are the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The values in `P` must lie on the interval [0 1].

The t inverse function in terms of the *t* cdf is

$$x = F^{-1}(p \mid \nu) = \{x : F(x \mid \nu) = p\}$$

where

$$p = F(x \mid \nu) = \int_{-\infty}^{x} \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{t^2}{\nu}\right)^{\frac{\nu+1}{2}}} dt$$

The result, *x*, is the solution of the cdf integral with parameter ν, where you supply the desired probability *p*.

Examples

What is the 99th percentile of the *t* distribution for one to six degrees of freedom?

```
percentile = tinv(0.99,1:6)
percentile =
  31.8205  6.9646  4.5407  3.7469  3.3649  3.1427
```

See Also

`icdf` | `tcdf` | `tpdf` | `trnd` | `tstat`

How To

- "Student's t Distribution" on page B-95

Purpose

Student's t probability density function

Syntax

```
Y = tpdf(X,V)
```

Description

`Y = tpdf(X,V)` computes Student's t pdf at each of the values in `X` using the corresponding degrees of freedom in `V`. `X` and `V` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

Student's t pdf is

$$y = f(x \mid \nu) = \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{x^2}{\nu}\right)^{\frac{\nu+1}{2}}}$$

Examples

The mode of the t distribution is at $x = 0$. This example shows that the value of the function at the mode is an increasing function of the degrees of freedom.

```
tpdf(0,1:6)
ans =
  0.3183   0.3536   0.3676   0.3750   0.3796   0.3827
```

The t distribution converges to the standard normal distribution as the degrees of freedom approaches infinity. How good is the approximation for $\nu = 30$?

```
difference = tpdf(-2.5:2.5,30)-normpdf(-2.5:2.5)
difference =
  0.0035   -0.0006   -0.0042   -0.0042   -0.0006   0.0035
```

See Also

`pdf` | `tcdf` | `tinv` | `tstat` | `trnd`

How To

- "Student's t Distribution" on page B-95

Purpose

Training indices for cross-validation

Syntax

```
idx = training(c)
idx = training(c,i)
```

Description

`idx = training(c)` returns the logical vector `idx` of training indices for an object `c` of the `cvpartition` class of type `'holdout'` or `'resubstitution'`.

If `c.Type` is `'holdout'`, `idx` specifies the observations in the training set.

If `c.Type` is `'resubstitution'`, `idx` specifies all observations.

`idx = training(c,i)` returns the logical vector `idx` of training indices for repetition `i` of an object `c` of the `cvpartition` class of type `'kfold'` or `'leaveout'`.

If `c.Type` is `'kfold'`, `idx` specifies the observations in the training set in fold `i`.

If `c.Type` is `'leaveout'`, `idx` specifies the observations left in at repetition `i`.

Examples

Identify the training indices in the first fold of a partition of 10 observations for 3-fold cross-validation:

```
c = cvpartition(10,'kfold',3)
c =
K-fold cross validation partition
             N: 10
   NumTestSets: 3
     TrainSize: 7  6  7
      TestSize: 3  4  3

training(c,1)
ans =
     0
     0
```

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

See Also

`cvpartition` | `test`

Purpose

Size of each training set

Description

Value is a vector in partitions of type `'kfold'` and `'leaveout'`. Value is a scalar in partitions of type `'holdout'` and `'resubstitution'`.

See Also

`type`

categorical.transpose

Purpose

Transpose categorical matrix

Syntax

```
B = transpose(A)
```

Description

`B = transpose(A)` returns the transpose of the 2-D categorical matrix `A`. `ctranspose` is identical to `transpose` for categorical arrays. The syntax `A.'` calls `transpose`.

See Also

`ctranspose` | `permute`

Purpose

Cell array of arguments for `classregtree`

Description

The `TreeArgs` property is a cell array of arguments for the `classregtree` constructor. `TreeBagger` uses these arguments in growing new trees for the ensemble.

TreeBagger

Purpose

Bootstrap aggregation for ensemble of decision trees

Description

`TreeBagger` bags an ensemble of decision trees for either classification or regression. Bagging stands for bootstrap aggregation. Every tree in the ensemble is grown on an independently drawn bootstrap replica of input data. Observations not included in this replica are "out of bag" for this tree. To compute prediction of an ensemble of trees for unseen data, `TreeBagger` takes an average of predictions from individual trees. To estimate the prediction error of the bagged ensemble, you can compute predictions for each tree on its out-of-bag observations, average these predictions over the entire ensemble for each observation and then compare the predicted out-of-bag response with the true value at this observation.

`TreeBagger` relies on the `classregtree` functionality for growing individual trees. In particular, `classregtree` accepts the number of features selected at random for each decision split as an optional input argument.

The `Compact` property contains another class, `CompactTreeBagger`, with sufficient information to make predictions using new data. This information includes the tree ensemble, variable names, and class names (for classification). `CompactTreeBagger` requires less memory than `TreeBagger`, but only `TreeBagger` has methods for growing more trees for the ensemble. Once you grow an ensemble of trees using `TreeBagger` and no longer need access to the training data, you can opt to work with the compact version of the trained ensemble from then on.

Construction

TreeBagger	Create ensemble of bagged decision trees

Methods

append	Append new trees to ensemble
compact	Compact ensemble of decision trees

error	Error (misclassification probability or MSE)
fillProximities	Proximity matrix for training data
growTrees	Train additional trees and add to ensemble
margin	Classification margin
mdsProx	Multidimensional scaling of proximity matrix
meanMargin	Mean classification margin
oobError	Out-of-bag error
oobMargin	Out-of-bag margins
oobMeanMargin	Out-of-bag mean margins
oobPredict	Ensemble predictions for out-of-bag observations
predict	Predict response

Properties

`ClassNames`

A cell array containing the class names for the response variable `Y`. This property is empty for regression trees.

`ComputeOOBPrediction`

A logical flag specifying whether out-of-bag predictions for training observations should be computed. The default is `false`.

If this flag is true, the following properties are available:

- `OOBIndices`
- `OOBInstanceWeight`

If this flag is true, the following methods can be called:

- `oobError`
- `oobMargin`
- `oobMeanMargin`

See also `oobError`, `OOBIndices`, `OOBInstanceWeight`, `oobMargin`, `oobMeanMargin`.

`Cost`

A matrix with misclassification costs. This property is empty for ensembles of regression trees.

See also `classregtree`.

`DeltaCritDecisionSplit`

A numeric array of size 1-by-*Nvars* of changes in the split criterion summed over splits on each variable, averaged across the entire ensemble of grown trees.

See also `classregtree.varimportance`.

`NVarSplit`

A numeric array of size 1-by-*Nvars*, where every element gives a number of splits on this predictor summed over all trees.

`OOBPermutedVarDeltaError`

A numeric array of size 1-by-*Nvars* containing a measure of importance for each predictor variable (feature). For any variable, the measure is the increase in prediction error if the values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble.

`OOBPermutedVarDeltaMeanMargin`

A numeric array of size 1-by-*Nvars* containing a measure of importance for each predictor variable (feature). For any variable, the measure is the decrease in the classification margin if the

values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble. This property is empty for regression trees.

`OutlierMeasure`

A numeric array of size *Nobs*-by-1, where *Nobs* is the number of observations in the training data, containing outlier measures for each observation.

See also `CompactTreeBagger.OutlierMeasure`.

`Prior`

A vector with prior probabilities for classes. This property is empty for ensembles of regression trees.

See also `classregtree`.

`Proximity`

A numeric matrix of size *Nobs*-by-*Nobs*, where *Nobs* is the number of observations in the training data, containing measures of the proximity between observations. For any two observations, their proximity is defined as the fraction of trees for which these observations land on the same leaf. This is a symmetric matrix with 1s on the diagonal and off-diagonal elements ranging from 0 to 1.

See also `CompactTreeBagger.proximity`, `classregtree.varimportance`.

`Prune`

The `Prune` property is true if decision trees are pruned and false if they are not. Pruning decision trees is not recommended for ensembles. The default value is false.

See also `classregtree.prune`.

`SampleWithReplacement`

A logical flag specifying if data are sampled for each decision tree with replacement. True if `TreeBagger` samples data with replacement and false otherwise. True by default.

`Trees`

A cell array of size *NTrees*-by-1 containing the trees in the ensemble.

See also `NTrees`.

`VarAssoc`

A matrix of size *Nvars*-by-*Nvars* with predictive measures of variable association, averaged across the entire ensemble of grown trees. If you grew the ensemble setting `'surrogate'` to `'on'`, this matrix for each tree is filled with predictive measures of association averaged over the surrogate splits. If you grew the ensemble setting `'surrogate'` to `'off'` (default), `VarAssoc` is diagonal.

`VarNames`

A cell array containing the names of the predictor variables (features). `TreeBagger` takes these names from the optional `'names'` parameter. The default names are `'x1'`, `'x2'`, etc.

`X`

A numeric matrix of size *Nobs*-by-*Nvars*, where *Nobs* is the number of observations (rows) and *Nvars* is the number of variables (columns) in the training data. This matrix contains the predictor (or feature) values.

`Y`

An array of true class labels for classification, or response values for regression. `Y` can be a numeric column vector, a character matrix, or a cell array of strings.

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

How To

- "Ensemble Methods" on page 13-51
- "Classification Trees and Regression Trees" on page 13-27
- Grouped Data

TreeBagger

Purpose

Create ensemble of bagged decision trees

Syntax

```
B = TreeBagger(ntrees,X,Y)
B = TreeBagger(ntrees,X,Y,'param1',val1,'param2',val2,...)
```

Description

`B = TreeBagger(ntrees,X,Y)` creates an ensemble `B` of `ntrees` decision trees for predicting response `Y` as a function of predictors `X`. By default `TreeBagger` builds an ensemble of classification trees. The function can build an ensemble of regression trees by setting the optional input argument `'method'` to `'regression'`.

`X` is a numeric matrix of training data. Each row represents an observation and each column represents a predictor or feature. `Y` is an array of true class labels for classification or numeric function values for regression. True class labels can be a numeric vector, character matrix, vector cell array of strings or categorical vector. `TreeBagger` converts labels to a cell array of strings for classification.

For more information on grouping variables, see "Grouped Data" on page 2-34.

`B = TreeBagger(ntrees,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'FBoot'`	Fraction of input data to sample with replacement from the input data for growing each new tree. Default value is 1.
`'OOBPred'`	`'on'` to store info on what observations are out of bag for each tree. This info can be used by `oobPredict` to compute the predicted class probabilities for each tree in the ensemble. Default is `'off'`.
`'OOBVarImp'`	`'on'` to store out-of-bag estimates of feature importance in the ensemble. Default is `'off'`. Specifying `'on'` also sets the `'OOBPred'` value to `'on'`.

`'Method'`	Either `'classification'` or `'regression'`. Regression requires a numeric `Y`.
`'NVarToSample'`	Number of variables to select at random for each decision split. Default is the square root of the number of variables for classification and one third of the number of variables for regression. Valid values are `'all'` or a positive integer. Setting this argument to any valid value but `'all'` invokes Breiman's 'random forest' algorithm.
`'NPrint'`	Number of training cycles (grown trees) after which `TreeBagger` displays a diagnostic message showing training progress. Default is no diagnostic messages.
`'MinLeaf'`	Minimum number of observations per tree leaf. Default is 1 for classification and 5 for regression.
`'Options'`	A structure that specifies options that govern the computation when growing the ensemble of decision trees. One option requests that the computation of decision trees on multiple bootstrap replicates uses multiple processors, if the Parallel Computing Toolbox is available. Two options specify the random number streams to use in selecting bootstrap replicates. You can create this argument with a call to `statset`. You can retrieve values of the individual fields with a call to `statget`. Applicable `statset` parameters are: • `'UseParallel'` — If `'always'` and if a `matlabpool` of the Parallel Computing Toolbox is open, compute decision trees drawn on separate boostrap replicates in parallel. If the Parallel Computing Toolbox is not installed, or a `matlabpool` is not open, computation occurs in serial mode. Default is `'never'`, or serial computation.

- 'UseSubstreams' — If 'always' select each bootstrap replicate using a separate Substream of the random number generator (aka Stream). This option is available only with RandStream types that support Substreams: 'mlfg6331_64' or 'mrg32k3a'. Default is 'never', do not use a different Substream to compute each bootstrap replicate.
- Streams — A RandStream object or cell array of such objects. If you do not specify Streams, TreeBagger uses the default stream or streams. If you choose to specify Streams, use a single object except in the case
  - You have an open MATLAB pool
  - UseParallel is 'always'
  - UseSubstreams is 'never'

  In that case, use a cell array the same size as the MATLAB pool.

For more information on using parallel computing, see Chapter 17, "Parallel Statistics".

In addition to the optional arguments above, this method accepts all optional classregtree arguments with the exception of 'minparent'. Refer to the documentation for classregtree for more detail.

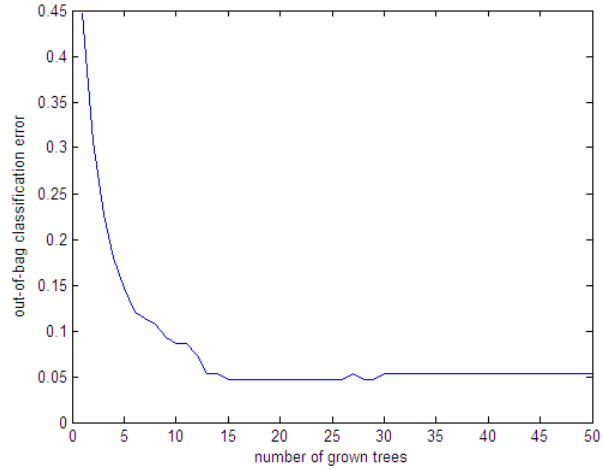
Examples

```
load fisheriris
b = TreeBagger(50,meas,species,'OOBPred','on')
plot(oobError(b))
xlabel('number of grown trees')
ylabel('out-of-bag classification error')
```

returns

```
b =
```

```
Ensemble with 50 bagged decision trees:
                Training X:              [150x4]
                Training Y:              [150x1]
                    Method:       classification
                     Nvars:                    4
            NVarToSample:                      2
                 MinLeaf:                      1
                   FBoot:                      1
    SampleWithReplacement:                     1
     ComputeOOBPrediction:                     1
         ComputeOOBVarImp:                     0
                Proximity:                    []
                    Prune:                     0
             MergeLeaves:                      0
                TreeArgs:
               ClassNames:'setosa'  'versicolor'  'virginica'
```



See Also

`classregtree` | `CompactTreeBagger`

How To

- “Ensemble Methods” on page 13-51

- “Grouped Data” on page 2-34

Purpose

Plot tree

Note `treedisp` will be removed in a future release. Use `classregtree.view` instead.

Syntax

```
treedisp(t)
treedisp(t,param1,val1,param2,val2,...)
```

Description

Note This function is superseded by the `view` method of the `classregtree` class and is maintained only for backwards compatibility. It accepts objects `t` created with the `classregtree` constructor.

`treedisp(t)` takes as input a decision tree `t` as computed by the `treefit` function, and displays it in a figure window. Each branch in the tree is labeled with its decision rule, and each terminal node is labeled with the predicted value for that node.

For each branch node, the left child node corresponds to the points that satisfy the condition, and the right child node corresponds to the points that do not satisfy the condition.

The **Click to display** pop-up menu at the top of the figure enables you to display more information about each node, as described in the following table.

Menu Choice	Displays
`Identity`	The node number, whether the node is a branch or a leaf, and the rule that governs the node
`Variable ranges`	The range of each of the predictor variables for that node
`Node statistics`	Descriptive statistics for the observations falling into this node

After you select the type of information you want, click any node to display the information for that node.

The **Pruning level** button displays the number of levels that have been cut from the tree and the number of levels in the unpruned tree. For example, `1 of 6` indicates that the unpruned tree has six levels, and that one level has been cut from the tree. Use the spin button to change the pruning level.

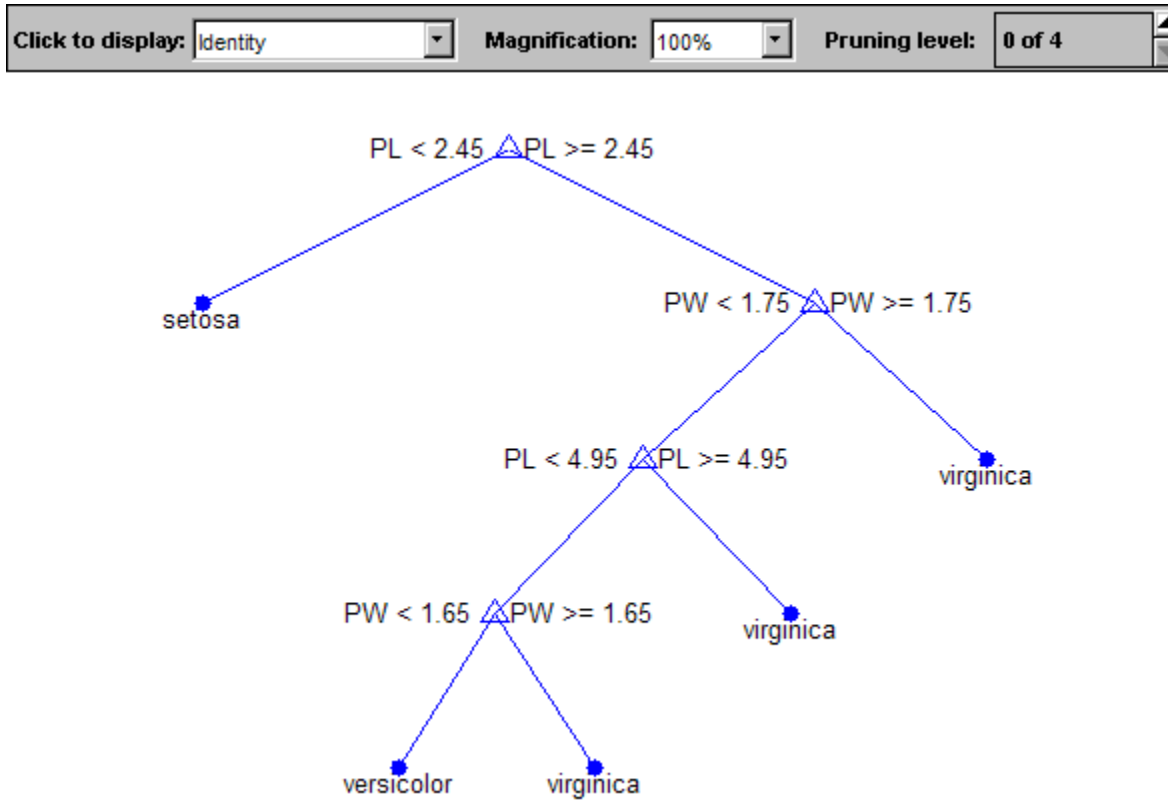
`treedisp(t,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` specifies optional parameter name-value pairs, listed in the following table.

Parameter	Value
`'names'`	A cell array of names for the predictor variables, in the order in which they appear in the `X` matrix from which the tree was created (see `treefit`)
`'prunelevel'`	Initial pruning level to display

Examples

Create and graph classification tree for Fisher's iris data. The names in this example are abbreviations for the column contents (sepal length, sepal width, petal length, and petal width).

```
load fisheriris;
t = treefit(meas,species);
treedisp(t,'names',{'SL' 'SW' 'PL' 'PW'});
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`treefit` | `treeprune` | `treetest`

treefit

Purpose

Fit tree

Note `treefit` will be removed in a future release. Use `classregtree` instead.

Syntax

```
t = treefit(X,y)
t = treefit(X,y,param1,val1,param2,val2,...)
```

Description

Note This function is superseded by the `classregtree` constructor of the `classregtree` class and is maintained only for backwards compatibility. It returns objects `t` in the `classregtree` class.

`t = treefit(X,y)` creates a decision tree `t` for predicting response `y` as a function of predictors `X`. `X` is an `n`-by-`m` matrix of predictor values. `y` is either a vector of `n` response values (for regression), or a character array or cell array of strings containing `n` class names (for classification). Either way, `t` is a binary tree where each non-terminal node is split based on the values of a column of `X`.

`t = treefit(X,y,param1,val1,param2,val2,...)` specifies optional parameter name-value pairs. Valid parameter strings are:

The following table lists parameters available for all trees.

Parameter	Value
`'catidx'`	Vector of indices of the columns of `X`. `treefit` treats these columns as unordered categorical values.
`'method'`	Either `'classification'` (default if `y` is text) or `'regression'` (default if `y` is numeric).

Parameter	Value
'splitmin'	A number n such that impure nodes must have n or more observations to be split (default 10).
'prune'	'on' (default) to compute the full tree and a sequence of pruned subtrees, or 'off' for the full tree without pruning.

The following table lists parameters available for classification trees only.

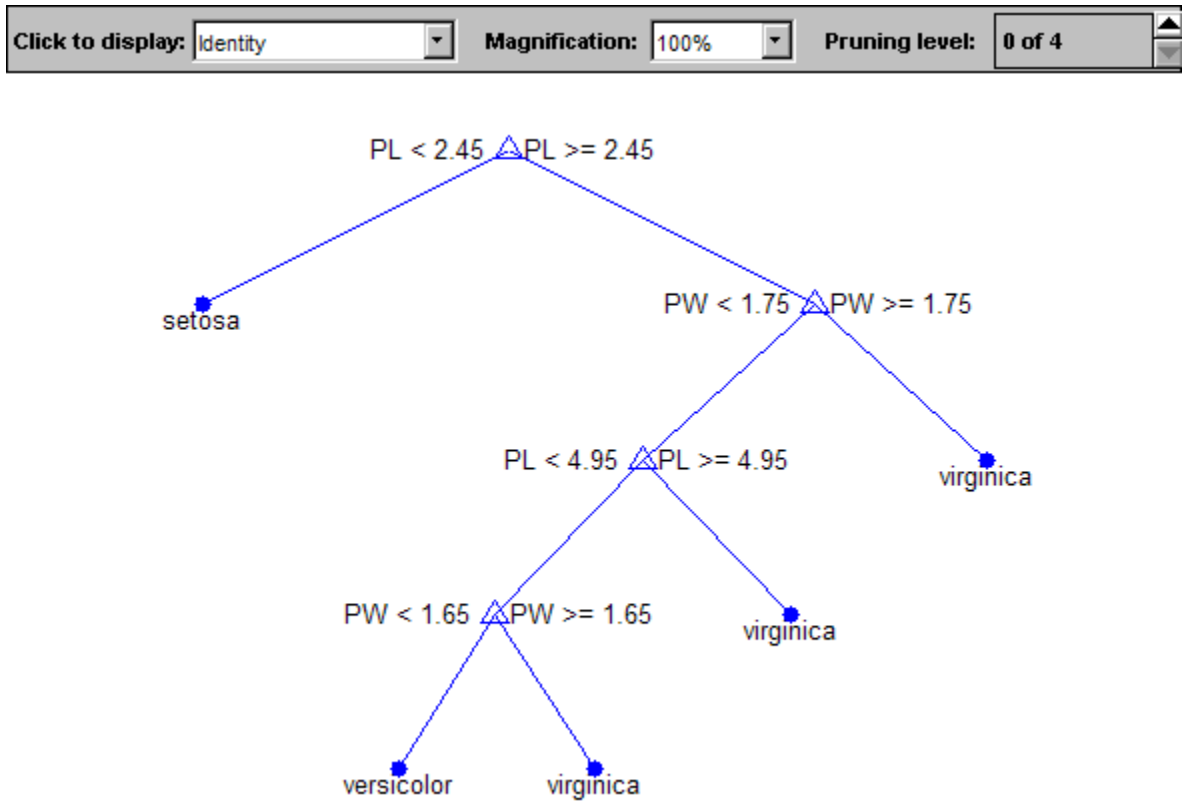
Parameter	Value
'cost'	p-by-p matrix C, where p is the number of distinct response values or class names in the input y. C(i,j) is the cost of classifying a point into class j if its true class is i. (The default has C(i,j)=1 if i~=j, and C(i,j)=0 if i=j.) C can also be a structure S with two fields: S.group containing the group names (see "Grouped Data" on page 2-34), and S.cost containing a matrix of cost values.
'splitcriterion'	Criterion for choosing a split: either 'gdi' (default) for Gini's diversity index, 'twoing' for the twoing rule, or 'deviance' for maximum deviance reduction.
'priorprob'	Prior probabilities for each class, specified as a vector (one value for each distinct group name) or as a structure S with two fields: S.group containing the group names, and S.prob containing a vector of corresponding probabilities.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;
t = treefit(meas,species);
```

```
treedisp(t,'names',{'SL' 'SW' 'PL' 'PW'});
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`treedisp` | `treetest`

How To

- "Grouped Data" on page 2-34

Purpose

Prune tree

Note `treeprune` will be removed in a future release. Use `classregtree.prune` instead.

Syntax

```
t2 = treeprune(t1,'level',level)
t2 = treeprune(t1,'nodes',nodes)
t2 = treeprune(t1)
```

Description

Note This function is superseded by the `prune` method of the `classregtree` class and is maintained only for backwards compatibility. It accepts objects `t1` created with the `classregtree` constructor and returns objects `t2` in the `classregtree` class.

`t2 = treeprune(t1,'level',level)` takes a decision tree `t1` as created by the `treefit` function, and a pruning level, and returns the decision tree `t2` pruned to that level. Setting `level` to `0` means no pruning. Trees are pruned based on an optimal pruning scheme that first prunes branches giving less improvement in error cost.

`t2 = treeprune(t1,'nodes',nodes)` prunes the nodes listed in the `nodes` vector from the tree. Any `t1` branch nodes listed in `nodes` become leaf nodes in `t2`, unless their parent nodes are also pruned. The `treedisp` function can display the node numbers for any node you select.

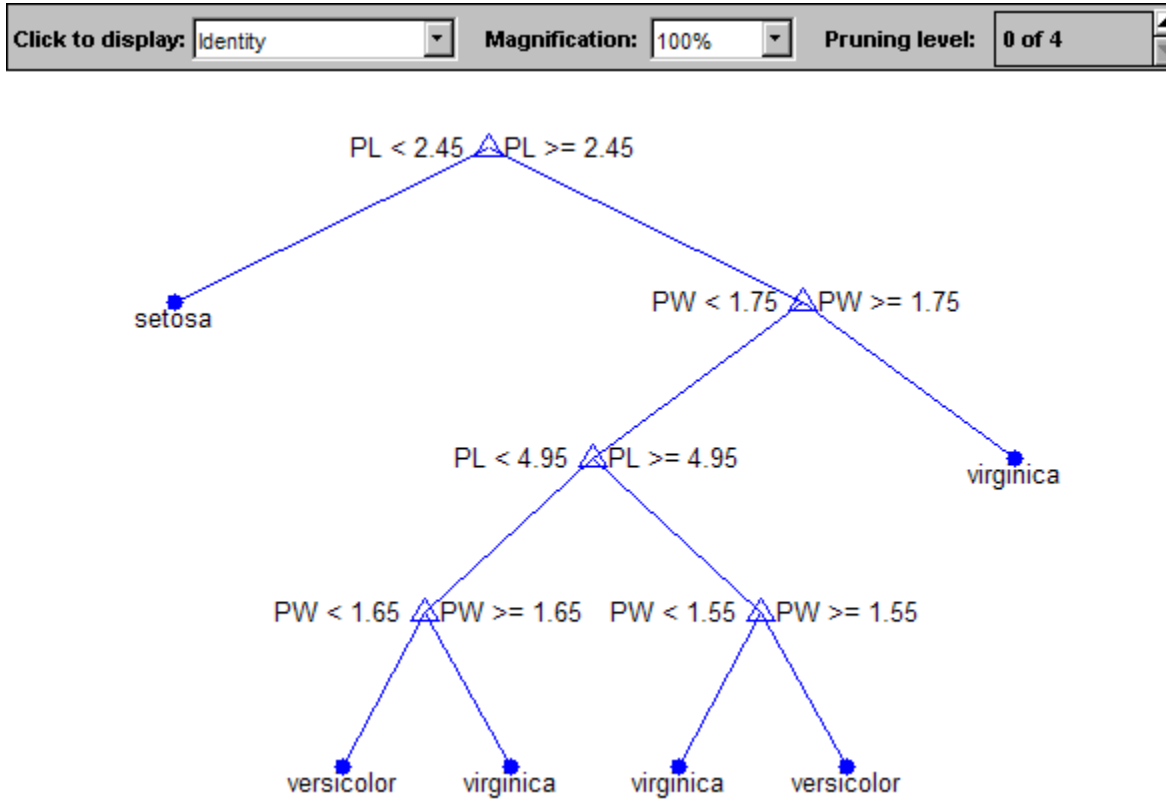
`t2 = treeprune(t1)` returns the decision tree `t2` that is the same as `t1`, but with the optimal pruning information added. This is useful only if you created `t1` by pruning another tree, or by using the `treefit` function with pruning set `'off'`. If you plan to prune a tree multiple times, it is more efficient to create the optimal pruning sequence first.

Pruning is the process of reducing a tree by turning some branch nodes into leaf nodes, and removing the leaf nodes under the original branch.

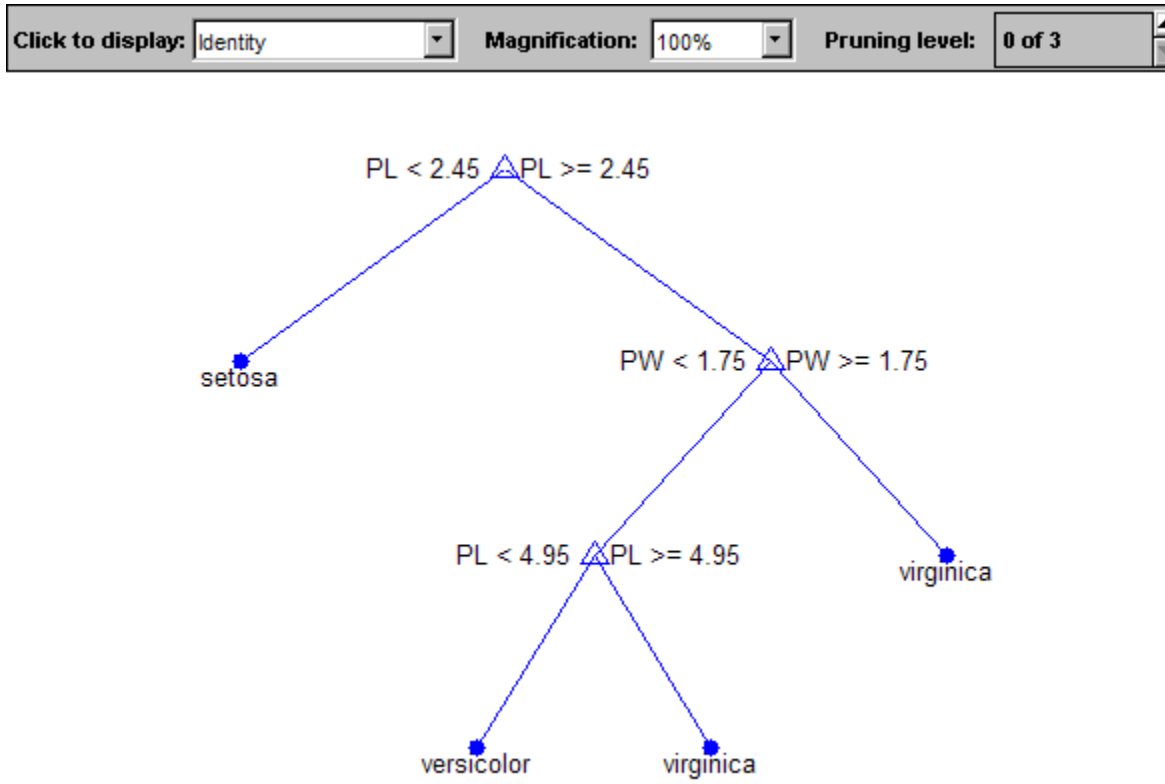
Examples

Display the full tree for Fisher's iris data, as well as the next largest tree from the optimal pruning sequence:

```
load fisheriris;
t1 = treefit(meas,species,'splitmin',5);
treedisp(t1,'names',{'SL' 'SW' 'PL' 'PW'});
```




```
t2 = treeprune(t1,'level',1);
treedisp(t2,'names',{'SL' 'SW' 'PL' 'PW'});
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`treefit` | `treetest` | `treedisp`

TreeBagger.Trees property

Purpose

Decision trees in ensemble

Description

The `Trees` property is a cell array of size `NTrees`-by-1 containing the trees in the ensemble.

See Also

`NTrees`

Purpose

Error rate

Syntax

```
cost = treetest(t,'resubstitution')
cost = treetest(t,'test',X,y)
cost = treetest(t,'crossvalidate',X,y)
[cost,secost,ntnodes,bestlevel] = treetest(...)
[...] = treetest(...,param1,val1,param2,val2,...)
```

Note `treetest` will be removed in a future release. Use `classregtree.test` instead.

Description

Note This function is superseded by the `test` method of the `classregtree` class class and is maintained only for backwards compatibility. It accepts objects `t` created with the `classregtree` constructor.

`cost = treetest(t,'resubstitution')` computes the cost of the tree `t` using a resubstitution method. `t` is a decision tree as created by the `treefit` function. The cost of the tree is the sum over all terminal nodes of the estimated probability of that node times the node's cost. If `t` is a classification tree, the cost of a node is the sum of the misclassification costs of the observations in that node. If `t` is a regression tree, the cost of a node is the average squared error over the observations in that node. `cost` is a vector of cost values for each subtree in the optimal pruning sequence for `t`. The resubstitution cost is based on the same sample that was used to create the original tree, so it underestimates the likely cost of applying the tree to new data.

`cost = treetest(t,'test',X,y)` uses the predictor matrix `X` and response `y` as a test sample, applies the decision tree `t` to that sample, and returns a vector `cost` of cost values computed for the test sample. `X` and `y` should not be the same as the learning sample, which is the sample that was used to fit the tree `t`.

`cost = treetest(t,'crossvalidate',X,y)` uses 10-fold cross-validation to compute the cost vector. `X` and `y` should be the learning sample, which is the sample that was used to fit the tree `t`. The function partitions the sample into 10 subsamples, chosen randomly but with roughly equal size. For classification trees, the subsamples also have roughly the same class proportions. For each subsample, `treetest` fits a tree to the remaining data and uses it to predict the subsample. It pools the information from all subsamples to compute the cost for the whole sample.

`[cost,secost,ntnodes,bestlevel] = treetest(...)` also returns the vector `secost` containing the standard error of each `cost` value, the vector `ntnodes` containing number of terminal nodes for each subtree, and the scalar `bestlevel` containing the estimated best level of pruning. `bestlevel = 0` means no pruning, i.e., the full unpruned tree. The best level is the one that produces the smallest tree that is within one standard error of the minimum-cost subtree.

`[...] = treetest(...,param1,val1,param2,val2,...)` specifies optional parameter name-value pairs chosen from the following table.

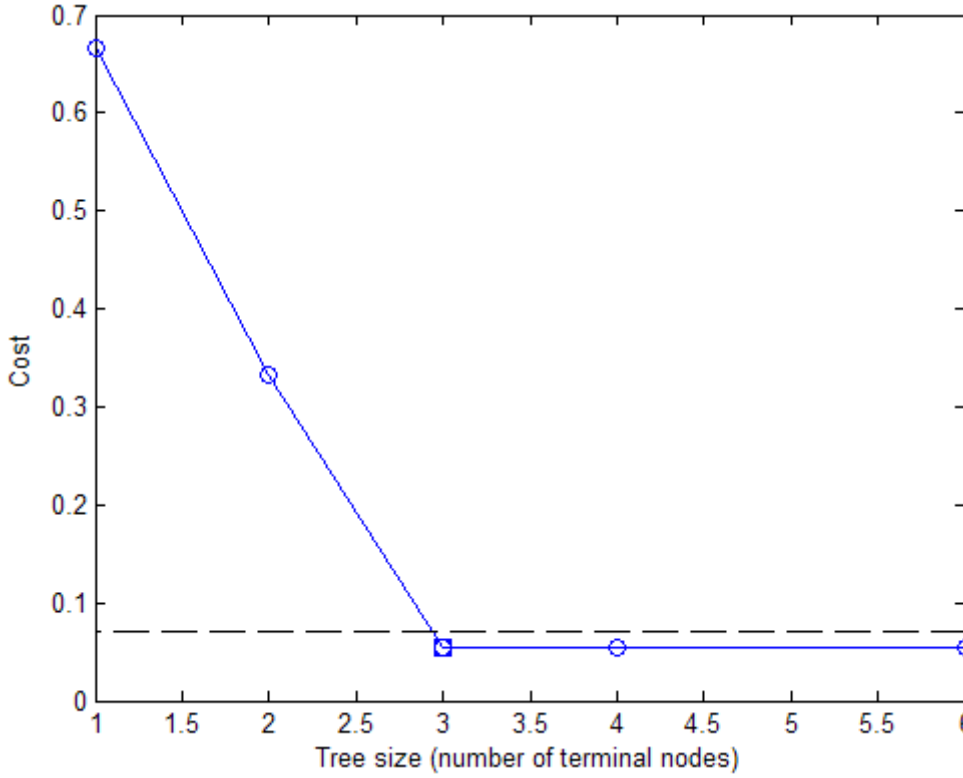
Parameter	Value
`'nsamples'`	The number of cross-validations samples (default is 10)
`'treesize'`	Either `'se'` (default) to choose the smallest tree whose cost is within one standard error of the minimum cost, or `'min'` to choose the minimal cost tree.

Examples

Find the best tree for Fisher's iris data using cross-validation. The solid line shows the estimated cost for each tree size, the dashed line marks one standard error above the minimum, and the square marks the smallest tree under the dashed line.

```
% Start with a large tree.
load fisheriris;
t = treefit(meas,species','splitmin',5);
```

```
% Find the minimum-cost tree.
[c,s,n,best] = treetest(t,'cross',meas,species);
tmin = treeprune(t,'level',best);

% Plot smallest tree within 1 std of minimum cost tree.
[mincost,minloc] = min(c);
plot(n,c,'b-o',...
     n(best+1),c(best+1),'bs',...
     n,(mincost+s(minloc))*ones(size(n)),'k--');
xlabel('Tree size (number of terminal nodes)')
ylabel('Cost')
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`treefit` | `treedisp`

Purpose

Predicted responses

Note `treeval` will be removed in a future release. Use `classregtree.eval` instead.

Syntax

```
yfit = treeval(t,X)
yfit = treeval(t,X,subtrees)
[yfit,node] = treeval(...)
[yfit,node,cname] = treeval(...)
```

Description

Note This function is superseded by the `eval` method of the `classregtree` class and is maintained only for backwards compatibility. It accepts objects `t` created with the `classregtree` constructor.

`yfit = treeval(t,X)` takes a classification or regression tree `t` as produced by the `treefit` function and a matrix `X` of predictor values, and produces a vector `yfit` of predicted response values. For a regression tree, `yfit(i)` is the fitted response value for a point having the predictor values `X(i,:)`. For a classification tree, `yfit(i)` is the class number into which the tree would assign the point with data `X(i,:)`. To convert the number into a class name, use the third output argument, `cname` (described below).

`yfit = treeval(t,X,subtrees)` takes an additional vector `subtrees` of pruning levels, with `0` representing the full, unpruned tree. `T` must include a pruning sequence as created by the `treefit` or `prunetree` function. If `subtree` has k elements and `X` has n rows, the output `yfit` is an n-by-k matrix, with the `j`th column containing the fitted values produced by the `subtrees(j)` subtree. `subtrees` must be sorted in ascending order.

`[yfit,node] = treeval(...)` also returns an array `node` of the same size as `yfit` containing the node number assigned to each row of `X`. The `treedisp` function can display the node numbers for any node you select.

`[yfit,node,cname] = treeval(...)` is valid only for classification trees. It returns a cell array `cname` containing the predicted class names.

Examples

Find the predicted classifications for Fisher's iris data:

```
load fisheriris;
t = treefit(meas,species);  % Create decision tree
sfit = treeval(t,meas);     % Find assigned class numbers
sfit = t.classname(sfit);   % Get class names
mean(strcmp(sfit,species))  % Proportion in correct class
ans =
   0.9800
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`treefit` | `treeprune` | `treetest`

Purpose

Mean excluding outliers

Syntax

```
m = trimmean(X,percent)
trimmean(X,percent,dim)
m = trimmean(X,percent,flag)
m = trimmean(x,percent,flag,dim)
```

Description

`m = trimmean(X,percent)` calculates the trimmed mean of the values in `X`. For a vector input, `m` is the mean of `X`, excluding the highest and lowest `k` data values, where `k=n*(percent/100)/2` and where `n` is the number of values in `X`. For a matrix input, `m` is a row vector containing the trimmed mean of each column of `X`. For `n`-D arrays, `trimmean` operates along the first non-singleton dimension. `percent` is a scalar between 0 and 100.

`trimmean(X,percent,dim)` takes the trimmed mean along dimension `dim` of `X`.

`m = trimmean(X,percent,flag)` controls how to trim when `k` is not an integer. `flag` can be chosen from the following:

`'round'`	Round `k` to the nearest integer (round to a smaller integer if `k` is a half integer). This is the default.
`'floor'`	Round `k` down to the next smaller integer.
`'weight'`	If `k=i+f` where `i` is the integer part and `f` is the fraction, compute a weighted mean with weight `(1-f)` for the `(i+1)th` and `(n-i)th` values, and full weight for the values between them.

`m = trimmean(x,percent,flag,dim)` takes the trimmed mean along dimension `dim` of `x`.

Tips

The trimmed mean is a robust estimate of the location of a sample. If there are outliers in the data, the trimmed mean is a more representative estimate of the center of the body of the data than the mean. However, if the data is all from the same probability distribution,

then the trimmed mean is less efficient than the sample mean as an estimator of the location of the data.

Examples

Example 1

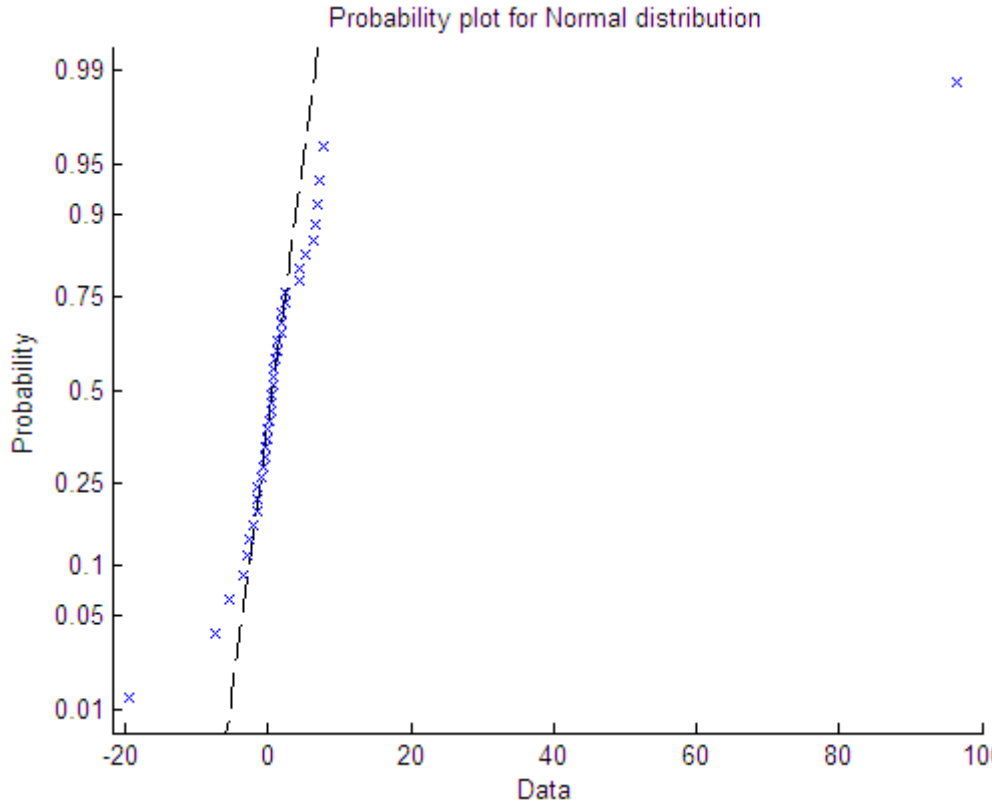
This example shows a Monte Carlo simulation of the efficiency of the 10% trimmed mean relative to the sample mean for normal data.

```
x = normrnd(0,1,100,100);
m = mean(x);
trim = trimmean(x,10);
sm = std(m);
strim = std(trim);
efficiency = (sm/strim).^2
efficiency =
  0.9702
```

Example 2

Generate random data from the `t` distribution, which tends to have outliers:

```
rng('default') % to reproduce the plot exactly
x = trnd(1,40,1);
probplot(x)
```



Though the distribution is symmetric around zero, there are several outliers which will affect the mean. The trimmed mean is much closer to zero, which is much more representative of the data:

```
mean(x)

ans =
2.7991

trimmean(x,25)

ans =
```

```
    0.8797
```

See Also

mean | median | geomean | harmmean

Purpose

Student's *t* random numbers

Syntax

```
R = trnd(V)
R = trnd(V,m,n,...)
R = trnd(V,[m,n,...])
```

Description

`R = trnd(V)` generates random numbers from Student's *t* distribution with `V` degrees of freedom. `V` can be a vector, a matrix, or a multidimensional array. The size of `R` is the size of `V`.

`R = trnd(V,m,n,...)` or `R = trnd(V,[m,n,...])` generates an `m`-by-`n`-by-... array. The `V` parameter can be a scalar or an array of the same size as `R`.

Examples

```
noisy = trnd(ones(1,6))
noisy =
  19.7250  0.3488  0.2843  0.4034  0.4816  -2.4190

numbers = trnd(1:6,[1 6])
numbers =
  -1.9500  -0.9611  -0.9038  0.0754  0.9820  1.0115

numbers = trnd(3,2,6)
numbers =
 -0.3177 -0.0812 -0.6627  0.1905 -1.5585 -0.0433
  0.2536  0.5502  0.8646  0.8060 -0.5216  0.0891
```

See Also

`random` | `tpdf` | `tcdf` | `tinv` | `tstat`

How To

- "Student's t Distribution" on page B-95

Purpose

Student's t mean and variance

Syntax

```
[M,V] = tstat(NU)
```

Description

`[M,V] = tstat(NU)` returns the mean of and variance for Student's t distribution using the degrees of freedom in `NU`. `M` and `V` are the same size as `NU`.

The mean of the Student's t distribution with parameter ν is zero for values of ν greater than 1. If ν is one, the mean does not exist. The variance for values of ν greater than 2 is $\nu/(\nu\text{-}2)$.

Examples

Find the mean of and variance for 1 to 30 degrees of freedom.

```
[m,v] = tstat(reshape(1:30,6,5))
m =
  NaN  0   0   0   0
   0   0   0   0   0
   0   0   0   0   0
   0   0   0   0   0
   0   0   0   0   0
   0   0   0   0   0

v =
    NaN   1.4000  1.1818  1.1176  1.0870
    NaN   1.3333  1.1667  1.1111  1.0833
  3.0000  1.2857  1.1538  1.1053  1.0800
  2.0000  1.2500  1.1429  1.1000  1.0769
  1.6667  1.2222  1.1333  1.0952  1.0741
  1.5000  1.2000  1.1250  1.0909  1.0714
```

Note that the variance does not exist for one and two degrees of freedom.

See Also

`tpdf` | `tcdf` | `tinv` | `trnd`

Purpose

One-sample and paired-sample *t*-test

Syntax

```
h = ttest(x)
h = ttest(x,m)
h = ttest(x,y)
h = ttest(...,alpha)
h = ttest(...,alpha,tail)
h = ttest(...,alpha,tail,dim)
[h,p] = ttest(...)
[h,p,ci] = ttest(...)
[h,p,ci,stats] = ttest(...)
```

Description

`h = ttest(x)` performs a *t*-test of the null hypothesis that data in the vector `x` are a random sample from a normal distribution with mean 0 and unknown variance, against the alternative that the mean is not 0. The result of the test is returned in `h`. `h = 1` indicates a rejection of the null hypothesis at the 5% significance level. `h = 0` indicates a failure to reject the null hypothesis at the 5% significance level.

`x` can also be a matrix or an *N*-dimensional array. For matrices, `ttest` performs separate *t*-tests along each column of `x` and returns a vector of results. For *N*-dimensional arrays, `ttest` works along the first non-singleton dimension of `x`.

The test treats `NaN` values as missing data, and ignores them.

`h = ttest(x,m)` performs a *t*-test of the null hypothesis that data in the vector `x` are a random sample from a normal distribution with mean `m` and unknown variance, against the alternative that the mean is not `m`.

`h = ttest(x,y)` performs a paired *t*-test of the null hypothesis that data in the difference `x-y` are a random sample from a normal distribution with mean 0 and unknown variance, against the alternative that the mean is not 0. `x` and `y` must be vectors of the same length, or arrays of the same size.

`h = ttest(...,alpha)` performs the test at the (100*`alpha`)% significance level. The default, when unspecified, is `alpha = 0.05`.

`h = ttest(...,alpha,tail)` performs the test against the alternative specified by the string `tail`. There are three options for `tail`:

- `'both'` — Mean is not 0 (or `m`) (two-tailed test). This is the default, when `tail` is unspecified.
- `'right'` — Mean is greater than 0 (or `m`) (right-tail test)
- `'left'` — Mean is less than 0 (or `m`) (left-tail test)

`tail` must be a single string, even when `x` is a matrix or an *N*-dimensional array.

`h = ttest(...,alpha,tail,dim)` works along dimension `dim` of `x`, or of `x-y` for a paired test. Use `[]` to pass in default values for `m`, `alpha`, or `tail`.

`[h,p] = ttest(...)` returns the *p* value of the test. The *p* value is the probability, under the null hypothesis, of observing a value as extreme or more extreme of the test statistic

$$t = \frac{\bar{x} - \mu}{s/\sqrt{n}}$$

where $\bar{x}$ is the sample mean, $\mu = 0$ (or `m`) is the hypothesized population mean, s is the sample standard deviation, and n is the sample size. Under the null hypothesis, the test statistic will have Student's t distribution with $n - 1$ degrees of freedom.

`[h,p,ci] = ttest(...)` returns a 100*(1 – `alpha`)% confidence interval on the population mean, or on the difference of population means for a paired test.

`[h,p,ci,stats] = ttest(...)` returns the structure `stats` with the following fields:

- `tstat` — Value of the test statistic
- `df` — Degrees of freedom of the test
- `sd` — Sample standard deviation

Examples

Simulate a random sample of size 100 from a normal distribution with mean 0.1:

```
x = normrnd(0.1,1,1,100);
```

Test the null hypothesis that the sample comes from a normal distribution with mean 0:

```
[h,p,ci] = ttest(x,0)
h =
     0
p =
    0.8323
ci =
   -0.1650    0.2045
```

The test fails to reject the null hypothesis at the default $\alpha = 0.05$ significance level. Under the null hypothesis, the probability of observing a value as extreme or more extreme of the test statistic, as indicated by the p value, is much greater than α. The 95% confidence interval on the mean contains 0.

Simulate a larger random sample of size 1000 from the same distribution:

```
y = normrnd(0.1,1,1,1000);
```

Test again if the sample comes from a normal distribution with mean 0:

```
[h,p,ci] = ttest(y,0)
h =
     1
p =
    0.0160
ci =
    0.0142    0.1379
```

This time the test rejects the null hypothesis at the default $\alpha = 0.05$ significance level. The p value has fallen below $\alpha = 0.05$ and the 95% confidence interval on the mean does not contain 0.

Because the p value of the sample `y` is greater than 0.01, the test will fail to reject the null hypothesis when the significance level is lowered to $\alpha = 0.01$:

```
[h,p,ci] = ttest(y,0,0.01)
h =
     0
p =
    0.0160
ci =
   -0.0053    0.1574
```

Notice that at the lowered significance level the 99% confidence interval on the mean widens to contain 0.

This example will produce slightly different results each time it is run, because of the random sampling.

See Also

`ttest2` | `ztest`

Purpose

Two-sample *t*-test

Syntax

```
h = ttest2(x,y)
h = ttest2(x,y,alpha)
h = ttest2(x,y,alpha,tail)
h = ttest2(x,y,alpha,tail,vartype)
h = ttest2(x,y,alpha,tail,vartype,dim)
[h,p] = ttest2(...)
[h,p,ci] = ttest2(...)
[h,p,ci,stats] = ttest2(...)
```

Description

`h = ttest2(x,y)` performs a *t*-test of the null hypothesis that data in the vectors `x` and `y` are independent random samples from normal distributions with equal means and equal but unknown variances, against the alternative that the means are not equal. The result of the test is returned in `h`. `h = 1` indicates a rejection of the null hypothesis at the 5% significance level. `h = 0` indicates a failure to reject the null hypothesis at the 5% significance level. `x` and `y` need not be vectors of the same length.

`x` and `y` can also be matrices or *N*-dimensional arrays. Matrices `x` and `y` must have the same number of columns, in which case `ttest2` performs separate *t*-tests along each column and returns a vector of results. *N*-dimensional arrays `x` and `y` must have the same size along all but the first non-singleton dimension, in which case `ttest2` works along the first non-singleton dimension.

The test treats `NaN` values as missing data, and ignores them.

`h = ttest2(x,y,alpha)` performs the test at the (100*`alpha`)% significance level. The default, when unspecified, is `alpha = 0.05`.

`h = ttest2(x,y,alpha,tail)` performs the test against the alternative specified by the string `tail`. There are three options for `tail`:

- `'both'` — Means are not equal (two-tailed test). This is the default, when `tail` is unspecified.
- `'right'` — Mean of `x` is greater than mean of `y` (right-tail test)

- `'left'` — Mean of `x` is less than mean of `y` (left-tail test)

`tail` must be a single string, even when `x` is a matrix or an *N*-dimensional array.

`h = ttest2(x,y,alpha,tail,vartype)` performs the test under the assumption of equal or unequal population variances, as specified by the string *`vartype`*. There are two options for *`vartype`*:

- `'equal'` — Assumes equal variances. This is the default, when `vartype` is unspecified.
- `'unequal'` — Does not assume equal variances. This is the Behrens-Fisher problem.

`vartype` must be a single string, even when `x` is a matrix or an *N*-dimensional array.

If `vartype` is `'equal'`, the test computes a pooled sample standard deviation using

$$s = \sqrt{\frac{(n-1)s_x^2 + (m-1)s_y^2}{n+m-2}}$$

where s_x and s_y are the sample standard deviations of `x` and `y`, respectively, and n and m are the sample sizes of `x` and `y`, respectively.

`h = ttest2(x,y,alpha,tail,vartype,dim)` works along dimension `dim` of `x` and `y`. Use `[]` to pass in default values for `alpha`, `tail`, or `vartype`.

`[h,p] = ttest2(...)` returns the p value of the test. The p value is the probability, under the null hypothesis, of observing a value as extreme or more extreme of the test statistic

$$t = \frac{\bar{x} - \bar{y}}{\sqrt{\frac{s_x^2}{n} + \frac{s_y^2}{m}}}$$

where $\bar{x}$ and $\bar{y}$ are the sample means, s_x and s_y are the sample standard deviations (replaced by the pooled standard deviation s in the default case where `vartype` is `'equal'`), and n and m are the sample sizes.

In the default case where `vartype` is `'equal'`, the test statistic, under the null hypothesis, has Student's t distribution with $n + m - 2$ degrees of freedom.

In the case where `vartype` is `'unequal'`, the test statistic, under the null hypothesis, has an approximate Student's t distribution with a number of degrees of freedom given by Satterthwaite's approximation.

`[h,p,ci] = ttest2(...)` returns a 100*(1 – `alpha`)% confidence interval on the difference of population means.

`[h,p,ci,stats] = ttest2(...)` returns structure `stats` with the following fields:

- `tstat` — Value of the test statistic
- `df` — Degrees of freedom of the test
- `sd` — Pooled sample standard deviation (in the default case where `vartype` is `'equal'`) or a vector with the sample standard deviations (in the case where `vartype` is `'unequal'`).

Examples

Simulate random samples of size 1000 from normal distributions with means 0 and 0.1, respectively, and standard deviations 1 and 2, respectively:

```
x = normrnd(0,1,1,1000);
y = normrnd(0.1,2,1,1000);
```

Test the null hypothesis that the samples come from populations with equal means, against the alternative that the means are unequal. Perform the test assuming unequal variances:

```
[h,p,ci] = ttest2(x,y,[],[],'unequal')
h =
     1
p =
    0.0102
ci =
   -0.3227   -0.0435
```

The test rejects the null hypothesis at the default $\alpha = 0.05$ significance level. Under the null hypothesis, the probability of observing a value as extreme or more extreme of the test statistic, as indicated by the p value, is less than α. The 95% confidence interval on the mean of the difference does not contain 0.

This example will produce slightly different results each time it is run, because of the random sampling.

See Also

`ttest` | `ztest`

Purpose

Tree type

Syntax

```
ttype = type(t)
```

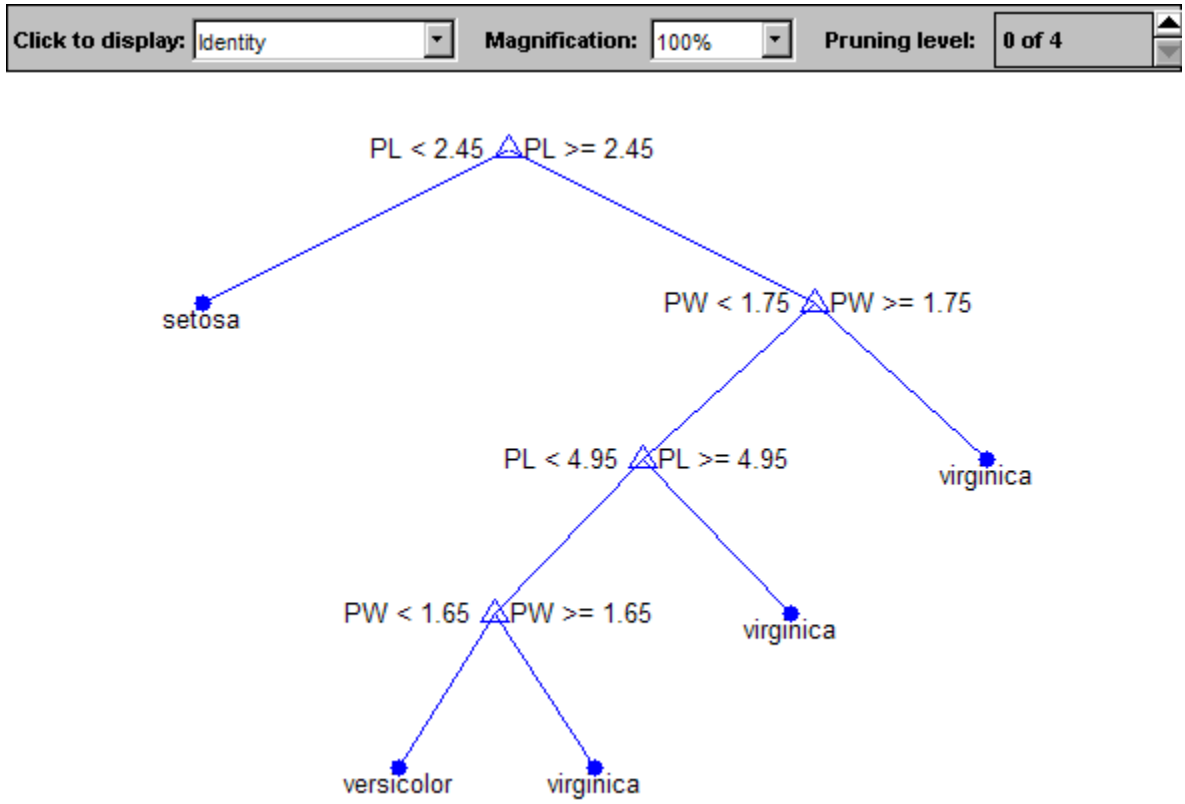
Description

`ttype = type(t)` returns the type of the tree `t`. `ttype` is `'regression'` for regression trees and `'classification'` for classification trees.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
ttype = type(t)
ttype =
classification
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree`

Purpose

Type of partition

Description

The type of validation partition. It is `'kfold'`, `'holdout'`, `'leaveout'`, or `'resubstitution'`.

See Also

`trainsize`

qrandset.Type property

Purpose

Name of sequence on which point set `P` is based

Description

`P.Type` returns a string that contains the name of the sequence on which the point set `P` is based, for example `'Sobol'`. You cannot change the `Type` property for a point set.

Purpose

Convert categorical array to unsigned 8-bit integers

Syntax

```
B = uint8(A)
```

Description

`B = uint8(A)` converts the categorical array `A` to unsigned 8-bit integers. Each element of `B` contains the internal categorical level code for the corresponding element of `A`. Undefined elements of `A` are assigned the value 0 in `B`. If `A` contains more than `intmax('uint8')` levels, the internal codes will saturate to `intmax('uint8')`when cast to `int8`.

See Also

`double` | `int8`

categorical.uint16

Purpose

Convert categorical array to unsigned 16-bit integers

Syntax

```
B = uint16(A)
```

Description

`B = uint16(A)` converts the categorical array `A` to unsigned 16-bit integers. Each element of `B` contains the internal categorical level code for the corresponding element of `A`.

Undefined elements of `A` are assigned the value 0 in `B`.

See Also

`double` | `int16`

Purpose

Convert categorical array to unsigned 32-bit integers

Syntax

```
B = uint32(A)
```

Description

`B = uint32(A)` converts the categorical array `A` to unsigned 32-bit integers. Each element of `B` contains the internal categorical level code for the corresponding element of `A`.

Undefined elements of `A` are assigned the value 0 in `B`.

See Also

`double` | `int32`

categorical.uint64

Purpose

Convert categorical array to unsigned 64-bit integers

Syntax

```
B = uint64(A)
```

Description

`B = uint64(A)` converts the categorical array `A` to unsigned 64-bit integers. Each element of `B` contains the internal categorical level code for the corresponding element of `A`.

Undefined elements of `A` are assigned the value 0 in `B`.

See Also

`double` | `int64`

Purpose

Text label for undefined levels

Description

Text label for undefined levels. Constant property with value `'<undefined>'`.

dataset.unique

Purpose

Unique observations in dataset array

Syntax

```
B = unique(A)
B = unique(A,vars)
[B,i,j] = unique(A)
[...] = unique(A,vars,'first')
```

Description

`B = unique(A)` returns a copy of the dataset A that contains only the sorted unique observations. `A` must contain only variables whose class has a `unique` method, including:

- numeric
- character
- logical
- categorical
- cell arrays of strings

For a variable with multiple columns, its class's `unique` method must support the `'rows'` flag.

`B = unique(A,vars)` returns a dataset that contains only one observation for each unique combination of values for the variables in `A` specified in `vars`. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. `B` includes all variables from `A`. The values in `B` for the variables not specified in `vars` are taken from the last occurrence among observations in `A` with each unique combination of values for the variables specified in `vars`.

`[B,i,j] = unique(A)` also returns index vectors `i` and `j` such that `B = A(i,:)` and `A = B(j,:)`.

`[...] = unique(A,vars,'first')` returns the vector `i` to index the first occurrence of each unique observation in `A`. `unique(A,vars,'last')`, the default, returns the vector `i` to index

the last occurrence. Specify `vars` as `[]` to use the default value of all variables.

See Also

`dataset | set | subsasgn`

dataset.Units property

Purpose

Units of variables in data set

Description

A cell array of strings giving the units of the variables in the data set. This property may be empty, but if not empty, the number of strings must equal the number of variables. Any individual string may be empty for a variable that does not have units defined. The default is an empty cell array.

Purpose

Discrete uniform cumulative distribution function

Syntax

```
P = unidcdf(X,N)
```

Description

`P = unidcdf(X,N)` computes the discrete uniform cdf at each of the values in `X` using the corresponding maximum observable value in `N`. `X` and `N` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The maximum observable values in `N` must be positive integers.

The discrete uniform cdf is

$$p = F(x \mid N) = \frac{floor(x)}{N} I_{(1,\ldots,N)}(x)$$

The result, p, is the probability that a single observation from the discrete uniform distribution with maximum N will be a positive integer less than or equal to x. The values x do not need to be integers.

Examples

What is the probability of drawing a number 20 or less from a hat with the numbers from 1 to 50 inside?

```
probability = unidcdf(20,50)
probability =
  0.4000
```

See Also

`cdf` | `unidpdf` | `unidinv` | `unidstat` | `unidrnd` | `mle`

How To

- “Uniform Distribution (Discrete)” on page B-101

unidinv

Purpose

Discrete uniform inverse cumulative distribution function

Syntax

```
X = unidinv(P,N)
```

Description

`X = unidinv(P,N)` returns the smallest positive integer `X` such that the discrete uniform cdf evaluated at `X` is equal to or exceeds `P`. You can think of `P` as the probability of drawing a number as large as `X` out of a hat with the numbers `1` through `N` inside.

`P` and `N` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `X`. A scalar input for `N` or `P` is expanded to a constant array with the same dimensions as the other input. The values in `P` must lie on the interval [0 1] and the values in `N` must be positive integers.

Examples

```
x = unidinv(0.7,20)
x =
    14

y = unidinv(0.7 + eps,20)
y =
    15
```

A small change in the first parameter produces a large jump in output. The cdf and its inverse are both step functions. The example shows what happens at a step.

See Also

`icdf` | `unidcdf` | `unidpdf` | `unidstat` | `unidrnd`

How To

- “Uniform Distribution (Discrete)” on page B-101

Purpose

Discrete uniform probability density function

Syntax

```
Y = unidpdf(X,N)
```

Description

`Y = unidpdf(X,N)` computes the discrete uniform pdf at each of the values in `X` using the corresponding maximum observable value in `N`. `X` and `N` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `N` must be positive integers.

The discrete uniform pdf is

$$y = f(x \mid N) = \frac{1}{N} I_{(1,\ldots,N)}(x)$$

You can think of y as the probability of observing any one number between 1 and n.

Examples

For fixed `n`, the uniform discrete pdf is a constant.

```
y = unidpdf(1:6,10)
y =
  0.1000   0.1000   0.1000   0.1000   0.1000   0.1000
```

Now fix `x`, and vary `n`.

```
likelihood = unidpdf(5,4:9)
likelihood =
  0   0.2000   0.1667   0.1429   0.1250   0.1111
```

See Also

`pdf` | `unidcdf` | `unidinv` | `unidstat` | `unidrnd`

How To

- "Uniform Distribution (Discrete)" on page B-101

unidrnd

Purpose

Discrete uniform random numbers

Syntax

```
R = unidrnd(N)
R = unidrnd(N,m,n,...)
R = unidrnd(N,[m,n,...])
```

Description

`R = unidrnd(N)` generates random numbers for the discrete uniform distribution with maximum `N`. The parameters in `N` must be positive integers. `N` can be a vector, a matrix, or a multidimensional array. The size of `R` is the size of `N`. The discrete uniform distribution arises from experiments equivalent to drawing a number from one to `N` out of a hat.

`R = unidrnd(N,m,n,...)` or `R = unidrnd(N,[m,n,...])` generates an `m`-by-`n`-by-... array. The `N` parameter can be a scalar or an array of the same size as `R`.

Examples

In the Massachusetts lottery, a player chooses a four-digit number. Generate random numbers for Monday through Saturday.

```
numbers = unidrnd(10000,1,6)-1
numbers =
    4564  185  8214  4447  6154  7919
```

See Also

`random` | `unidpdf` | `unidcdf` | `unidinv` | `unidstat`

How To

- "Uniform Distribution (Discrete)" on page B-101

Purpose

Discrete uniform mean and variance

Syntax

```
[M,V] = unidstat(N)
```

Description

`[M,V] = unidstat(N)` returns the mean and variance of the discrete uniform distribution with minimum value `1` and maximum value `N`.

The mean of the discrete uniform distribution with parameter N is $(N + 1)/2$. The variance is $(N^2 - 1)/12$.

Examples

```
[m,v] = unidstat(1:6)
m =
  1.0000   1.5000   2.0000   2.5000   3.0000   3.5000
v =
  0   0.2500   0.6667   1.2500   2.0000   2.9167
```

See Also

`unidpdf` | `unidcdf` | `unidinv` | `unidrnd`

How To

- "Uniform Distribution (Discrete)" on page B-101

unifcdf

Purpose

Continuous uniform cumulative distribution function

Syntax

```
P = unifcdf(X,A,B)
```

Description

`P = unifcdf(X,A,B)` computes the uniform cdf at each of the values in `X` using the corresponding lower endpoint (minimum), `A` and upper endpoint (maximum), `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant matrix with the same dimensions as the other inputs.

The uniform cdf is

$$p = F(x \mid a,b) = \frac{x-a}{b-a} I_{[a,b]}(x)$$

The standard uniform distribution has A = `0` and B = `1`.

Examples

What is the probability that an observation from a standard uniform distribution will be less than 0.75?

```
probability = unifcdf(0.75)
probability =
  0.7500
```

What is the probability that an observation from a uniform distribution with `a = -1` and `b = 1` will be less than 0.75?

```
probability = unifcdf(0.75,-1,1)
probability =
  0.8750
```

See Also

`cdf` | `unifpdf` | `unifinv` | `unifstat` | `unifit` | `unifrnd`

How To

- "Uniform Distribution (Continuous)" on page B-99

Purpose

Continuous uniform inverse cumulative distribution function

Syntax

```
X = unifinv(P,A,B)
```

Description

`X = unifinv(P,A,B)` computes the inverse of the uniform cdf with parameters `A` and `B` (the minimum and maximum values, respectively) at the corresponding probabilities in `P`. `P`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

The inverse of the uniform cdf is

$$x = F^{-1}(p \mid a,b) = a + p(a-b)I_{[0,1]}(p)$$

The standard uniform distribution has A = `0` and B = `1`.

Examples

What is the median of the standard uniform distribution?

```
median_value = unifinv(0.5)
median_value =
  0.5000
```

What is the 99th percentile of the uniform distribution between -1 and 1?

```
percentile = unifinv(0.99,-1,1)
percentile =
  0.9800
```

See Also

`icdf` | `unifcdf` | `unifpdf` | `unifstat` | `unifit` | `unifrnd`

How To

- "Uniform Distribution (Continuous)" on page B-99

unifit

Purpose

Continuous uniform parameter estimates

Syntax

```
[ahat,bhat] = unifit(data)
[ahat,bhat,ACI,BCI] = unifit(data)
[ahat,bhat,ACI,BCI] = unifit(data,alpha)
```

Description

`[ahat,bhat] = unifit(data)` returns the maximum likelihood estimates (MLEs) of the parameters of the uniform distribution given the data in `data`.

`[ahat,bhat,ACI,BCI] = unifit(data)` also returns 95% confidence intervals, `ACI` and `BCI`, which are matrices with two rows. The first row contains the lower bound of the interval for each column of the matrix `data`. The second row contains the upper bound of the interval.

`[ahat,bhat,ACI,BCI] = unifit(data,alpha)` enables you to control of the confidence level `alpha`. For example, if `alpha = 0.01` then `ACI` and `BCI` are 99% confidence intervals.

Examples

```
r = unifrnd(10,12,100,2);
[ahat,bhat,aci,bci] = unifit(r)
ahat =
  10.0154  10.0060
bhat =
  11.9989  11.9743
aci =
  9.9551  9.9461
  10.0154  10.0060
bci =
  11.9989  11.9743
  12.0592  12.0341
```

See Also

`mle` | `unifpdf` | `unifcdf` | `unifinv` | `unifstat` | `unifrnd`

How To

- "Uniform Distribution (Continuous)" on page B-99

Purpose

Continuous uniform probability density function

Syntax

```
Y = unifpdf(X,A,B)
```

Description

`Y = unifpdf(X,A,B)` computes the continuous uniform pdf at each of the values in `X` using the corresponding lower endpoint (minimum), `A` and upper endpoint (maximum), `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `B` must be greater than those in `A`.

The continuous uniform distribution pdf is

$$y = f(x \mid a,b) = \frac{1}{b-a} I_{[a,b]}(x)$$

The standard uniform distribution has A = `0` and B = `1`.

Examples

For fixed `a` and `b`, the uniform pdf is constant.

```
x = 0.1:0.1:0.6;
y = unifpdf(x)
y =
   1   1   1   1   1   1
```

What if `x` is not between `a` and `b`?

```
y = unifpdf(-1,0,1)
y =
   0
```

See Also

`pdf` | `unifcdf` | `unifinv` | `unifstat` | `unifit` | `unifrnd`

How To

- "Uniform Distribution (Continuous)" on page B-99

unifrnd

Purpose

Continuous uniform random numbers

Syntax

```
R = unifrnd(A,B)
R = unifrnd(A,B,m,n,...)
R = unifrnd(A,B,[m,n,...])
```

Description

`R = unifrnd(A,B)` returns an array `R` of random numbers generated from the continuous uniform distributions with lower and upper endpoints specified by `A` and `B`, respectively. If `A` and `B` are arrays, `R(i,j)` is generated from the distribution specified by the corresponding elements of `A` and `B`. If either `A` or `B` is a scalar, it is expanded to the size of the other input.

`R = unifrnd(A,B,m,n,...)` or `R = unifrnd(A,B,[m,n,...])` returns an `m`-by-`n`-by-... array. If `A` and `B` are scalars, all elements of `R` are generated from the same distribution. If either `A` or `B` is an array, they must be `m`-by-`n`-by-... .

Examples

Generate one random number each from the continuous uniform distributions on the intervals (0,1), (0,2), ..., (0,5):

```
a = 0; b = 1:5;
r1 = unifrnd(a,b)
r1 =
    0.8147    1.8116    0.3810    3.6535    3.1618
```

Generate five random numbers each from the same distributions:

```
B = repmat(b,5,1);
R = unifrnd(a,B)
R =
    0.0975    0.3152    0.4257    2.6230    3.7887
    0.2785    1.9412    1.2653    0.1428    3.7157
    0.5469    1.9143    2.7472    3.3965    1.9611
    0.9575    0.9708    2.3766    3.7360    3.2774
    0.9649    1.6006    2.8785    2.7149    0.8559
```

Generate five random numbers from the continuous uniform distribution on (0,2):

```
r2 = unifrnd(a,b(2),1,5)
r2 =
    1.4121    0.0637    0.5538    0.0923    0.1943
```

See Also

rand | random | unifpdf | unifcdf | unifinv | unifstat | unifit

How To

- "Uniform Distribution (Continuous)" on page B-99

unifstat

Purpose

Continuous uniform mean and variance

Syntax

```
[M,V] = unifstat(A,B)
```

Description

`[M,V] = unifstat(A,B)` returns the mean of and variance for the continuous uniform distribution using the corresponding lower endpoint (minimum), `A` and upper endpoint (maximum), `B`. Vector or matrix inputs for `A` and `B` must have the same size, which is also the size of `M` and `V`. A scalar input for `A` or `B` is expanded to a constant matrix with the same dimensions as the other input.

The mean of the continuous uniform distribution with parameters a and b is $(a + b)/2$, and the variance is $(a - b)^2/12$.

Examples

```
a = 1:6;
b = 2.*a;
[m,v] = unifstat(a,b)
m =
  1.5000  3.0000  4.5000  6.0000  7.5000  9.0000
v =
  0.0833  0.3333  0.7500  1.3333  2.0833  3.0000
```

See Also

`unifpdf` | `unifcdf` | `unifinv` | `unifit` | `unifrnd`

How To

- "Uniform Distribution (Continuous)" on page B-99

Purpose

Set union for categorical arrays

Syntax

```
C = union(A,B)
[C,IA,IB] = union(A,B)
```

Description

`C = union(A,B)` when `A` and `B` are categorical arrays returns a categorical vector `C` containing the combined values from `A` and `B` but with no repetitions. The result `C` is sorted. The set of categorical levels for `C` is the sorted union of the sets of levels of the inputs, as determined by their labels.

`[C,IA,IB] = union(A,B)` also returns index vectors `IA` and `IB` such that `C` is a sorted combination of the elements `A(IA)` and `B(IB)`.

See Also

`intersect` | `ismember` | `setdiff` | `setxor` | `unique`

categorical.unique

Purpose

Unique values in categorical array

Syntax

```
B = unique(A)
[B,I,J] = unique(A)
[B,I,J] = unique(A,'first')
```

Description

`B = unique(A)` returns a categorical array containing the unique elements of `A`, sorted by the order of `A`'s levels.

`[B,I,J] = unique(A)` also returns index vectors `I` and `J` such that `B = A(I)` and `A = B(J)`.

`[B,I,J] = unique(A,'first')` returns the vector `I` to index the first occurrence of each unique value in `A`. `unique(A,'last')`, the default, returns the vector `I` to index the last occurrence.

See Also

`intersect` | `ismember` | `setdiff` | `setxor` | `union`

Purpose

Unstack data from single variable into multiple variables

Syntax

```
wide = unstack(tall,datavar,indvar)
[wide,itall] = unstack(tall,datavar,indvar)
wide = unstack(tall,datavar,indvar,'Parameter',value)
```

Description

`wide = unstack(tall,datavar,indvar)` converts a dataset array `tall` to an equivalent dataset array `wide` that is in wide format, by unstacking a single variable in `tall` into multiple variables in `wide`. In general `wide` contains more variables, but fewer observations, than `tall`.

`datavar` specifies the data variable in `tall` to unstack. `indvar` specifies an indicator variable in `tall` that determines which variable in `wide` each value in `datavar` is unstacked into. `unstack` treats the remaining variables in `tall` as grouping variables. Each unique combination of their values defines a group of observations in `tall` that will be unstacked into a single observation in `wide`.

`unstack` creates `m` data variables in `wide`, where `m` is the number of group levels in `indvar`. The values in `indvar` indicate which of those `m` variables receive which values from `datavar`. The `j`-th data variable in `wide` contains the values from `datavar` that correspond to observations whose `indvar` value was the `j`-th of the `m` possible levels. Elements of those `m` variables for which no corresponding data value in `tall` exists contain a default value.

`datavar` is a positive integer, a variable name, or a logical vector containing a single true value. `indvar` is a positive integer, a variable name, or a logical vector containing a single true value.

`[wide,itall] = unstack(tall,datavar,indvar)` returns an index vector `itall` indicating the correspondence between observations in `wide` and those in `tall`. For each observation in `wide`, `itall` contains the index of the first in the corresponding group of observations in `tall`.

For more information on grouping variables, see “Grouping Variables” on page 2-34.

Input Arguments

`wide = unstack(tall,datavar,indvar,'Parameter',value)` uses the following parameter name/value pairs to control how `unstack` converts variables in `tall` to variables in `wide`:

`'GroupVars'`	Grouping variables in `tall` that define groups of observations. `groupvars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. The default is all variables in `tall` not listed in `datavar` or `indvar`.
`'NewDataVarNames'`	A cell array of strings containing names for the data variables `unstack` should create in `wide`. Default is the group names of the grouping variable specified in `indvar`.
`'AggregationFun'`	A function handle that accepts a subset of values from `datavar` and returns a single value. `stack` applies this function to observations from the same group that have the same value of `indvar`. The function must aggregate the data values into a single value, and in such cases it is not possible to recover `tall` from `wide` using `stack`. The default is `@sum` for numeric data variables. For non-numeric variables, there is no default, and you must specify `'AggregationFun'` if multiple observations in the same group have the same values of `indvar`.
`'ConstVars'`	Variables in `tall` to copy to `wide` without unstacking. The values for these variables in `wide` are taken from the first observation in each group in `tall`, so these variables should typically be constant within each group. `ConstVars` is a positive integer, a vector of positive integers, a variable name, a cell array

	containing one or more variable names, or a logical vector. The default is no variables.

You can also specify more than one data variable in `tall`, each of which becomes a set of `m` variables in `wide`. In this case, specify `datavar` as a vector of positive integers, a cell array containing variable names, or a logical vector. You may specify only one variable with `indvar`. The names of each set of data variables in `wide` are the name of the corresponding data variable in `tall` concatenated with the names specified in `'NewDataVarNames'`. The function specified in `'AggregationFun'` must return a value with a single row.

Examples

Convert a "wide format" data set to "tall format", and then back to a different "wide format":

```
load flu

% FLU has a 'Date' variable, and 10 variables for estimated
% influenza rates (in 9 different regions, estimated from
% Google searches, plus a nationwide extimate from the
% CDC). Combine those 10 variables into a "tall" array that
% has a single data variable, 'FluRate', and an indicator
% variable, 'Region', that says which region each estimate
% is from.
[flu2,iflu] = stack(flu, 2:11, 'NewDataVarName','FluRate', ...
    'IndVarName','Region')

% The second observation in FLU is for 10/16/2005.  Find the
% observations in FLU2 that correspond to that date.
flu(2,:)
flu2(iflu==2,:)

% Use the 'Date' variable from that tall array to split
% 'FluRate' into 52 separate variables, each containing the
% estimated influenza rates for each unique date.  The new
% "wide" array has one observation for each region.  In
% effect, this is the original array FLU "on its side".
dateNames = cellstr(datestr(flu.Date,'mmm_DD_YYYY'));
```

```
[flu3,iflu2] = unstack(flu2, 'FluRate', 'Date', ...
    'NewDataVarNames',dateNames)

% Since observations in FLU3 represent regions, IFLU2
% indicates the first occurrence in FLU2 of each region.
flu2(iflu2,:)
```

See Also

dataset.stack | dataset.join | dataset.grpstats

How To

- “Grouping Variables” on page 2-34

Purpose

Upper Pareto tails parameters

Syntax

```
params = upperparams(obj)
```

Description

`params = upperparams(obj)` returns the 2-element vector `params` of shape and scale parameters, respectively, of the upper tail of the Pareto tails object `obj`. `upperparams` does not return a location parameter.

Examples

Fit Pareto tails to a t distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);

lowerparams(obj)
ans =
   -0.1901    1.1898
upperparams(obj)
ans =
    0.3646    0.5103
```

See Also

`paretotails` | `lowerparams`

dataset.UserData property

Purpose

Variable containing additional information associated with data set

Description

Any variable containing additional information to be associated with the data set. The default is an empty array.

Purpose

Return variance of ProbDistUnivParam object

Syntax

```
V = var(PD)
```

Description

`V = var(PD)` returns *V*, the variance of the ProbDistUnivParam object *PD*.

Input Arguments

PD	An object of the class `ProbDistUnivParam`.

Output Arguments

V	The variance of the ProbDistUnivParam object *PD*.

See Also

`var`

dataset.VarDescription property

Purpose

Cell array of strings giving descriptions of variables in data set

Description

A cell array of strings giving the descriptions of the variables in the data set. This property may be empty, but if not empty, the number of strings must equal the number of variables. Any individual string may be empty for a variable that does not have a description defined. The default is an empty cell array.

Purpose

Compute embedded estimates of input feature importance

Syntax

```
imp = varimportance(t)
```

Description

`imp = varimportance(t)` computes estimates of input feature importance for tree `t` by summing changes in the risk due to splits on every feature. The returned vector `imp` has one element for each input variable in the data used to train this tree. At each node, the risk is estimated as node impurity if impurity was used to split nodes and node error otherwise. This risk is weighted by the node probability. Variable importance associated with this split is computed as the difference between the risk for the parent node and the total risk for the two children.

See Also

`risk`

dataset.VarNames property

Purpose

Cell array giving names of variables in data set

Description

A cell array of nonempty, distinct strings giving the names of the variables in the data set. The number of strings must equal the number of variables. The default is the cell array of string names for the variables used to create the data set.

Purpose

Variable names

Description

The `VarNames` property is a cell array containing the names of the predictor variables (features). `TreeBagger` takes these names from the optional `'names'` parameter. The default names are `'x1'`, `'x2'`, etc.

Purpose

Chi-square variance test

Syntax

```
H = vartest(X,V)
H = vartest(X,V,alpha)
H = vartest(X,V,alpha,tail)
[H,P] = vartest(...)
[H,P,CI] = vartest(...)
[H,P,CI,STATS] = vartest(...)
[...] = vartest(X,V,alpha,tail,dim)
```

Description

`H = vartest(X,V)` performs a chi-square test of the hypothesis that the data in the vector `X` comes from a normal distribution with variance `V`, against the alternative that `X` comes from a normal distribution with a different variance. The result is `H = 0` if the null hypothesis (variance is `V`) cannot be rejected at the 5% significance level, or `H = 1` if the null hypothesis can be rejected at the 5% level.

`X` may also be a matrix or an n-dimensional array. For matrices, `vartest` performs separate tests along each column of `X`, and returns a row vector of results. For n-dimensional arrays, `vartest` works along the first nonsingleton dimension of `X`. `V` must be a scalar.

`H = vartest(X,V,alpha)` performs the test at the significance level `(100*alpha)`%. `alpha` has a default value of 0.05 and must be a scalar.

`H = vartest(X,V,alpha,tail)` performs the test against the alternative hypothesis specified by *`tail`*, where *`tail`* is a single string from the following choices:

- `'both'` — Variance is not `V` (two-tailed test). This is the default.
- `'right'` — Variance is greater than `V` (right-tailed test).
- `'left'` — Variance is less than `V` (left-tailed test).

`[H,P] = vartest(...)` returns the *p* value, i.e., the probability of observing the given result, or one more extreme, by chance if the null hypothesis is true. Small values of `P` cast doubt on the validity of the null hypothesis.

`[H,P,CI] = vartest(...)` returns a `100*(1-alpha)`% confidence interval for the true variance.

`[H,P,CI,STATS] = vartest(...)` returns the structure `STATS` with the following fields:

- `'chisqstat'` — Value of the test statistic
- `'df'` — Degrees of freedom of the test

`[...] = vartest(X,V,alpha,tail,dim)` works along dimension `dim` of `X`. Pass in `[]` for `alpha` or `tail` to use their default values.

Examples

Determine whether the standard deviation is significantly different from 7?

```
load carsmall

[h,p,ci] = vartest(MPG,7^2)
```

See Also

`ttest` | `ztest` | `vartest2`

Purpose

Two-sample *F*-test for equal variances

Syntax

```
H = vartest2(X,Y)
H = vartest2(X,Y,alpha)
H = vartest2(X,Y,alpha,tail)
[H,P] = vartest2(...)
[H,P,CI] = vartest2(...)
[H,P,CI,STATS] = vartest2(...)
[...] = vartest2(X,Y,alpha,tail,dim)
```

Description

`H = vartest2(X,Y)` performs an *F* test of the hypothesis that two independent samples, in the vectors `X` and `Y`, come from normal distributions with the same variance, against the alternative that they come from normal distributions with different variances. The result is `H = 0` if the null hypothesis (variances are equal) cannot be rejected at the 5% significance level, or `H = 1` if the null hypothesis can be rejected at the 5% level. `X` and `Y` can have different lengths. `X` and `Y` can also be matrices or n-dimensional arrays.

For matrices, `vartest2` performs separate tests along each column, and returns a vector of results. `X` and `Y` must have the same number of columns. For n-dimensional arrays, `vartest2` works along the first nonsingleton dimension. `X` and `Y` must have the same size along all the remaining dimensions.

`H = vartest2(X,Y,alpha)` performs the test at the significance level `(100*alpha)`%. `alpha` must be a scalar.

`H = vartest2(X,Y,alpha,tail)` performs the test against the alternative hypothesis specified by *`tail`*, where *`tail`* is one of the following single strings:

- `'both'` — Variance is not `Y` (two-tailed test). This is the default.
- `'right'` — Variance is greater than `Y` (right-tailed test).
- `'left'` — Variance is less than `Y` (left-tailed test).

`[H,P] = vartest2(...)` returns the *p* value, i.e., the probability of observing the given result, or one more extreme, by chance if the null hypothesis is true. Small values of `P` cast doubt on the validity of the null hypothesis.

`[H,P,CI] = vartest2(...)` returns a `100*(1-alpha)`% confidence interval for the true variance ratio `var(X)/var(Y)`.

`[H,P,CI,STATS] = vartest2(...)` returns a structure with the following fields:

- `'fstat'` — Value of the test statistic
- `'df1'` — Numerator degrees of freedom of the test
- `'df2'` — Denominator degrees of freedom of the test

`[...] = vartest2(X,Y,alpha,tail,dim)` works along dimension `dim` of `X`. To pass in the default values for `alpha` or `tail` use `[]`.

Examples

Is the variance significantly different for two model years, and what is a confidence interval for the ratio of these variances?

```
load carsmall

[H,P,CI] =
vartest2(MPG(Model_Year==82),MPG(Model_Year==76))
```

See Also

`ansaribradley` | `vartest` | `vartestn` | `ttest2`

Purpose

Bartlett multiple-sample test for equal variances

Syntax

```
vartestn(X)
vartestn(X,group)
p = vartestn(...)
[p,STATS] = vartestn(...)
[...] = vartestn(...,displayopt)
[...] = vartestn(...,testtype)
```

Description

`vartestn(X)` performs Bartlett's test for equal variances for the columns of the matrix `X`. This is a test of the null hypothesis that the columns of `X` come from normal distributions with the same variance, against the alternative that they come from normal distributions with different variances. The result is a display of a box plot of the groups, and a summary table of statistics.

`vartestn(X,group)` requires a vector `X`, and a `group` argument that is a categorical variable, vector, string array, or cell array of strings with one row for each element of `X`. The `X` values corresponding to the same value of `group` are placed in the same group. (See "Grouped Data" on page 2-34.) The function tests for equal variances across groups.

`vartestn` treats `NaN`s as missing values and ignores them.

`p = vartestn(...)` returns the *p* value, i.e., the probability of observing the given result, or one more extreme, by chance if the null hypothesis of equal variances is true. Small values of `p` cast doubt on the validity of the null hypothesis.

`[p,STATS] = vartestn(...)` returns a structure with the following fields:

- `'chistat'` — Value of the test statistic
- `'df'` — Degrees of freedom of the test

`[...] = vartestn(...,displayopt)` determines if a box plot and table are displayed. *`displayopt`* may be `'on'` (the default) or `'off'` .

`[...] = vartestn(...,testtype)` sets the test type. When *`testtype`* is `'robust'`, `vartestn` performs Levene's test in place of Bartlett's test, which is a useful alternative when the sample distributions are not normal, and especially when they are prone to outliers. For this test the `STATS` output structure has a field named `'fstat'` containing the test statistic, and `'df1'` and `'df2'` containing its numerator and denominator degrees of freedom. When *`testtype`* is `'classical'` `vartestn` performs Bartlett's test.

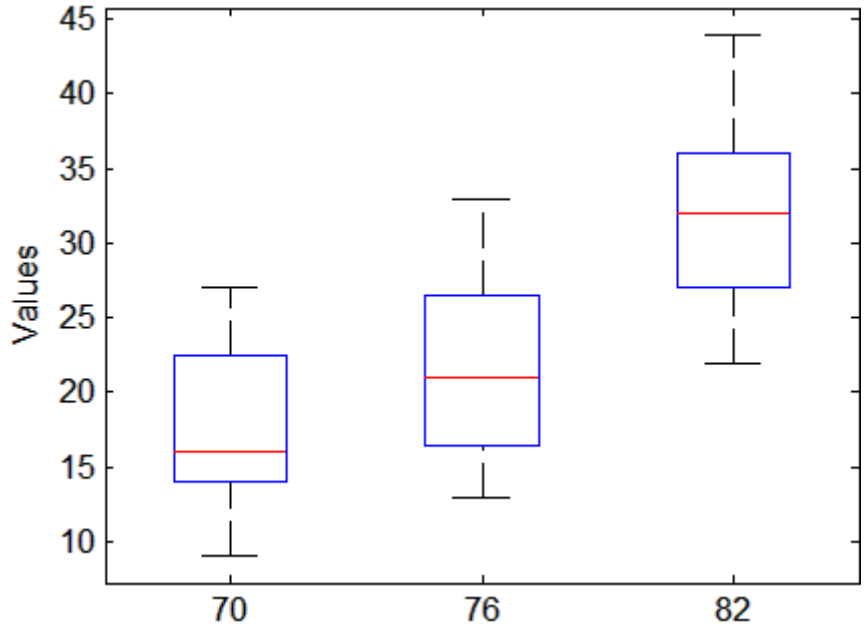
Examples

Does the variance of mileage measurements differ significantly from one model year to another?

```
load carsmall
p = vartestn(MPG,Model_Year)
p =
    0.8327
```

Group Summary Table

Group	Count	Mean	Std Dev
70	29	17.6897	5.33923
76	34	21.5735	5.8893
82	31	31.7097	5.39255
Pooled	94	23.7181	5.562
Bartlett's statistic	0.36619		
Degrees of freedom	2		
p-value	0.83269		



See Also `vartest` | `vartest2` | `anova1`

How To

- “Grouped Data” on page 2-34

Purpose

Vertical concatenation for categorical arrays

Syntax

```
C = vertcat(dim,A,B,...)
C = vertcat(A,B)
```

Description

`C = vertcat(dim,A,B,...)` vertically concatenates the categorical arrays `A,B,...` . For matrices, all inputs must have the same number of rows. For `n`-D arrays, all inputs must have the same sizes except in the second dimension. The set of categorical levels for `C` is the sorted union of the sets of levels of the inputs, as determined by their labels.

`C = vertcat(A,B)` is called for the syntax `[A B]`.

See Also

`cat` | `horzcat`

dataset.vertcat

Purpose

Vertical concatenation for dataset arrays

Syntax

```
ds = vertcat(ds1, ds2, ...)
```

Description

`ds = vertcat(ds1, ds2, ...)` vertically concatenates the dataset arrays `ds1, ds2, ...` . Observation names, when present, must be unique across datasets. `vertcat` fills in default observation names for the output when some of the inputs have names and some do not.

Variable names for all dataset arrays must be identical except for order. `vertcat` concatenates by matching variable names. `vertcat` assigns values for the "per-variable" properties (e.g., `Units` and `VarDescription`) in `ds` from the corresponding property values in `ds1`.

See Also

`cat | horzcat`

Purpose

Plot tree

Syntax

```
view(t)
view(t,param1,val1,param2,val2,...)
```

Description

`view(t)` displays the decision tree `t` as computed by `classregtree` in a figure window. Each branch in the tree is labeled with its decision rule, and each terminal node is labeled with the predicted value for that node. Click any node to get more information about it. The information displayed is specified by the **Click to display** pop-up menu at the top of the figure.

`view(t,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs:

- `'names'` — A cell array of names for the predictor variables, in the order in which they appear in the matrix `X` from which the tree was created. (See `classregtree`.)
- `'prunelevel'` — Initial pruning level to display.

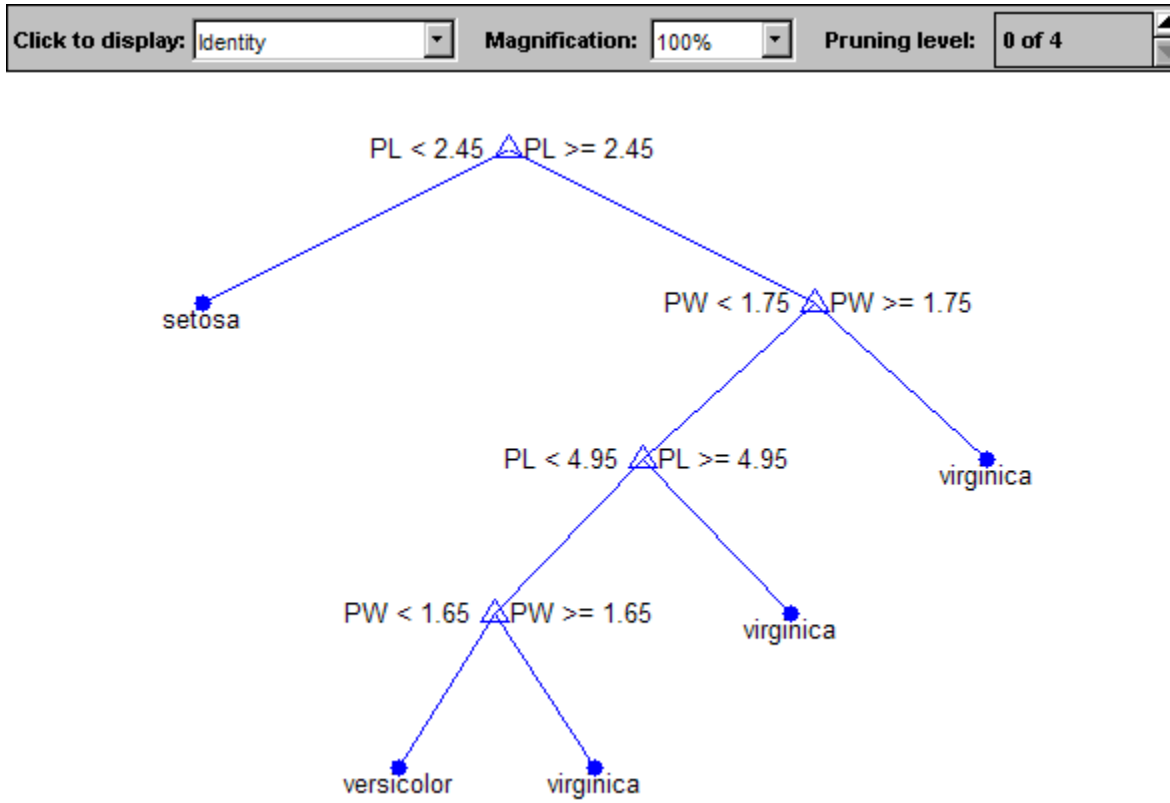
For each branch node, the left child node corresponds to the points that satisfy the condition, and the right child node corresponds to the points that do not satisfy the condition.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
```

```
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `eval` | `prune` | `test`

CompactClassificationTree.view

Purpose

View tree

Syntax

```
view(tree)
view(tree,Name,Value)
```

Description

`view(tree)` returns a text description of `tree`, a decision tree.

`view(tree,Name,Value)` describes `tree` with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`tree`

A classification tree or compact classification tree created by `ClassificationTree.fit` or `compact`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`mode`

String describing the display of `tree`, either `'graph'` or `'text'`. `'graph'` opens a GUI displaying `tree`, and containing controls for querying the tree. `'text'` sends output to the Command Window describing `tree`.

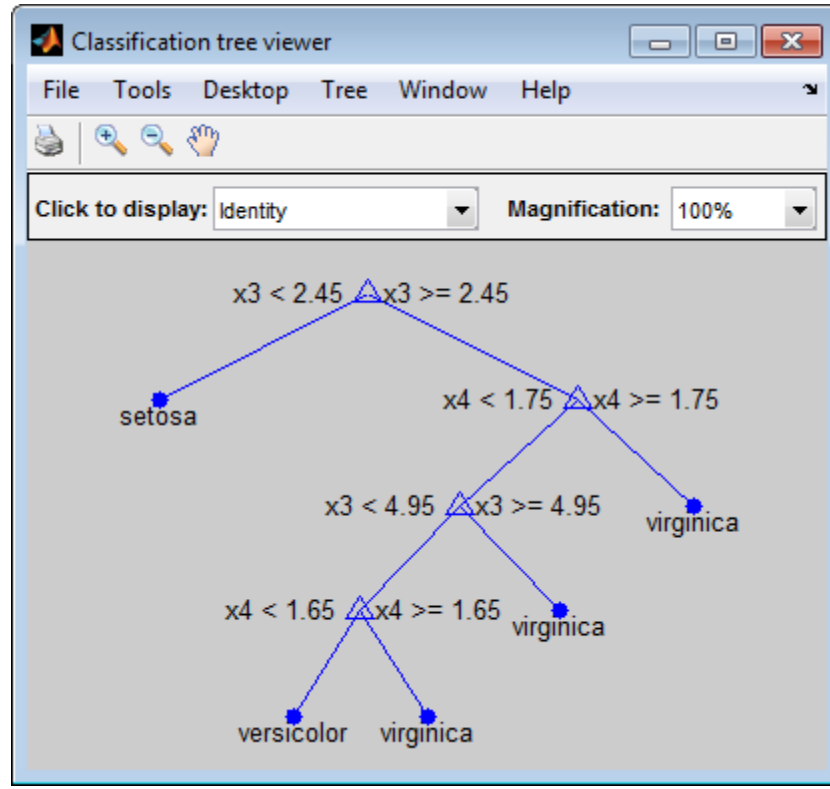
Default: `'text'`

Examples

View the classification tree for Fisher's iris model in both textual and graphical displays:

```
load fisheriris
tree = ClassificationTree.fit(meas,species);
view(tree)

Decision tree for classification
```

```
1  if x3<2.45 then node 2 elseif x3>=2.45 then node 3 else setosa
2  class = setosa
3  if x4<1.75 then node 4 elseif x4>=1.75 then node 5 else versicolor
4  if x3<4.95 then node 6 elseif x3>=4.95 then node 7 else versicolor
5  class = virginica
6  if x4<1.65 then node 8 elseif x4>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(tree,'mode','graph')
```



See Also `ClassificationTree`

How To

- Chapter 13, “Nonparametric Supervised Learning”

Purpose

View tree

Syntax

```
view(tree)
view(tree,Name,Value)
```

Description

`view(tree)` returns a text description of `tree`, a decision tree.

`view(tree,Name,Value)` describes `tree` with additional options specified by one or more `Name,Value` pair arguments.

Input Arguments

`tree`

A regression tree or compact regression tree created by `RegressionTree.fit` or `compact`.

Name-Value Pair Arguments

Optional comma-separated pairs of `Name,Value` arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`''`). You can specify several name-value pair arguments in any order as `Name1,Value1, ,NameN,ValueN`.

`mode`

String describing the display of `tree`, either `'graph'` or `'text'`. `'graph'` opens a GUI displaying `tree`, and containing controls for querying the tree. `'text'` sends output to the Command Window describing `tree`.

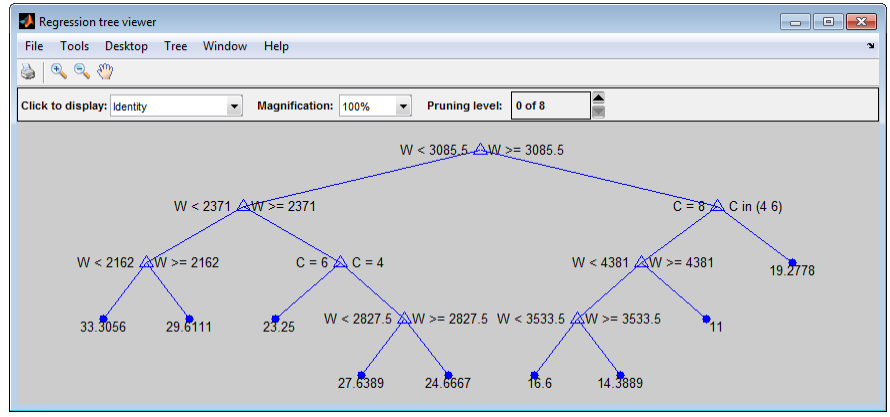
Default: `'text'`

Examples

View a regression tree for the `carsmall` data in both textual and graphical displays:

```
load carsmall
tree = RegressionTree.fit([Weight, Cylinders],MPG,...
                'categoricalpredictors',2,'MinParent',20,...
                'PredictorNames',{'W','C'});
view(tree)
```

```
Decision tree for regression
 1  if W<3085.5 then node 2 elseif W>=3085.5 then node 3 else 23.7181
 2  if W<2371 then node 4 elseif W>=2371 then node 5 else 28.7931
 3  if C=8 then node 6 elseif C in {4 6} then node 7 else 15.5417
 4  if W<2162 then node 8 elseif W>=2162 then node 9 else 32.0741
 5  if C=6 then node 10 elseif C=4 then node 11 else 25.9355
 6  if W<4381 then node 12 elseif W>=4381 then node 13 else 14.2963
 7  fit = 19.2778
 8  fit = 33.3056
 9  fit = 29.6111
10  fit = 23.25
11  if W<2827.5 then node 14 elseif W>=2827.5 then node 15 else 27.2143
12  if W<3533.5 then node 16 elseif W>=3533.5 then node 17 else 14.8696
13  fit = 11
14  fit = 27.6389
15  fit = 24.6667
16  fit = 16.6
17  fit = 14.3889

view(tree,'mode','graph')
```



See Also

RegressionTree

How To

- Chapter 13, “Nonparametric Supervised Learning”

wblcdf

Purpose

Weibull cumulative distribution function

Syntax

```
P = wblcdf(X,A,B)
[P,PLO,PUP] = wblcdf(X,A,B,PCOV,alpha)
```

Description

`P = wblcdf(X,A,B)` computes the cdf of the Weibull distribution with scale parameter `A` and shape parameter `B`, at each of the values in `X`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The default values for `A` and `B` are both `1`. The parameters `A` and `B` must be positive.

`[P,PLO,PUP] = wblcdf(X,A,B,PCOV,alpha)` returns confidence bounds for `P` when the input parameters `A` and `B` are estimates. `PCOV` is the 2-by-2 covariance matrix of the estimated parameters. `alpha` has a default value of 0.05, and specifies 100(1 - `alpha`)% confidence bounds. `PLO` and `PUP` are arrays of the same size as `P` containing the lower and upper confidence bounds.

The function `wblcdf` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\hat{b}\left(\log x - \log \hat{a}\right)$$

and then transforms those bounds to the scale of the output `P`. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `PCOV` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The Weibull cdf is

$$p = F\left(x \mid a,b\right) = \int_0^x b a^{-b} t^{b-1} e^{-\left(\frac{t}{a}\right)^b} dt = 1 - e^{-\left(\frac{x}{a}\right)^b} I_{(0,\infty)}(x)$$

Examples

What is the probability that a value from a Weibull distribution with parameters `a = 0.15` and `b = 0.8` is less than 0.5?

```
probability = wblcdf(0.5, 0.15, 0.8)
probability =
  0.9272
```

How sensitive is this result to small changes in the parameters?

```
[A, B] = meshgrid(0.1:0.05:0.2,0.2:0.05:0.3);
probability = wblcdf(0.5, A, B)
probability =
  0.7484  0.7198  0.6991
  0.7758  0.7411  0.7156
  0.8022  0.7619  0.7319
```

See Also

cdf | wblpdf | wblinv | wblstat | wblfit | wbllike | wblrnd

How To

- “Weibull Distribution” on page B-103

wblfit

Purpose

Weibull parameter estimates

Syntax

```
parmhat = wblfit(data)
[parmhat,parmci] = wblfit(data)
[parmhat,parmci] = wblfit(data,alpha)
[...] = wblfit(data,alpha,censoring)
[...] = wblfit(data,alpha,censoring,freq)
[...] = wblfit(...,options)
```

Description

`parmhat = wblfit(data)` returns the maximum likelihood estimates, `parmhat`, of the parameters of the Weibull distribution given the values in the vector `data`, which must be positive. `parmhat` is a two-element row vector: `parmhat(1)` estimates the Weibull parameter a, and `parmhat(2)` estimates the Weibull parameter b, in the pdf

$$y = f(x \mid a,b) = ba^{-b}x^{b-1}e^{-\left(\frac{x}{a}\right)^{b}} I_{(0,\infty)}(x)$$

`[parmhat,parmci] = wblfit(data)` returns 95% confidence intervals for the estimates of a and b in the 2-by-2 matrix `parmci`. The first row contains the lower bounds of the confidence intervals for the parameters, and the second row contains the upper bounds of the confidence intervals.

`[[parmhat,parmci] = wblfit(data,alpha)` returns 100(1 - `alpha`)% confidence intervals for the parameter estimates.

`[...] = wblfit(data,alpha,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is `1` for observations that are right-censored and `0` for observations that are observed exactly.

`[...] = wblfit(data,alpha,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. The vector `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any non-negative values. Pass in `[]` for `alpha`, `censoring`, or `freq` to use their default values.

`[...] = wblfit(...,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates. The Weibull fit function accepts an `options` structure that can be created using the function `statset`. Enter `statset ('wblfit')` to see the names and default values of the parameters that `lognfit` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

Examples

```
data = wblrnd(0.5,0.8,100,1);
[parmhat, parmci] = wblfit(data)
parmhat =
  0.5861  0.8567
parmci =
  0.4606  0.7360
  0.7459  0.9973
```

See Also

`mle` | `wbllike` | `wblpdf` | `wblcdf` | `wblinv` | `wblstat` | `wblrnd`

How To

- "Weibull Distribution" on page B-103

wblinv

Purpose

Weibull inverse cumulative distribution function

Syntax

```
X = wblinv(P,A,B)
[X,XLO,XUP] = wblinv(P,A,B,PCOV,alpha)
```

Description

`X = wblinv(P,A,B)` returns the inverse cumulative distribution function (cdf) for a Weibull distribution with scale parameter `A` and shape parameter `B`, evaluated at the values in `P`. `P`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The default values for `A` and `B` are both `1`.

`[X,XLO,XUP] = wblinv(P,A,B,PCOV,alpha)` returns confidence bounds for `X` when the input parameters `A` and `B` are estimates. `PCOV` is a 2-by-2 matrix containing the covariance matrix of the estimated parameters. `alpha` has a default value of 0.05, and specifies 100(1 - `alpha`)% confidence bounds. `XLO` and `XUP` are arrays of the same size as `X` containing the lower and upper confidence bounds.

The function `wblinv` computes confidence bounds for `X` using a normal approximation to the distribution of the estimate

$$\log a + \frac{\log q}{b}$$

where q is the `P`th quantile from a Weibull distribution with scale and shape parameters both equal to 1. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `PCOV` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The inverse of the Weibull cdf is

$$x = F^{-1}(p \mid a,b) = -a\left[\ln\left(1-p\right)\right]^{1/b} I_{[0,1]}(p)$$

Examples

The lifetimes (in hours) of a batch of light bulbs has a Weibull distribution with parameters `a = 200` and `b = 6`.

Find the median lifetime of the bulbs:

```
life = wblinv(0.5, 200, 6)
life =
 188.1486
```

Generate 100 random values from this distribution, and estimate the 90th percentile (with confidence bounds) from the random sample

```
x = wblrnd(200,6,100,1);
p = wblfit(x)
[nlogl,pcov] = wbllike(p,x)
[q90,q90lo,q90up] = wblinv(0.9,p(1),p(2),pcov)
p =

  204.8918    6.3920


nlogl =

  496.8915


pcov =

   11.3392    0.5233
    0.5233    0.2573


q90 =

  233.4489


q90lo =
```

```
    226.0092

q90up =

    241.1335
```

See Also

icdf | wblcdf | wblpdf | wblstat | wblfit | wbllike | wblrnd

How To

- “Weibull Distribution” on page B-103

Purpose

Weibull negative log-likelihood

Syntax

```
nlogL = wbllike(params,data)
[logL,AVAR] = wbllike(params,data)
[...] = wbllike(params,data,censoring)
[...] = wbllike(params,data,censoring,freq)
```

Description

`nlogL = wbllike(params,data)` returns the Weibull log-likelihood. `params(1)` is the scale parameter, `A`, and `params(2)` is the shape parameter, `B`.

`[logL,AVAR] = wbllike(params,data)` also returns `AVAR`, which is the asymptotic variance-covariance matrix of the parameter estimates if the values in `params` are the maximum likelihood estimates. `AVAR` is the inverse of Fisher's information matrix. The diagonal elements of `AVAR` are the asymptotic variances of their respective parameters.

`[...] = wbllike(params,data,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = wbllike(params,data,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `censoring` to use its default value.

The Weibull negative log-likelihood for uncensored data is

$$(-\log L) = -\log \prod_{i=1} f(a,b \mid x_i) = -\sum_{i=1}^{n} \log f(a,b \mid x_i)$$

where f is the Weibull pdf.

`wbllike` is a utility function for maximum likelihood estimation.

Examples

This example continues the example from `wblfit`.

```
r = wblrnd(0.5,0.8,100,1);
```

```
[logL, AVAR] = wbllike(wblfit(r),r)
logL =
  47.3349
AVAR =
  0.0048  0.0014
  0.0014  0.0040
```

References

[1] Patel, J. K., C. H. Kapadia, and D. B. Owen. *Handbook of Statistical Distributions*. New York: Marcel Dekker, 1976.

See Also

`wblfit` | `wblpdf` | `wblcdf` | `wblinv` | `wblstat` | `wblrnd`

How To

- "Weibull Distribution" on page B-103

Purpose

Weibull probability density function

Syntax

```
Y = wblpdf(X,A,B)
```

Description

`Y = wblpdf(X,A,B)` computes the Weibull pdf at each of the values in `X` using the corresponding scale parameter, `A` and shape parameter, `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The parameters in `A` and `B` must be positive.

The Weibull pdf is

$$y = f(x \mid a,b) = ba^{-b}x^{b-1}e^{-\left(\frac{x}{a}\right)^{b}} I_{(0,\infty)}(x)$$

Some references refer to the Weibull distribution with a single parameter. This corresponds to `wblpdf` with `A = 1`.

Examples

The exponential distribution is a special case of the Weibull distribution.

```
lambda = 1:6;
y = wblpdf(0.1:0.1:0.6,lambda,1)
y =
  0.9048  0.4524  0.3016  0.2262  0.1810  0.1508

y1 = exppdf(0.1:0.1:0.6,lambda)
y1 =
  0.9048  0.4524  0.3016  0.2262  0.1810  0.1508
```

References

[1] Devroye, L. *Non-Uniform Random Variate Generation*. New York: Springer-Verlag, 1986.

See Also

`pdf | wblcdf`

How To

- `wblfit`
- `wblinv`
- `wbllike`
- `wblplot`
- `wblrnd`
- `wblstat`
- “Weibull Distribution” on page B-103

Purpose

Weibull probability plot

Syntax

```
wblplot(X)
h = wblplot(X)
```

Description

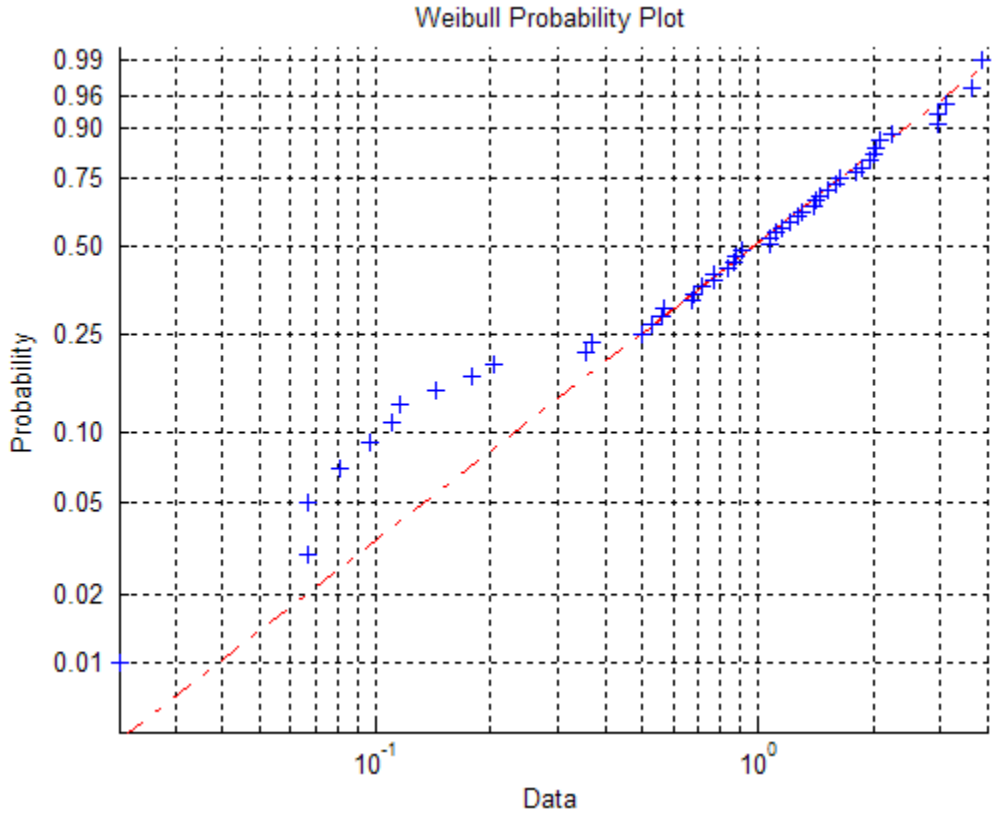
`wblplot(X)` displays a Weibull probability plot of the data in `X`. If `X` is a matrix, `wblplot` displays a plot for each column.

`h = wblplot(X)` returns handles to the plotted lines.

The purpose of a Weibull probability plot is to graphically assess whether the data in `X` could come from a Weibull distribution. If the data are Weibull the plot will be linear. Other distribution types might introduce curvature in the plot. `wblplot` uses midpoint probability plotting positions. Use `probplot` when the data included censored observations.

Examples

```
r = wblrnd(1.2,1.5,50,1);
wblplot(r)
```



See Also

`probplot` | `normplot` | `wblcdf`

How To

- `wblfit`
- `wblinv`
- `wbllike`
- `wblpdf`
- `wblrnd`

- `wblstat`
- “Weibull Distribution” on page B-103

wblrnd

Purpose

Weibull random numbers

Syntax

```
R = wblrnd(A,B)
R = wblrnd(A,B,m,n,...)
R = wblrnd(A,B,[m,n,...])
```

Description

`R = wblrnd(A,B)` generates random numbers for the Weibull distribution with scale parameter, `A` and shape parameter, `B`. The input arguments `A` and `B` can be either scalars or matrices. `A` and `B`, can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other input.

`R = wblrnd(A,B,m,n,...)` or `R = wblrnd(A,B,[m,n,...])` generates an `m`-by-`n`-by-... array. The `A`, `B` parameters can each be scalars or arrays of the same size as `R`.

Devroye [1] refers to the Weibull distribution with a single parameter; this is `wblrnd` with A = 1.

Examples

```
n1 = wblrnd(0.5:0.5:2,0.5:0.5:2)
n1 =
  0.0178  0.0860  2.5216  0.9124

n2 = wblrnd(1/2,1/2,[1 6])
n2 =
  0.0046  1.7214  2.2108  0.0367  0.0531  0.0917
```

References

[1] Devroye, L. *Non-Uniform Random Variate Generation*. New York: Springer-Verlag, 1986.

See Also

`random` | `wblpdf` | `wblcdf` | `wblinv` | `wblstat` | `wblfit` | `wbllike`

How To

• "Weibull Distribution" on page B-103

Purpose

Weibull mean and variance

Syntax

```
[M,V] = wblstat(A,B)
```

Description

`[M,V] = wblstat(A,B)` returns the mean of and variance for the Weibull distribution with scale parameter, `A` and shape parameter, `B`. Vector or matrix inputs for `A` and `B` must have the same size, which is also the size of `M` and `V`. A scalar input for `A` or `B` is expanded to a constant matrix with the same dimensions as the other input.

The mean of the Weibull distribution with parameters a and b is

$$a\left[\Gamma\left(1+b^{-1}\right)\right]$$

and the variance is

$$a^2\left[\Gamma\left(1+2b^{-1}\right)-\Gamma\left(1+b^{-1}\right)^2\right]$$

Examples

```
[m,v] = wblstat(1:4,1:4)
m =
  1.0000  1.7725  2.6789  3.6256
v =
  1.0000  0.8584  0.9480  1.0346

wblstat(0.5,0.7)
ans =
  0.6329
```

See Also

`wblpdf` | `wblcdf` | `wblinv` | `wblfit` | `wbllike` | `wblrnd`

How To

- "Weibull Distribution" on page B-103

wishrnd

Purpose

Wishart random numbers

Syntax

```
W = wishrnd(Sigma,df)
W = wishrnd(Sigma,df,D)
[W,D] = wishrnd(Sigma,df)
```

Description

`W = wishrnd(Sigma,df)` generates a random matrix `W` having the Wishart distribution with covariance matrix `Sigma` and with `df` degrees of freedom. The inverse of `W` has the Inverse Wishart distribution with parameters `Tau = inv(Sigma)` and `df` degrees of freedom.

`W = wishrnd(Sigma,df,D)` expects `D` to be the Cholesky factor of `Sigma`. If you call `wishrnd` multiple times using the same value of `Sigma`, it's more efficient to supply `D` instead of computing it each time.

`[W,D] = wishrnd(Sigma,df)` returns `D` so you can provide it as input in future calls to `wishrnd`.

This function defines the parameter `Sigma` so that the mean of the output matrix is `Sigma*df`

See Also

`iwishrnd`

How To

- "Wishart Distribution" on page B-106

Purpose

X data used to create ensemble

Description

The `X` property is a numeric matrix of size `Nobs`-by-`Nvars`, where `Nobs` is the number of observations (rows) and `Nvars` is the number of variables (columns) in the training data. This matrix contains the predictor (or feature) values.

xptread

Purpose

Create dataset array from data stored in SAS XPORT format file

Syntax

```
data = xptread
data = xptread(filename)
[data,missing] = xptread(filename)
xptread(...,'ReadObsNames',true)
```

Description

`data = xptread` displays a dialog box for selecting a file, then reads data from the file into a dataset array. The file must be in the `SAS XPORT` format.

`data = xptread(filename)` retrieves data from a `SAS XPORT` format file `filename`. The `XPORT` format allows for 28 missing data types, represented in the file by an upper case letter, `'.'` or `'_'`. `xptread` converts All missing data to `NaN` values in `data`. However, if you need the specific missing types then you can recover this information by specifying a second output.

`[data,missing] = xptread(filename)` returns a nominal array, `missing`, of the same size as `data` containing the missing data type information from the `xport` format file. The entries are undefined for values that are not present and are one of `'.'`, `'_'`, `'A'`,...,`'Z'` for missing values.

`xptread(...,'ReadObsNames',true)` treats the first variable in the file as observation names. The default value is false.

`xptread` only supports single data sets per file. `xptread` does not support compressed files.

Examples

Read in a `SAS XPORT` format dataset:

```
data = xptread('sample.xpt')
```

See Also

`dataset | dataset.export`

Purpose

Convert predictor matrix to design matrix

Syntax

```
D = x2fx(X,model)
D = x2fx(X,model,categ)
D = x2fx(X,model,categ,catlevels)
```

Description

`D = x2fx(X,model)` converts a matrix of predictors `X` to a design matrix `D` for regression analysis. Distinct predictor variables should appear in different columns of `X`.

The optional input *`model`* controls the regression model. By default, `x2fx` returns the design matrix for a linear additive model with a constant term. *`model`* is one of the following strings:

- `'linear'` — Constant and linear terms. This is the default.
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms
- `'purequadratic'` — Constant, linear, and squared terms

If `X` has n columns, the order of the columns of `D` for a full quadratic model is:

1. The constant term
2. The linear terms (the columns of `X`, in order 1, 2, ..., n)
3. The interaction terms (pairwise products of the columns of `X`, in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n–1, n))
4. The squared terms (in order 1, 2, ..., n)

Other models use a subset of these terms, in the same order.

Alternatively, *`model`* can be a matrix specifying polynomial terms of arbitrary order. In this case, *`model`* should have one column for each column in `X` and one row for each term in the model. The entries in any row of *`model`* are powers for the corresponding columns of `X`. For

example, if X has columns X1, X2, and X3, then a row [0 1 2] in *model* specifies the term (X1.^0).*(X2.^1).*(X3.^2). A row of all zeros in *model* specifies a constant term, which can be omitted.

D = x2fx(X,*model*,categ) treats columns with numbers listed in the vector categ as categorical variables. Terms involving categorical variables produce dummy variable columns in D. Dummy variables are computed under the assumption that possible categorical levels are completely enumerated by the unique values that appear in the corresponding column of X.

D = x2fx(X,*model*,categ,catlevels) accepts a vector catlevels the same length as categ, specifying the number of levels in each categorical variable. In this case, values in the corresponding column of X must be integers in the range from 1 to the specified number of levels. Not all of the levels need to appear in X.

Examples

Example 1

The following converts 2 predictors X1 and X2 (the columns of X) into a design matrix for a full quadratic model with terms constant, X1, X2, X1.*X2, X1.^2, and X2.^2.

```
X = [1 10
     2 20
     3 10
     4 20
     5 15
     6 15];

D = x2fx(X,'quadratic')
D =
     1     1    10    10     1   100
     1     2    20    40     4   400
     1     3    10    30     9   100
     1     4    20    80    16   400
     1     5    15    75    25   225
     1     6    15    90    36   225
```

Example 2

The following converts 2 predictors `X1` and `X2` (the columns of `X`) into a design matrix for a quadratic model with terms `constant`, `X1`, `X2`, `X1.*X2`, and `X1.^2`.

```
X = [1 10
     2 20
     3 10
     4 20
     5 15
     6 15];
model = [0 0
         1 0
         0 1
         1 1
         2 0];

D = x2fx(X,model)
D =
     1     1    10    10     1
     1     2    20    40     4
     1     3    10    30     9
     1     4    20    80    16
     1     5    15    75    25
     1     6    15    90    36
```

See Also

`regstats` | `rstool` | `candexch` | `candgen` | `cordexch` | `rowexch`

TreeBagger.Y property

Purpose

Y data used to create ensemble

Description

The `Y` property is an array of true class labels for classification, or response values for regression. `Y` can be a numeric column vector, a character matrix, or a cell array of strings.

Purpose

Standardized *z*-scores

Syntax

```
Z = zscore(X)
[Z,mu,sigma] = zscore(X)
[...] = zscore(X,1)
[...] = zscore(X,flag,dim)
```

Description

`Z = zscore(X)` returns a centered, scaled version of `X`, the same size as `X`. For vector input `x`, output is the vector of *z*-scores `z = (x mean(x))./std(x)`. For matrix input `X`, *z*-scores are computed using the mean and standard deviation along each column of `X`. For higher-dimensional arrays, *z*-scores are computed using the mean and standard deviation along the first non-singleton dimension.

The columns of `Z` have mean zero and standard deviation one (unless a column of `X` is constant, in which case that column of `Z` is constant at `0`). *z*-scores are used to put data on the same scale before further analysis.

`[Z,mu,sigma] = zscore(X)` also returns `mean(X)` in `mu` and `std(X)` in `sigma`.

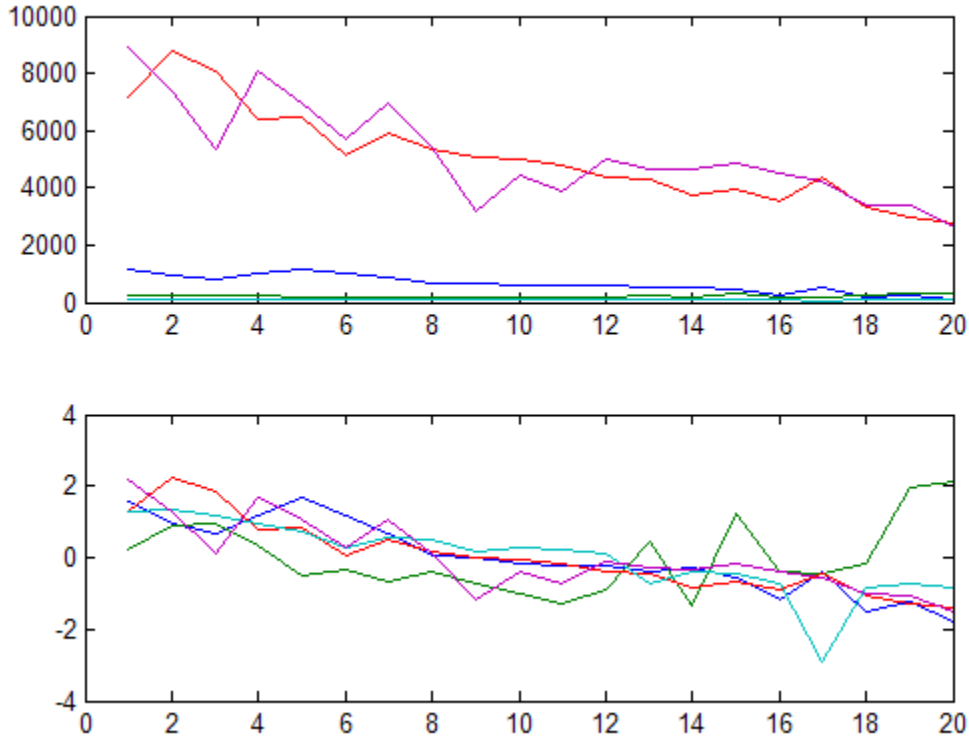
`[...] = zscore(X,1)` normalizes `X` using `std(X,1)`, that is, by computing the standard deviation(s) using n rather than $n–1$, where n is the length of the dimension along which `zscore` works. `zscore(X,0)` is the same as `zscore(X)`.

`[...] = zscore(X,flag,dim)` standardizes `X` by working along the dimension `dim` of `X`. Set `flag` to `0` to use the default normalization by $n–1$; set `flag` to `1` to use n.

Examples

Compare the predictors in the Moore data on original and standardized scales:

```
load moore
predictors = moore(:,1:5);
subplot(2,1,1),plot(predictors)
subplot(2,1,2),plot(zscore(predictors))
```



See Also

`mean` | `std`

Purpose

z-test

Syntax

```
h = ztest(x,m,sigma)
h = ztest(...,alpha)
h = ztest(...,alpha,tail)
h = ztest(...,alpha,tail,dim)
[h,p] = ztest(...)
[h,p,ci] = ztest(...)
[h,p,ci,zval] = ztest(...)
```

Description

`h = ztest(x,m,sigma)` performs a *z*-test of the null hypothesis that data in the vector `x` are a random sample from a normal distribution with mean `m` and standard deviation `sigma`, against the alternative that the mean is not `m`. The result of the test is returned in `h`. `h = 1` indicates a rejection of the null hypothesis at the 5% significance level. `h = 0` indicates a failure to reject the null hypothesis at the 5% significance level.

`x` can also be a matrix or an *N*-dimensional array. For matrices, `ztest` performs separate *z*-tests along each column of `x` and returns a vector of results. For *N*-dimensional arrays, `ztest` works along the first non-singleton dimension of `x`.

The test treats `NaN` values as missing data, and ignores them.

`h = ztest(...,alpha)` performs the test at the (100*`alpha`)% significance level. The default, when unspecified, is `alpha = 0.05`.

`h = ztest(...,alpha,tail)` performs the test against the alternative specified by the string *`tail`*. There are three options for *`tail`*:

- `'both'` — Mean is not `m` (two-tailed test). This is the default, when `tail` is unspecified.
- `'right'` — Mean is greater than `m` (right-tail test)
- `'left'` — Mean is less than `m` (left-tail test)

`tail` must be a single string, even when `x` is a matrix or an *N*-dimensional array.

`h = ztest(...,alpha,tail,dim)` works along dimension `dim` of `x`. Use `[]` to pass in default values for `alpha` or `tail`.

`[h,p] = ztest(...)` returns the p value of the test. The p value is the probability, under the null hypothesis, of observing a value as extreme or more extreme of the test statistic

$$z = \frac{\bar{x} - \mu}{\sigma / \sqrt{n}}$$

where $\bar{x}$ is the sample mean, μ = `m` is the hypothesized population mean, σ is the population standard deviation, and n is the sample size. Under the null hypothesis, the test statistic will have a standard normal distribution, $N(0,1)$.

`[h,p,ci] = ztest(...)` returns a 100*(1 – `alpha`)% confidence interval on the population mean.

`[h,p,ci,zval] = ztest(...)` returns the value of the test statistic.

Examples

Simulate a random sample of size 100 from a normal distribution with mean 0.1 and standard deviation 1:

```
x = normrnd(0.1,1,1,100);
```

Test the null hypothesis that the sample comes from a standard normal distribution:

```
[h,p,ci] = ztest(x,0,1)
h =
     0
p =
    0.1391
ci =
   -0.0481    0.3439
```

The test fails to reject the null hypothesis at the default $\alpha = 0.05$ significance level. Under the null hypothesis, the probability of observing a value as extreme or more extreme of the test statistic, as

indicated by the p value, is greater than α. The 95% confidence interval on the mean contains 0.

Simulate a larger random sample of size 1000 from the same distribution:

```
y = normrnd(0.1,1,1,1000);
```

Test again if the sample comes from a normal distribution with mean 0:

```
[h,p,ci] = ztest(y,0,1)
h =
     1
p =
  5.5160e-005
ci =
    0.0655    0.1895
```

This time the test rejects the null hypothesis at the default $\alpha = 0.05$ significance level. The p value has fallen below $\alpha = 0.05$ and the 95% confidence interval on the mean does not contain 0.

Because the p value of the sample `y` is less than 0.01, the test will still reject the null hypothesis when the significance level is lowered to $\alpha = 0.01$:

```
[h,p,ci] = ztest(y,0,1,0.01)
h =
     1
p =
  5.5160e-005
ci =
    0.0461    0.2090
```

This example will produce slightly different results each time it is run, because of the random sampling.

See Also

`ttest` | `ttest2`

A

Data Sets

Statistics Toolbox software includes the sample data sets in the following table.

To load a data set into the MATLAB workspace, type:

```
load filename
```

where *filename* is one of the files listed in the table.

Data sets contain individual data variables, description variables with references, and dataset arrays encapsulating the data set and its description, as appropriate.

File	Description of Data Set
acetylene.mat	Chemical reaction data with correlated predictors
arrhythmia.mat	Cardiac arrhythmia data from the UCI machine learning repository
carbig.mat	Measurements of cars, 1970–1982
carsmall.mat	Subset of carbig.mat. Measurements of cars, 1970, 1976, 1982
cereal.mat	Breakfast cereal ingredients
cities.mat	Quality of life ratings for U.S. metropolitan areas
discrim.mat	A version of cities.mat used for discriminant analysis
examgrades.mat	Exam grades on a scale of 0–100
fisheriris.mat	Fisher's 1936 iris data
flu.mat	Google Flu Trends estimated ILI (influenza-like illness) percentage for various regions of the US, and CDC weighted ILI percentage based on sentinel provider reports
gas.mat	Gasoline prices around the state of Massachusetts in 1993
hald.mat	Heat of cement vs. mix of ingredients
hogg.mat	Bacteria counts in different shipments of milk

File	Description of Data Set
hospital.mat	Simulated hospital data
imports-85.mat	1985 Auto Imports Database from the UCI repository
ionosphere.mat	Ionosphere dataset from the UCI machine learning repository
kmeansdata.mat	Four-dimensional clustered data
lawdata.mat	Grade point average and LSAT scores from 15 law schools
mileage.mat	Mileage data for three car models from two factories
moore.mat	Biochemical oxygen demand on five predictors
morse.mat	Recognition of Morse code distinctions by non-coders
ovariancancer.mat	Grouped observations on 4000 predictors
parts.mat	Dimensional run-out on 36 circular parts
polydata.mat	Sample data for polynomial fitting
popcorn.mat	Popcorn yield by popper type and brand
reaction.mat	Reaction kinetics for Hougen-Watson model
sat.dat	Scholastic Aptitude Test averages by gender and test (table)
sat2.dat	Scholastic Aptitude Test averages by gender and test (csv)
spectra.mat	NIR spectra and octane numbers of 60 gasoline samples
stockreturns.mat	Simulated stock returns

B

Distribution Reference

Bernoulli Distribution

Definition of the Bernoulli Distribution

The Bernoulli distribution is a special case of the binomial distribution, with $n = 1$.

See Also

"Discrete Distributions" on page 5-7

Beta Distribution

In this section...

Definition

The beta pdf is

$$y = f(x \mid a,b) = \frac{1}{B(a,b)} x^{a-1}(1-x)^{b-1} I_{(0,1)}(x)$$

where $B(\cdot)$ is the Beta function. The indicator function $I_{(0,1)}(x)$ ensures that only values of x in the range (0 1) have nonzero probability.

Background

The beta distribution describes a family of curves that are unique in that they are nonzero only on the interval (0 1). A more general version of the function assigns parameters to the endpoints of the interval.

The beta cdf is the same as the incomplete beta function.

The beta distribution has a functional relationship with the t distribution. If Y is an observation from Student's t distribution with ν degrees of freedom, then the following transformation generates X, which is beta distributed.

$$X = \frac{1}{2} + \frac{1}{2} \frac{Y}{\sqrt{\nu + Y^2}}$$

If $Y \sim t(\upsilon)$, then $X \sim \beta\left(\frac{\nu}{2}, \frac{\nu}{2}\right)$

This relationship is used to compute values of the t cdf and inverse function as well as generating t distributed random numbers.

Parameters

Suppose you are collecting data that has hard lower and upper bounds of zero and one respectively. Parameter estimation is the process of determining the parameters of the beta distribution that fit this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the beta pdf. But for the pdf, the parameters are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the x's) are already observed. So they are the fixed constants. The variables are the unknown parameters. Maximum likelihood estimation (MLE) involves calculating the values of the parameters that give the highest likelihood given the particular set of data.

The function `betafit` returns the MLEs and confidence intervals for the parameters of the beta distribution. Here is an example using random numbers from the beta distribution with $a = 5$ and $b = 0.2$.

```
r = betarnd(5,0.2,100,1);
[phat, pci] = betafit(r)

phat =
    4.5330    0.2301

pci =
    2.8051    0.1771
    6.2610    0.2832
```

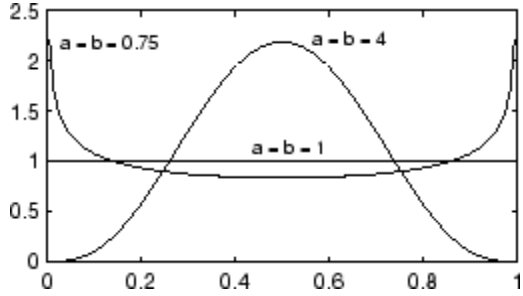
The MLE for parameter a is 4.5330, compared to the true value of 5. The 95% confidence interval for a goes from 2.8051 to 6.2610, which includes the true value.

Similarly the MLE for parameter b is 0.2301, compared to the true value of 0.2. The 95% confidence interval for b goes from 0.1771 to 0.2832, which

also includes the true value. In this made-up example you know the "true value." In experimentation you do not.

Example

The shape of the beta distribution is quite variable depending on the values of the parameters, as illustrated by the plot below.



The constant pdf (the flat line) shows that the standard uniform distribution is a special case of the beta distribution.

See Also

"Continuous Distributions (Data)" on page 5-4

Binomial Distribution

In this section...

Definition

The binomial pdf is

$$f(k \mid n, p) = \binom{n}{k} p^k (1-p)^{n-k}$$

where k is the number of successes in n trials of a Bernoulli process with probability of success p.

The binomial distribution is discrete, defined for integers $k = 0, 1, 2, \ldots n$, where it is nonzero.

Background

The binomial distribution models the total number of successes in repeated trials from an infinite population under the following conditions:

- Only two outcomes are possible on each of n trials.
- The probability of success for each trial is constant.
- All trials are independent of each other.

The binomial distribution is a generalization of the Bernoulli distribution; it generalizes to the multinomial distribution.

Parameters

Suppose you are collecting data from a widget manufacturing process, and you record the number of widgets within specification in each batch of 100. You might be interested in the probability that an individual widget is within specification. Parameter estimation is the process of determining the parameter, p, of the binomial distribution that fits this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the binomial pdf above. But for the pdf, the parameters (n and p) are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the x's) are already observed. So they are the fixed constants. The variables are the unknown parameters. MLE involves calculating the value of p that give the highest likelihood given the particular set of data.

The function `binofit` returns the MLEs and confidence intervals for the parameters of the binomial distribution. Here is an example using random numbers from the binomial distribution with $n = 100$ and $p = 0.9$.

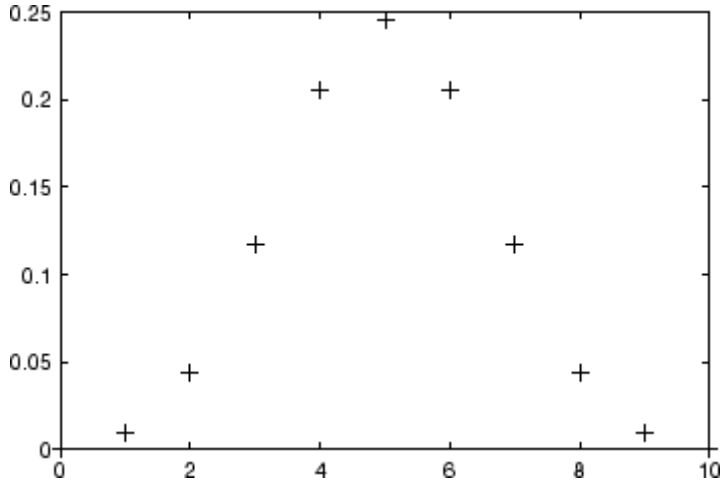
```
r = binornd(100,0.9)

r =
    88

[phat, pci] = binofit(r,100)

phat =
    0.8800

pci =
    0.7998
    0.9364
```

The MLE for parameter p is 0.8800, compared to the true value of 0.9. The 95% confidence interval for p goes from 0.7998 to 0.9364, which includes the true value. In this made-up example you know the "true value" of p. In experimentation you do not.

Example

The following commands generate a plot of the binomial pdf for $n = 10$ and $p = 1/2$.

```
x = 0:10;
y = binopdf(x,10,0.5);
plot(x,y,'+')
```



See Also

"Discrete Distributions" on page 5-7

Birnbaum-Saunders Distribution

In this section...

Definition

The Birnbaum-Saunders distribution has the density function

$$\frac{1}{\sqrt{2\pi}}\exp\left\{-\frac{\left(\sqrt{x/\beta}-\sqrt{\beta/x}\right)^2}{2\gamma^2}\right\}\left(\frac{\left(\sqrt{x/\beta}+\sqrt{\beta/x}\right)}{2\gamma x}\right)$$

with scale parameter ß > 0 and shape parameter $\gamma > 0$, for $x > 0$.

If x has a Birnbaum-Saunders distribution with parameters ß and γ, then

$$\frac{\left(\sqrt{x/\beta}-\sqrt{\beta/x}\right)}{\gamma}$$

has a standard normal distribution.

Background

The Birnbaum-Saunders distribution was originally proposed as a lifetime model for materials subject to cyclic patterns of stress and strain, where the ultimate failure of the material comes from the growth of a prominent flaw. In materials science, Miner's Rule suggests that the damage occurring after n cycles, at a stress level with an expected lifetime of N cycles, is proportional

to n / N. Whenever Miner's Rule applies, the Birnbaum-Saunders model is a reasonable choice for a lifetime distribution model.

Parameters

See `mle`, `dfittool`.

See Also

"Continuous Distributions (Data)" on page 5-4

Chi-Square Distribution

In this section...

Definition

The χ^2 pdf is

$$y = f(x \mid \nu) = \frac{x^{(\nu-2)/2} e^{-x/2}}{2^{\frac{\nu}{2}} \Gamma(\nu/2)}$$

where $\Gamma(\cdot)$ is the Gamma function, and v is the degrees of freedom.

Background

The χ^2 distribution is a special case of the gamma distribution where $b = 2$ in the equation for gamma distribution below.

$$y = f(x \mid a,b) = \frac{1}{b^a \Gamma(a)} x^{a-1} e^{\frac{x}{b}}$$

The χ^2 distribution gets special attention because of its importance in normal sampling theory. If a set of n observations is normally distributed with variance σ^2, and s^2 is the sample standard deviation, then

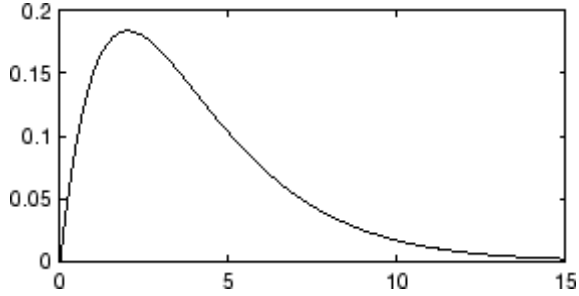
$$\frac{(n-1)s^2}{\sigma^2} \sim \chi^2(n-1)$$

This relationship is used to calculate confidence intervals for the estimate of the normal parameter σ^2 in the function `normfit`.

Example

The χ^2 distribution is skewed to the right especially for few degrees of freedom (ν). The plot shows the χ^2 distribution with four degrees of freedom.

```
x = 0:0.2:15;
y = chi2pdf(x,4);
plot(x,y)
```



See Also

"Continuous Distributions (Statistics)" on page 5-6

Copulas

See “Copulas” on page 5-107.

Custom Distributions

User-defined custom distributions, created using files and function handles, are supported by the Statistics Toolbox functions `pdf`, `cdf`, `icdf`, and `mle`, and the Statistics Toolbox GUI `dfittool`.

Exponential Distribution

In this section...

Definition

The exponential pdf is

$$y = f(x \mid \mu) = \frac{1}{\mu} e^{\frac{-x}{\mu}}$$

Background

Like the chi-square distribution, the exponential distribution is a special case of the gamma distribution (obtained by setting $a = 1$)

$$y = f(x \mid a, b) = \frac{1}{b^a \Gamma(a)} x^{a-1} e^{\frac{x}{b}}$$

where $\Gamma(\cdot)$ is the Gamma function.

The exponential distribution is special because of its utility in modeling events that occur randomly over time. The main application area is in studies of lifetimes.

Parameters

Suppose you are stress testing light bulbs and collecting data on their lifetimes. You assume that these lifetimes follow an exponential distribution.

You want to know how long you can expect the average light bulb to last. Parameter estimation is the process of determining the parameters of the exponential distribution that fit this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the exponential pdf above. But for the pdf, the parameters are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the x's) are already observed. So they are the fixed constants. The variables are the unknown parameters. MLE involves calculating the values of the parameters that give the highest likelihood given the particular set of data.

The function `expfit` returns the MLEs and confidence intervals for the parameters of the exponential distribution. Here is an example using random numbers from the exponential distribution with $\mu = 700$.

```
lifetimes = exprnd(700,100,1);
[muhat, muci] = expfit(lifetimes)

muhat =

  672.8207

muci =

  547.4338
  810.9437
```

The MLE for parameter μ is 672, compared to the true value of 700. The 95% confidence interval for μ goes from 547 to 811, which includes the true value.

In the life tests you do not know the true value of μ so it is nice to have a confidence interval on the parameter to give a range of likely values.

Example

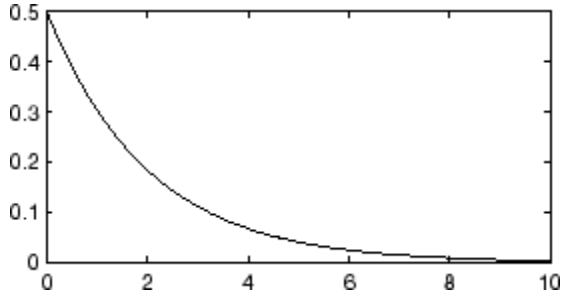
For exponentially distributed lifetimes, the probability that an item will survive an extra unit of time is independent of the current age of the item. The example shows a specific case of this special property.

```
l = 10:10:60;
```

```
lpd = l+0.1;
deltap = (expcdf(lpd,50)-expcdf(l,50))./(1-expcdf(l,50))

deltap =
    0.0020    0.0020    0.0020    0.0020    0.0020    0.0020
```

The following commands generate a plot of the exponential pdf with its parameter (and mean), μ, set to 2.

```
x = 0:0.1:10;
y = exppdf(x,2);
plot(x,y)
```



See Also

"Continuous Distributions (Data)" on page 5-4

Extreme Value Distribution

In this section...

Definition

The probability density function for the extreme value distribution with location parameter μ and scale parameter σ is

$$y = f(x \mid \mu,\sigma) = \sigma^{-1} \exp\left(\frac{x-\mu}{\sigma}\right)\exp\left(-\exp\left(\frac{x-\mu}{\sigma}\right)\right)$$

If T has a Weibull distribution with parameters a and b, then $\log T$ has an extreme value distribution with parameters $\mu = \log a$ and $\sigma = 1/b$.

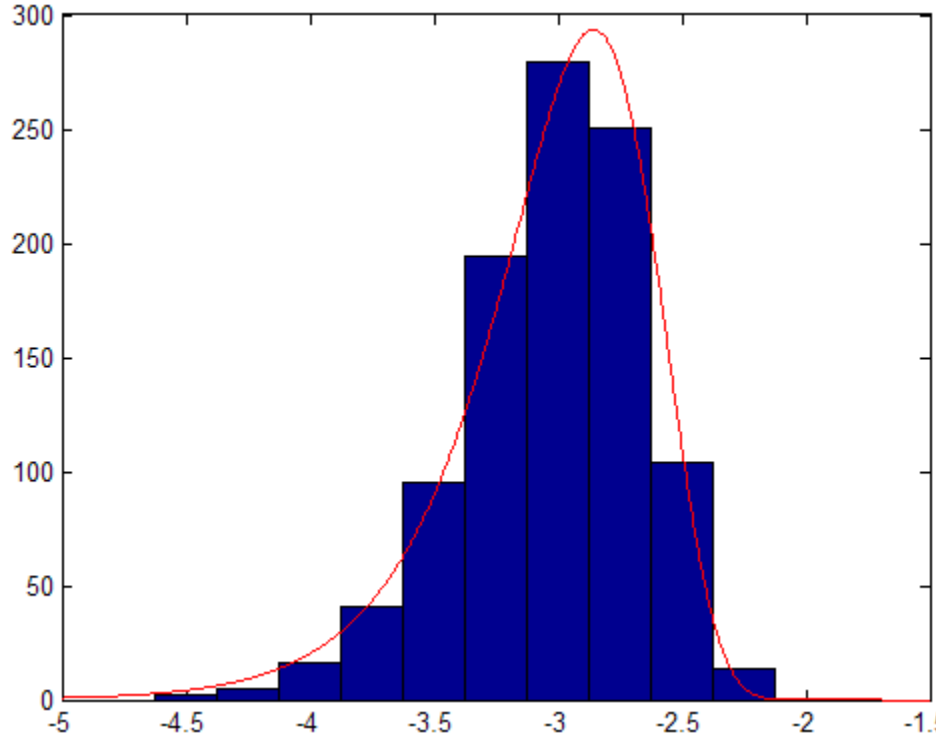
Background

Extreme value distributions are often used to model the smallest or largest value among a large set of independent, identically distributed random values representing measurements or observations. The extreme value distribution is appropriate for modeling the smallest value from a distribution whose tails decay exponentially fast, for example, the normal distribution. It can also model the largest value from a distribution, such as the normal or exponential distributions, by using the negative of the original values.

For example, the following fits an extreme value distribution to minimum values taken over 1000 sets of 500 observations from a normal distribution:

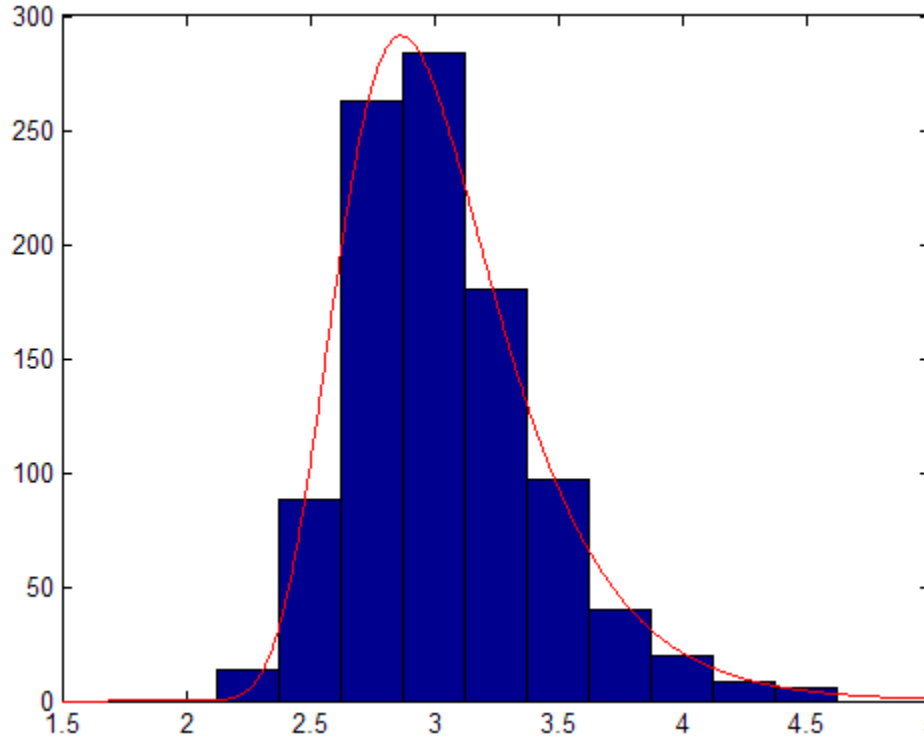
```
xMinima = min(randn(1000,500), [], 2);
paramEstsMinima = evfit(xMinima);
y = linspace(-5,-1.5,1001);
```

```
hist(xMinima,-4.75:.25:-1.75);
p = evpdf(y,paramEstsMinima(1),paramEstsMinima(2));
line(y,.25*length(xMinima)*p,'color','r')
```



The following fits an extreme value distribution to the maximum values in each set of observations:

```
xMaxima = max(randn(1000,500), [], 2);
paramEstsMaxima = evfit(-xMaxima);
y = linspace(1.5,5,1001);
hist(xMaxima,1.75:.25:4.75);
p = evpdf(-y,paramEstsMaxima(1),paramEstsMaxima(2));
line(y,.25*length(xMaxima)*p,'color','r')
```



Although the extreme value distribution is most often used as a model for extreme values, you can also use it as a model for other types of continuous data. For example, extreme value distributions are closely related to the Weibull distribution. If `T` has a Weibull distribution, then `log(T)` has a type 1 extreme value distribution.

Parameters

The function `evfit` returns the maximum likelihood estimates (MLEs) and confidence intervals for the parameters of the extreme value distribution. The following example shows how to fit some sample data using `evfit`, including estimates of the mean and variance from the fitted distribution.

Suppose you want to model the size of the smallest washer in each batch of 1000 from a manufacturing process. If you believe that the sizes are

independent within and between each batch, you can fit an extreme value distribution to measurements of the minimum diameter from a series of eight experimental batches. The following code returns the MLEs of the distribution parameters as `parmhat` and the confidence intervals as the columns of `parmci`.

```
x = [19.774 20.141 19.44 20.511 21.377 19.003 19.66 18.83];
[parmhat, parmci] = evfit(x)

parmhat =
   20.2506    0.8223

parmci =
   19.644 0.49861
   20.857 1.3562
```

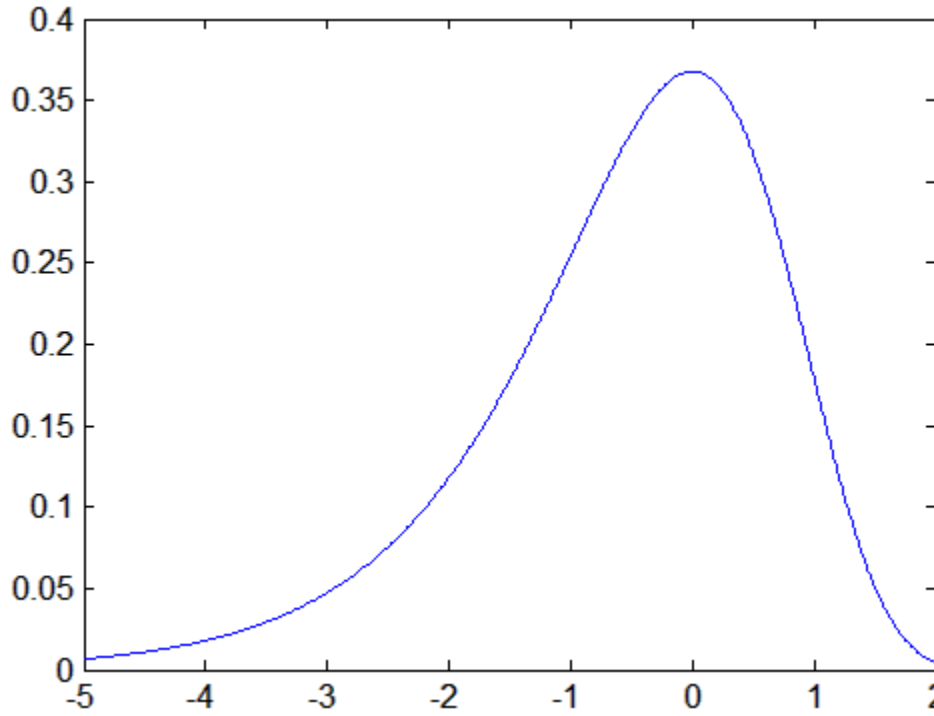
You can find mean and variance of the extreme value distribution with these parameters using the function `evstat`.

```
[meanfit, varfit] = evstat(parmhat(1),parmhat(2))

meanfit =
   19.776

varfit =
   1.1123
```

Example

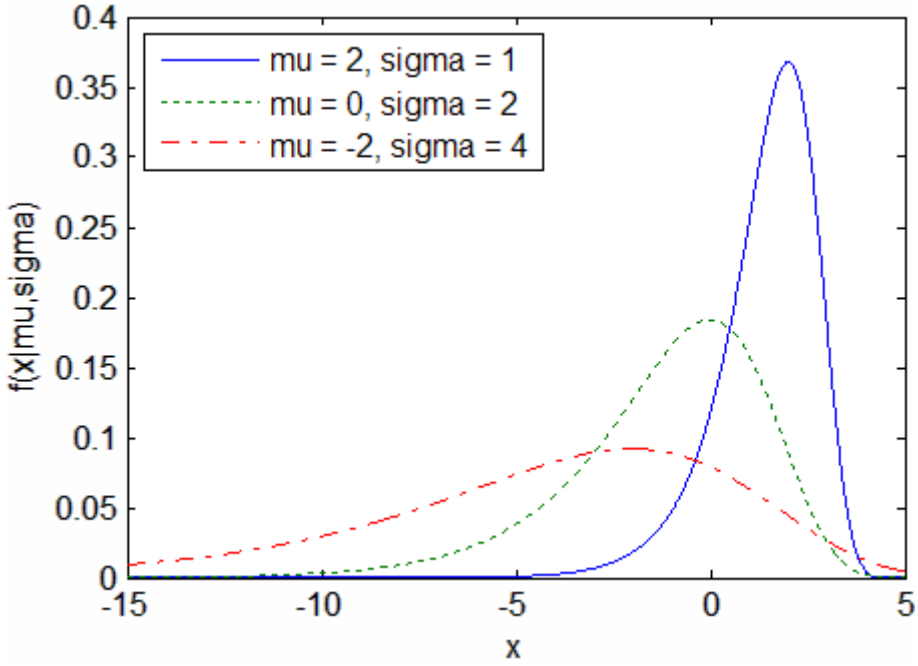
The following code generates a plot of the pdf for the extreme value distribution.

```
t = [-5:.01:2];
y = evpdf(t);
plot(t,y)
```



The extreme value distribution is skewed to the left, and its general shape remains the same for all parameter values. The location parameter, `mu`, shifts the distribution along the real line, and the scale parameter, `sigma`, expands or contracts the distribution. This example plots the probability function for different combinations of `mu` and `sigma`.

```
x = -15:.01:5;
plot(x,evpdf(x,2,1),'-', ...
     x,evpdf(x,0,2),':', ...
     x,evpdf(x,-2,4),'-.');
legend({'mu = 2, sigma = 1', ...
        'mu = 0, sigma = 2', ...
        'mu = -2, sigma = 4'}, ...
       'Location','NW')
xlabel('x')
ylabel('f(x|mu,sigma)')
```



See Also

"Continuous Distributions (Data)" on page 5-4

F Distribution

In this section...

Definition

The pdf for the F distribution is

$$y = f(x \mid \nu_1, \nu_2) = \frac{\Gamma\left[\frac{(\nu_1 + \nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}} \frac{x^{\frac{\nu_1 - 2}{2}}}{\left[1 + \left(\frac{\nu_1}{\nu_2}\right)x\right]^{\frac{\nu_1 + \nu_2}{2}}}$$

where $\Gamma(\cdot)$ is the Gamma function.

Background

The F distribution has a natural relationship with the chi-square distribution. If χ_1 and χ_2 are both chi-square with ν_1 and ν_2 degrees of freedom respectively, then the statistic F below is F-distributed.

$$F(\nu_1, \nu_2) = \frac{\chi_1 / \nu_1}{\chi_2 / \nu_2}$$

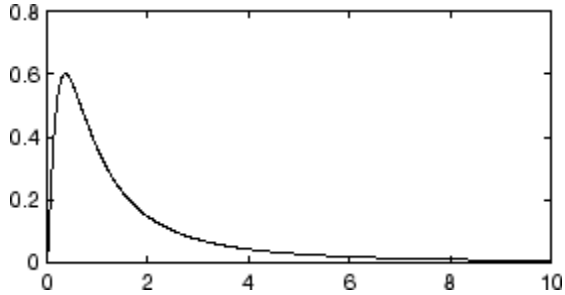
The two parameters, ν_1 and ν_2, are the numerator and denominator degrees of freedom. That is, ν_1 and ν_2 are the number of independent pieces of information used to calculate χ_1 and χ_2, respectively.

Example

The most common application of the *F* distribution is in standard tests of hypotheses in analysis of variance and regression.

The plot shows that the *F* distribution exists on the positive real numbers and is skewed to the right.

```
x = 0:0.01:10;
y = fpdf(x,5,3);
plot(x,y)
```



See Also

"Continuous Distributions (Statistics)" on page 5-6

Gamma Distribution

In this section...

Definition

The gamma pdf is

$$y = f(x \mid a,b) = \frac{1}{b^a \Gamma(a)} x^{a-1} e^{\frac{-x}{b}}$$

where $\Gamma(\cdot)$ is the Gamma function.

Background

The gamma distribution models sums of exponentially distributed random variables.

The gamma distribution family is based on two parameters. The chi-square and exponential distributions, which are children of the gamma distribution, are one-parameter distributions that fix one of the two gamma parameters.

The gamma distribution has the following relationship with the incomplete Gamma function.

$$f(x \mid a,b) = \text{gammainc}\left(\frac{x}{b}, a\right)$$

When a is large, the gamma distribution closely approximates a normal distribution with the advantage that the gamma distribution has density only for positive real numbers.

Parameters

Suppose you are stress testing computer memory chips and collecting data on their lifetimes. You assume that these lifetimes follow a gamma distribution. You want to know how long you can expect the average computer memory chip to last. Parameter estimation is the process of determining the parameters of the gamma distribution that fit this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the gamma pdf above. But for the pdf, the parameters are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the x's) are already observed. So they are the fixed constants. The variables are the unknown parameters. MLE involves calculating the values of the parameters that give the highest likelihood given the particular set of data.

The function `gamfit` returns the MLEs and confidence intervals for the parameters of the gamma distribution. Here is an example using random numbers from the gamma distribution with $a = 10$ and $b = 5$.

```
lifetimes = gamrnd(10,5,100,1);
[phat, pci] = gamfit(lifetimes)

phat =

    10.9821    4.7258

pci =

    7.4001    3.1543
   14.5640    6.2974
```

Note `phat(1)` = $\hat{a}$ and `phat(2)` = $\hat{b}$. The MLE for parameter a is 10.98, compared to the true value of 10. The 95% confidence interval for a goes from 7.4 to 14.6, which includes the true value.

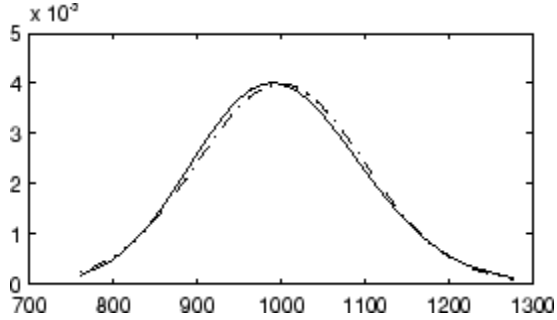
Similarly the MLE for parameter b is 4.7, compared to the true value of 5. The 95% confidence interval for b goes from 3.2 to 6.3, which also includes the true value.

In the life tests you do not know the true value of a and b so it is nice to have a confidence interval on the parameters to give a range of likely values.

Example

In the example the gamma pdf is plotted with the solid line. The normal pdf has a dashed line type.

```
x = gaminv((0.005:0.01:0.995),100,10);
y = gampdf(x,100,10);
y1 = normpdf(x,1000,100);
plot(x,y,'-',x,y1,'-.')
```



See Also

"Continuous Distributions (Data)" on page 5-4

Gaussian Distribution

See “Normal Distribution” on page B-83.

Gaussian Mixture Distributions

See the discussion of the `gmdistribution` class in the "Gaussian Mixture Models" on page 5-99 section of "Probability Distributions Used for Multivariate Modeling" on page 5-99 and the "Gaussian Mixture Models" on page 11-28 section of Chapter 11, "Cluster Analysis".

Generalized Extreme Value Distribution

In this section...

Definition

The probability density function for the generalized extreme value distribution with location parameter μ, scale parameter σ, and shape parameter $k \neq 0$ is

$$y = f(x \mid k,\mu,\sigma) = \left(\frac{1}{\sigma}\right)\exp\left(-\left(1+k\frac{(x-\mu)}{\sigma}\right)^{-\frac{1}{k}}\right)\left(1+k\frac{(x-\mu)}{\sigma}\right)^{-1-\frac{1}{k}}$$

for

$$1 + k\frac{(x-\mu)}{\sigma} > 0$$

$k > 0$ corresponds to the Type II case, while $k < 0$ corresponds to the Type III case. For $k = 0$, corresponding to the Type I case, the density is

$$y = f(x \mid 0,\mu,\sigma) = \left(\frac{1}{\sigma}\right)\exp\left(-\exp\left(-\frac{(x-\mu)}{\sigma}\right)-\frac{(x-\mu)}{\sigma}\right)$$

Background

Like the extreme value distribution, the generalized extreme value distribution is often used to model the smallest or largest value among a large set of independent, identically distributed random values representing measurements or observations. For example, you might have batches of 1000

washers from a manufacturing process. If you record the size of the largest washer in each batch, the data are known as block maxima (or minima if you record the smallest). You can use the generalized extreme value distribution as a model for those block maxima.

The generalized extreme value combines three simpler distributions into a single form, allowing a continuous range of possible shapes that includes all three of the simpler distributions. You can use any one of those distributions to model a particular dataset of block maxima. The generalized extreme value distribution allows you to "let the data decide" which distribution is appropriate.

The three cases covered by the generalized extreme value distribution are often referred to as the Types I, II, and III. Each type corresponds to the limiting distribution of block maxima from a different class of underlying distributions. Distributions whose tails decrease exponentially, such as the normal, lead to the Type I. Distributions whose tails decrease as a polynomial, such as Student's *t*, lead to the Type II. Distributions whose tails are finite, such as the beta, lead to the Type III.

Types I, II, and III are sometimes also referred to as the Gumbel, Frechet, and Weibull types, though this terminology can be slightly confusing. The Type I (Gumbel) and Type III (Weibull) cases actually correspond to the mirror images of the usual Gumbel and Weibull distributions, for example, as computed by the functions `evcdf` and `evfit` , or `wblcdf` and `wblfit`, respectively. Finally, the Type II (Frechet) case is equivalent to taking the reciprocal of values from a standard Weibull distribution.

Parameters

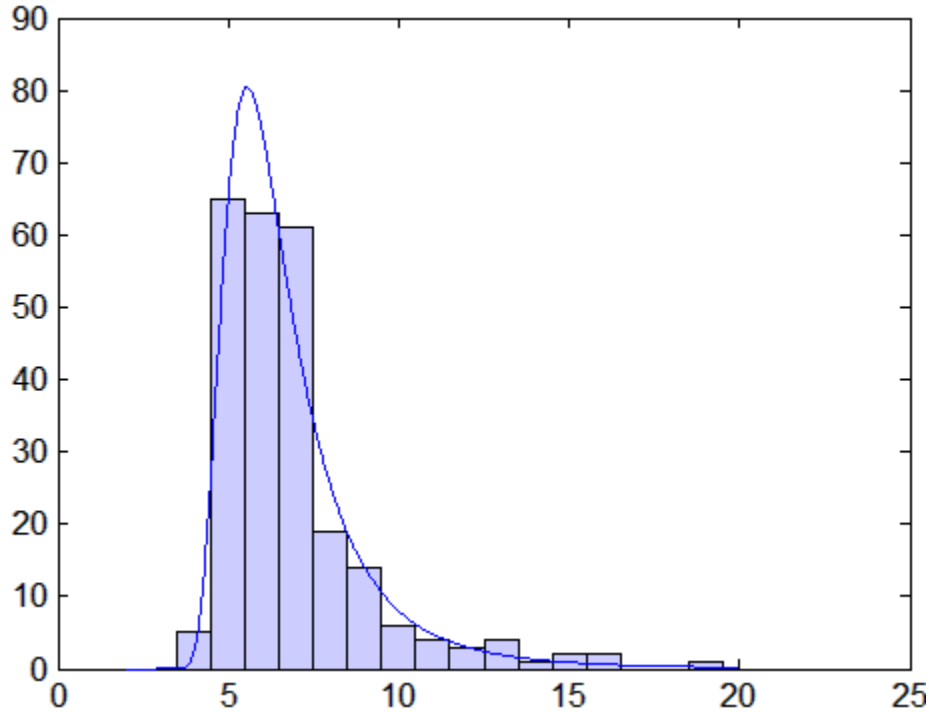
If you generate 250 blocks of 1000 random values drawn from Student's *t* distribution with 5 degrees of freedom, and take their maxima, you can fit a generalized extreme value distribution to those maxima.

```
blocksize = 1000;
nblocks = 250;
t = trnd(5,blocksize,nblocks);
x = max(t); % 250 column maxima
paramEsts = gevfit(x)
paramEsts =
```

```
    0.2438    1.1760    5.8045
```

Notice that the shape parameter estimate (the first element) is positive, which is what you would expect based on block maxima from a Student's *t* distribution.

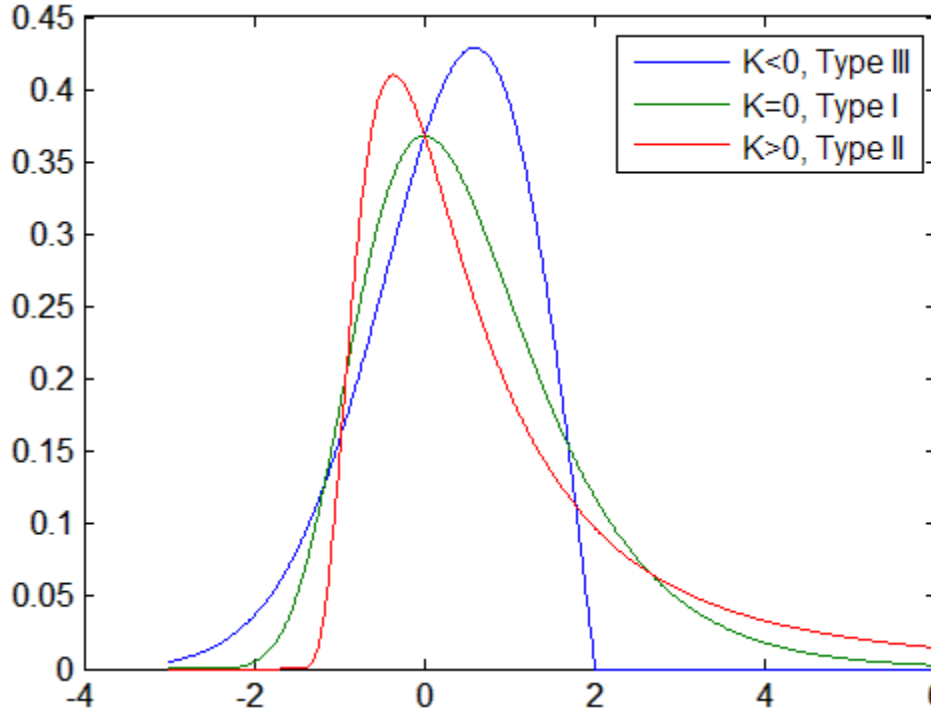
```
hist(x,2:20);
set(get(gca,'child'),'FaceColor',[.8 .8 1])
xgrid = linspace(2,20,1000);
line(xgrid,nblocks*...
     gevpdf(xgrid,paramEsts(1),paramEsts(2),paramEsts(3)));
```



Example

The following code generates examples of probability density functions for the three basic forms of the generalized extreme value distribution.

```
x = linspace(-3,6,1000);
y1 = gevpdf(x,-.5,1,0);
y2 = gevpdf(x,0,1,0);
y3 = gevpdf(x,.5,1,0)
plot(x,y1,'-', x,y2,'-', x,y3,'-')
legend({'K<0, Type III' 'K=0, Type I' 'K>0, Type II'});
```



Notice that for `k > 0`, the distribution has zero probability density for `x` such that

$$x < -\frac{\sigma}{k} + \mu$$

For `k < 0`, the distribution has zero probability density for

$$x > -\frac{\sigma}{k} + \mu$$

For $k = 0$, there is no upper or lower bound.

See Also

"Continuous Distributions (Data)" on page 5-4

Generalized Pareto Distribution

In this section...

Definition

The probability density function for the generalized Pareto distribution with shape parameter $k \neq 0$, scale parameter σ, and threshold parameter θ, is

$$y = f(x \mid k,\sigma,\theta) = \left(\frac{1}{\sigma}\right)\left(1 + k\frac{(x-\theta)}{\sigma}\right)^{-1-\frac{1}{k}}$$

for $\theta < x$, when $k > 0$, or for $\theta < x < -\sigma/k$ when $k < 0$.

For $k = 0$, the density is

$$y = f(x \mid 0,\sigma,\theta) = \left(\frac{1}{\sigma}\right)e^{-\frac{(x-\theta)}{\sigma}}$$

for $\theta < x$.

If $k = 0$ and $\theta = 0$, the generalized Pareto distribution is equivalent to the exponential distribution. If $k > 0$ and $\theta = \sigma/k$, the generalized Pareto distribution is equivalent to the Pareto distribution.

Background

Like the exponential distribution, the generalized Pareto distribution is often used to model the tails of another distribution. For example, you might have washers from a manufacturing process. If random influences in the process lead to differences in the sizes of the washers, a standard probability

distribution, such as the normal, could be used to model those sizes. However, while the normal distribution might be a good model near its mode, it might not be a good fit to real data in the tails and a more complex model might be needed to describe the full range of the data. On the other hand, only recording the sizes of washers larger (or smaller) than a certain threshold means you can fit a separate model to those tail data, which are known as *exceedences*. You can use the generalized Pareto distribution in this way, to provide a good fit to extremes of complicated data.

The generalized Pareto distribution allows a continuous range of possible shapes that includes both the exponential and Pareto distributions as special cases. You can use either of those distributions to model a particular dataset of exceedences. The generalized Pareto distribution allows you to "let the data decide" which distribution is appropriate.

The generalized Pareto distribution has three basic forms, each corresponding to a limiting distribution of exceedence data from a different class of underlying distributions.

- Distributions whose tails decrease exponentially, such as the normal, lead to a generalized Pareto shape parameter of zero.
- Distributions whose tails decrease as a polynomial, such as Student's *t*, lead to a positive shape parameter.
- Distributions whose tails are finite, such as the beta, lead to a negative shape parameter.

The generalized Pareto distribution is used in the tails of distribution fit objects of the `paretotails` class.

Parameters

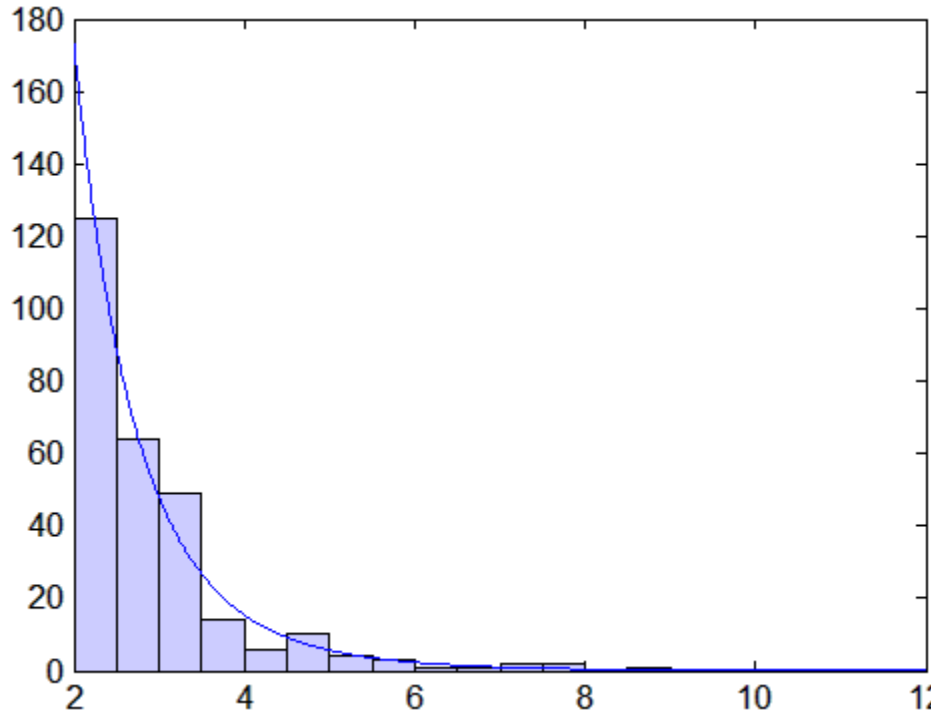
If you generate a large number of random values from a Student's *t* distribution with 5 degrees of freedom, and then discard everything less than 2, you can fit a generalized Pareto distribution to those exceedences.

```
t = trnd(5,5000,1);
y = t(t > 2) - 2;
paramEsts = gpfit(y)
paramEsts =
```

```
    0.1267    0.8134
```

Notice that the shape parameter estimate (the first element) is positive, which is what you would expect based on exceedences from a Student's *t* distribution.

```
hist(y+2,2.25:.5:11.75);
set(get(gca,'child'),'FaceColor',[.8 .8 1])
xgrid = linspace(2,12,1000);
line(xgrid,.5*length(y)*...
     gppdf(xgrid,paramEsts(1),paramEsts(2),2));
```

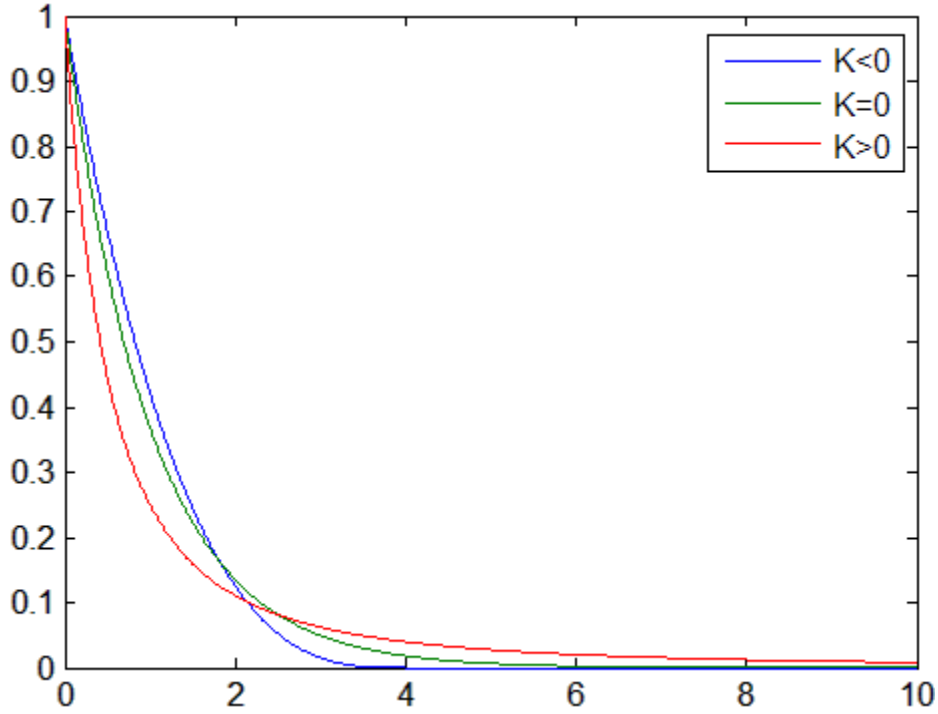


Example

The following code generates examples of the probability density functions for the three basic forms of the generalized Pareto distribution.

```
x = linspace(0,10,1000);
```

```
y1 = gppdf(x,-.25,1,0);
y2 = gppdf(x,0,1,0);
y3 = gppdf(x,1,1,0)
plot(x,y1,'-', x,y2,'-', x,y3,'-')
legend({'K<0' 'K=0' 'K>0'});
```



Notice that for `k < 0`, the distribution has zero probability density for $x > -\frac{\sigma}{k}$, while for $k \geq 0$, there is no upper bound.

See Also

"Continuous Distributions (Data)" on page 5-4

Geometric Distribution

In this section...

Definition

The geometric pdf is

$$y = f(x \mid p) = pq^x I_{(0,1,\ldots)}(x)$$

where $q = 1 - p$. The geometric distribution is a special case of the negative binomial distribution, with $r = 1$.

Background

The geometric distribution is discrete, existing only on the nonnegative integers. It is useful for modeling the runs of consecutive successes (or failures) in repeated independent trials of a system.

The geometric distribution models the number of successes before one failure in an independent succession of tests where each test results in success or failure.

Example

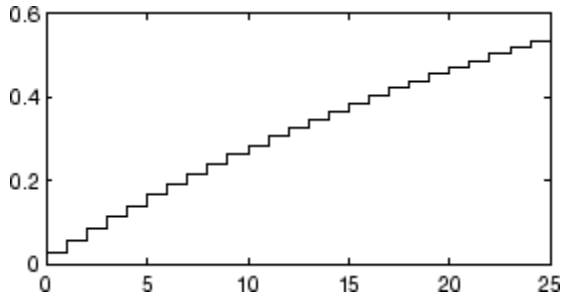
Suppose the probability of a five-year-old battery failing in cold weather is 0.03. What is the probability of starting 25 consecutive days during a long cold snap?

```
1 - geocdf(25,0.03)

ans =
```

```
    0.4530
```

The plot shows the cdf for this scenario.

```
x = 0:25;
y = geocdf(x,0.03);
stairs(x,y)
```



See Also

"Discrete Distributions" on page 5-7

Hypergeometric Distribution

In this section...

Definition

The hypergeometric pdf is

$$y = f(x \mid M, K, n) = \frac{\binom{K}{x}\binom{M-K}{n-x}}{\binom{M}{n}}$$

Background

The hypergeometric distribution models the total number of successes in a fixed-size sample drawn without replacement from a finite population.

The distribution is discrete, existing only for nonnegative integers less than the number of samples or the number of possible successes, whichever is greater. The hypergeometric distribution differs from the binomial only in that the population is finite and the sampling from the population is without replacement.

The hypergeometric distribution has three parameters that have direct physical interpretations.

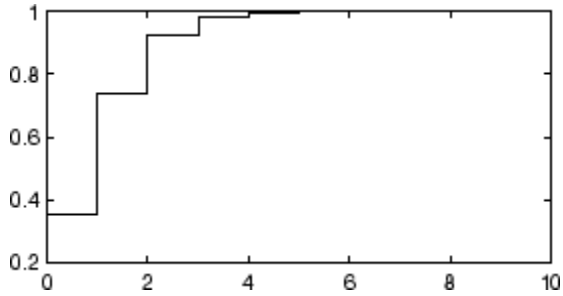
- M is the size of the population.
- K is the number of items with the desired characteristic in the population.
- n is the number of samples drawn.

Sampling “without replacement” means that once a particular sample is chosen, it is removed from the relevant population for all subsequent selections.

Example

The plot shows the cdf of an experiment taking 20 samples from a group of 1000 where there are 50 items of the desired type.

```
x = 0:10;
y = hygecdf(x,1000,50,20);
stairs(x,y)
```



See Also

“Discrete Distributions” on page 5-7

Inverse Gaussian Distribution

In this section...

Definition

The inverse Gaussian distribution has the density function

$$\sqrt{\frac{\lambda}{2\pi x^3}}\exp\left\{-\frac{\lambda}{2\mu^2 x}(x-\mu)^2\right\}$$

Background

Also known as the Wald distribution, the inverse Gaussian is used to model nonnegative positively skewed data. The distribution originated in the theory of Brownian motion, but has been used to model diverse phenomena. Inverse Gaussian distributions have many similarities to standard Gaussian (normal) distributions, which lead to applications in inferential statistics.

Parameters

See `mle`, `dfittool`.

See Also

"Continuous Distributions (Data)" on page 5-4

Inverse Wishart Distribution

Definition

The probability density function of the d-dimensional Inverse Wishart distribution is given by

$$y = f(\mathrm{X},\Sigma,\nu) = \frac{|T|^{(\nu/2)}\, e^{\left(-\frac{1}{2}\mathrm{trace}\left(TX^{-1}\right)\right)}}{2^{(\nu d)/2}\,\pi^{(d(d-1))/4}\,|X|^{(\nu+d+1)/2}\,\Gamma\left(\nu/2\right)\ldots\Gamma(\nu-(d-1))/2},$$

where X and T are d-by-d symmetric positive definite matrices, and ν is a scalar greater than or equal to d. While it is possible to define the Inverse Wishart for singular T, the density cannot be written as above.

If a random matrix has a Wishart distribution with parameters T^{-1} and ν, then the inverse of that random matrix has an inverse Wishart distribution with parameters T and ν. The mean of the distribution is given by

$$\frac{1}{\nu-d-1}T$$

where d is the number of rows and columns in T.

Only random matrix generation is supported for the inverse Wishart, including both singular and nonsingular T.

Background

The inverse Wishart distribution is based on the Wishart distribution. In Bayesian statistics it is used as the conjugate prior for the covariance matrix of a multivariate normal distribution.

Example

Notice that the sampling variability is quite large when the degrees of freedom is small.

```
Tau = [1 .5; .5 2];
df = 10; S1 = iwishrnd(Tau,df)*(df-2-1)
```

```
S1 =
       1.7959      0.64107
      0.64107       1.5496

df = 1000; S2 = iwishrnd(Tau,df)*(df-2-1)

S2 =
       0.9842      0.50158
      0.50158       2.1682
```

See Also

"Wishart Distribution" on page B-106, "Multivariate Distributions" on page 5-8

Johnson System

See “Pearson and Johnson Systems” on page 6-25.

Logistic Distribution

In this section...

Definition

The logistic distribution has the density function

$$\frac{e^{\frac{x-\mu}{\sigma}}}{\sigma\left(1+e^{\frac{x-\mu}{\sigma}}\right)^2}$$

with location parameter μ and scale parameter $\sigma > 0$, for all real x.

Background

The logistic distribution originated with Verhulst's work on demography in the early 1800s. The distribution has been used for various growth models, and is used in logistic regression. It has longer tails and a higher kurtosis than the normal distribution.

Parameters

See `mle`, `dfittool`.

See Also

"Continuous Distributions (Data)" on page 5-4

Loglogistic Distribution

In this section...

Definition

The variable x has a loglogistic distribution with location parameter μ and scale parameter $\sigma > 0$ if $\ln x$ has a logistic distribution with parameters μ and σ. The relationship is similar to that between the lognormal and normal distribution.

Parameters

See `mle`, `dfittool`.

See Also

"Continuous Distributions (Data)" on page 5-4

Lognormal Distribution

In this section...

Definition

The lognormal pdf is

$$y = f(x \mid \mu,\sigma) = \frac{1}{x\sigma\sqrt{2\pi}} e^{\frac{-(\ln x-\mu)^2}{2\sigma^2}}$$

Background

The normal and lognormal distributions are closely related. If X is distributed lognormally with parameters μ and σ, then log(X) is distributed normally with mean μ and standard deviation σ.

The mean m and variance v of a lognormal random variable are functions of μ and σ that can be calculated with the `lognstat` function. They are:

$$m = \exp\left(\mu + \sigma^2 / 2\right)$$
$$v = \exp\left(2\mu + \sigma^2\right)\left(\exp\left(\sigma^2\right) - 1\right)$$

A lognormal distribution with mean m and variance v has parameters

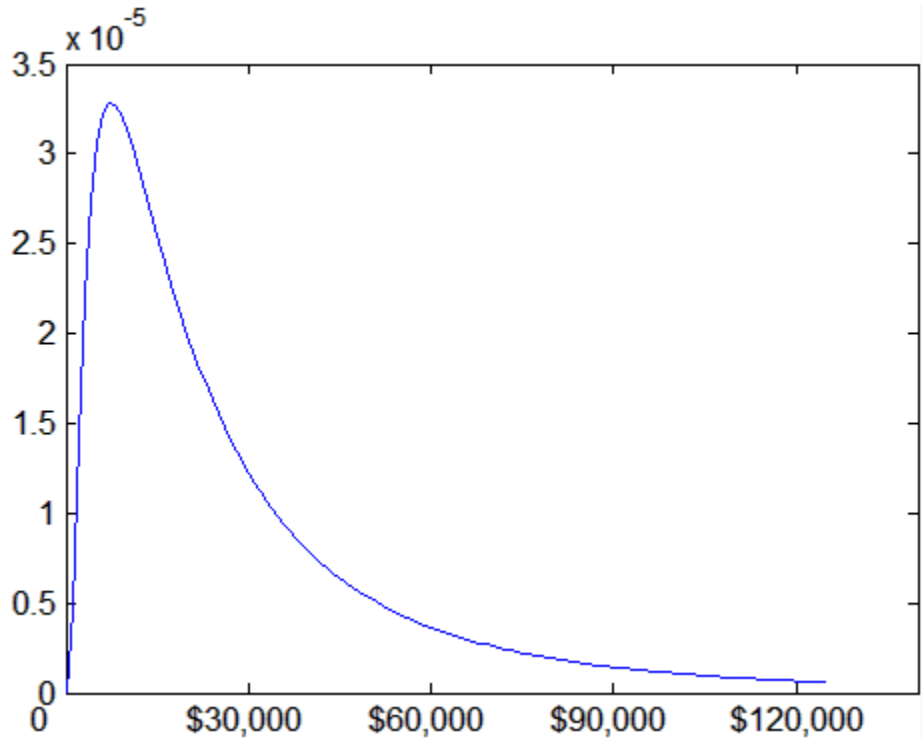
$$\mu = \log\left(m^2 / \sqrt{v + m^2}\right)$$
$$\sigma = \sqrt{\log\left(v / m^2 + 1\right)}$$

The lognormal distribution is applicable when the quantity of interest must be positive, since log(*X*) exists only when *X* is positive.

Example

Suppose the income of a family of four in the United States follows a lognormal distribution with $\mu = \log(20{,}000)$ and $\sigma^2 = 1.0$. Plot the income density.

```
x = (10:1000:125010)';
y = lognpdf(x,log(20000),1.0);
plot(x,y)
set(gca,'xtick',[0 30000 60000 90000 120000])
set(gca,'xticklabel',{'0','$30,000','$60,000',...
                              '$90,000','$120,000'})
```



See Also

"Continuous Distributions (Data)" on page 5-4

Multinomial Distribution

In this section...

Definition

The multinomial pdf is

$$f(x \mid n, p) = \frac{n!}{x_1! \cdots x_k!} p_1^{x_1} \cdots p_k^{x_k}$$

where $x = (x_1,..., x_k)$ gives the number of each of k outcomes in n trials of a process with fixed probabilities $p = (p_1,...,p_k)$ of individual outcomes in any one trial. The vector x has non-negative integer components that sum to n. The vector p has non-negative integer components that sum to 1.

Background

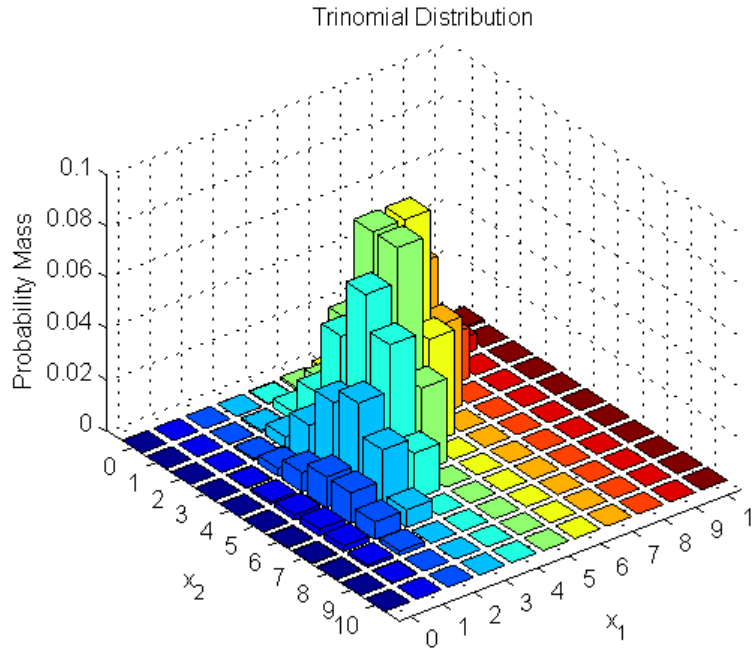
The multinomial distribution is a generalization of the binomial distribution. The binomial distribution gives the probability of the number of "successes" and "failures" in n independent trials of a two-outcome process. The probability of "success" and "failure" in any one trial is given by the fixed probabilities p and $q = 1–p$. The multinomial distribution gives the probability of each combination of outcomes in n independent trials of a k-outcome process. The probability of each outcome in any one trial is given by the fixed probabilities $p_1,...,p_k$.

The expected value of outcome i is np_i. The variance of outcome i is $np_i(1 - p_i)$. The covariance of outcomes i and j is $–np_ip_j$ for distinct i and j.

Example

The following uses `mnpdf` to produce a visualization of a trinomial distribution:

```
% Compute the distribution
p = [1/2 1/3 1/6]; % Outcome probabilities
n = 10; % Sample size
x1 = 0:n;
x2 = 0:n;
[X1,X2] = meshgrid(x1,x2);
X3 = n-(X1+X2);
Y = mnpdf([X1(:),X2(:),X3(:)],repmat(p,(n+1)^2,1));

% Plot the distribution
Y = reshape(Y,n+1,n+1);
bar3(Y)
set(gca,'XTickLabel',0:n)
set(gca,'YTickLabel',0:n)
xlabel('x_1')
ylabel('x_2')
zlabel('Probability Mass')
```



Note that the visualization does not show x_3, which is determined by the constraint $x_1 + x_2 + x_3 = n$.

Multivariate Gaussian Distribution

See “Multivariate Normal Distribution” on page B-58.

Multivariate Normal Distribution

In this section...

Definition

The probability density function of the d-dimensional multivariate normal distribution is given by

$$y = f(x,\mu,\Sigma) = \frac{1}{\sqrt{|\Sigma|(2\pi)^d}} e^{-\frac{1}{2}(x-\mu)\,\Sigma^{-1}(x-\mu)'}$$

where x and μ are 1-by-d vectors and Σ is a d-by-d symmetric positive definite matrix. While it is possible to define the multivariate normal for singular Σ, the density cannot be written as above. Only random vector generation is supported for the singular case. Note that while most textbooks define the multivariate normal with x and μ oriented as column vectors, for the purposes of data analysis software, it is more convenient to orient them as row vectors, and Statistics Toolbox software uses that orientation.

Background

The multivariate normal distribution is a generalization of the univariate normal to two or more variables. It is a distribution for random vectors of correlated variables, each element of which has a univariate normal distribution. In the simplest case, there is no correlation among variables, and elements of the vectors are independent univariate normal random variables.

The multivariate normal distribution is parameterized with a mean vector, μ, and a covariance matrix, Σ. These are analogous to the mean μ and variance σ^2 parameters of a univariate normal distribution. The diagonal elements of Σ

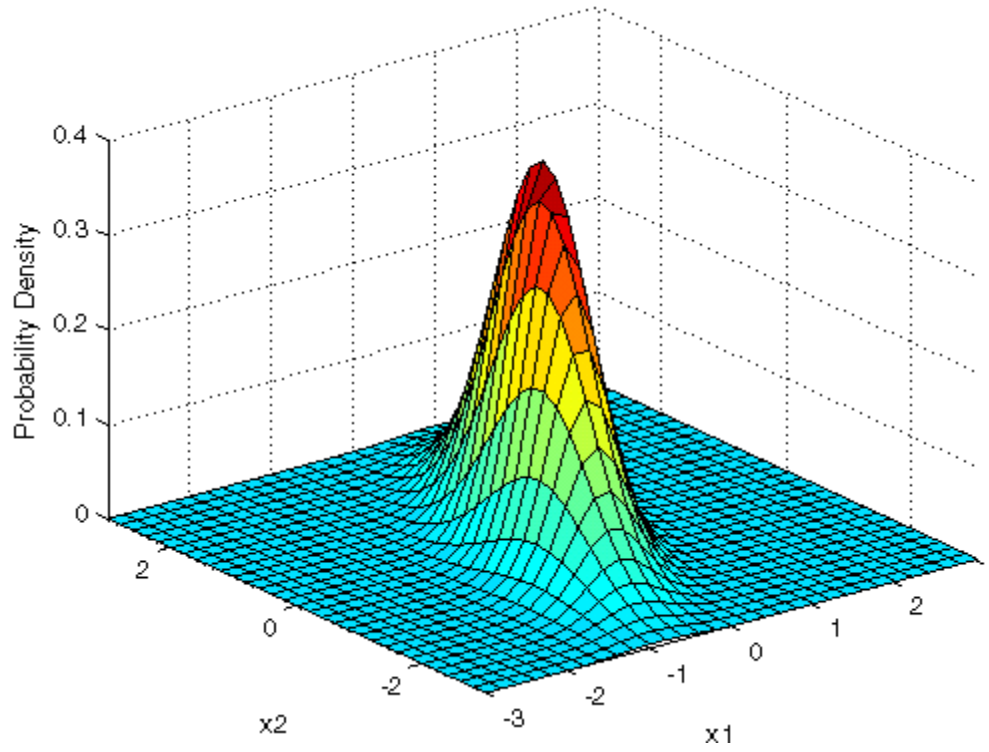
contain the variances for each variable, while the off-diagonal elements of Σ contain the covariances between variables.

The multivariate normal distribution is often used as a model for multivariate data, primarily because it is one of the few multivariate distributions that is tractable to work with.

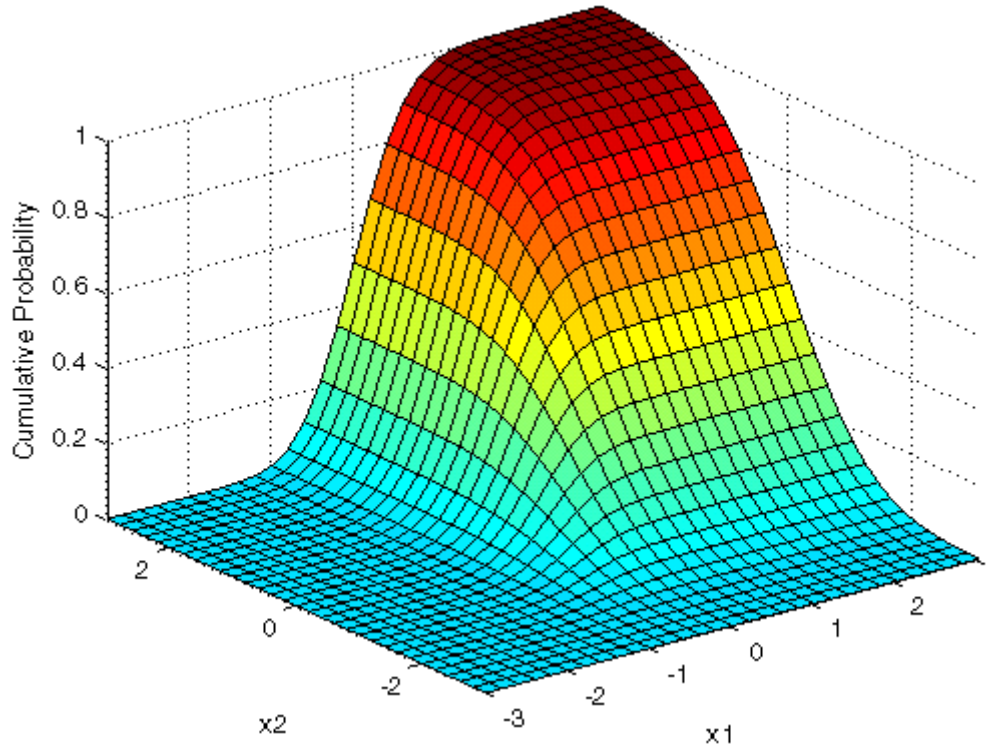
Example

This example shows the probability density function (pdf) and cumulative distribution function (cdf) for a bivariate normal distribution with unequal standard deviations. You can use the multivariate normal distribution in a higher number of dimensions as well, although visualization is not easy.

```
mu = [0 0];
Sigma = [.25 .3; .3 1];
x1 = -3:.2:3; x2 = -3:.2:3;
[X1,X2] = meshgrid(x1,x2);
F = mvnpdf([X1(:) X2(:)],mu,Sigma);
F = reshape(F,length(x2),length(x1));
surf(x1,x2,F);
caxis([min(F(:))-.5*range(F(:)),max(F(:))]);
axis([-3 3 -3 3 0 .4])
xlabel('x1'); ylabel('x2'); zlabel('Probability Density');
```

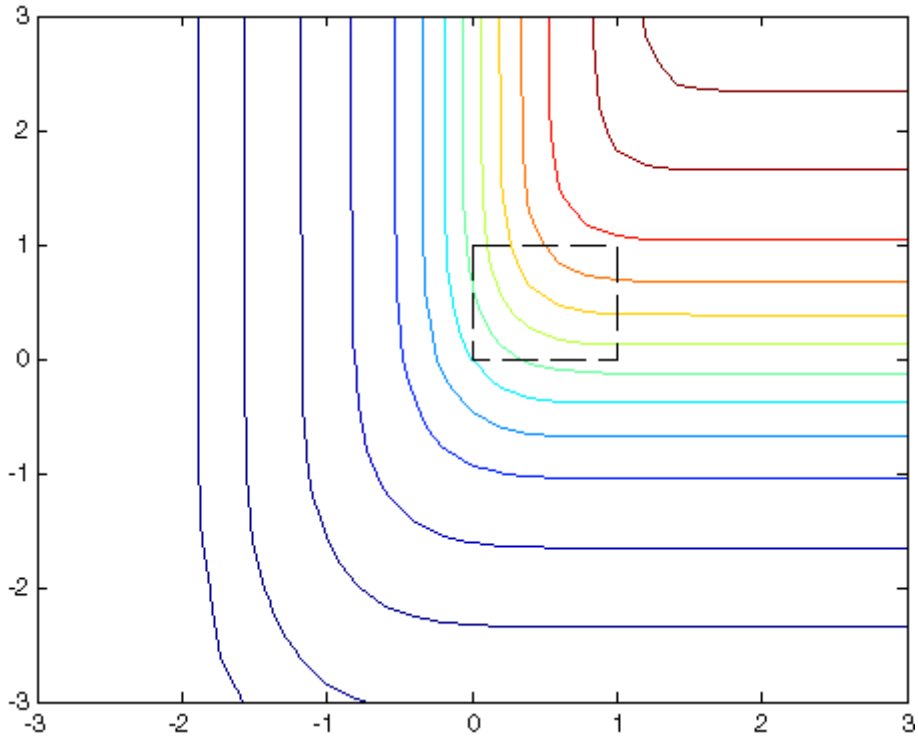



```
F = mvncdf([X1(:) X2(:)],mu,Sigma);
F = reshape(F,length(x2),length(x1));
surf(x1,x2,F);
caxis([min(F(:))-.5*range(F(:)),max(F(:))]);
axis([-3 3 -3 3 0 1])
xlabel('x1'); ylabel('x2'); zlabel('Cumulative Probability');
```



Since the bivariate normal distribution is defined on the plane, you can also compute cumulative probabilities over rectangular regions. For example, this contour plot illustrates the computation that follows, of the probability contained within the unit square.

```
contour(x1,x2,F,[.0001 .001 .01 .05:.1:.95 .99 .999 .9999]);
xlabel('x'); ylabel('y');
line([0 0 1 1 0],[1 0 0 1 1],'linestyle','--','color','k');
```




```
mvncdf([0 0],[1 1],mu,Sigma)
ans =
      0.20974
```

Computing a multivariate cumulative probability requires significantly more work than computing a univariate probability. By default, the `mvncdf` function computes values to less than full machine precision, and returns an estimate of the error as an optional second output:

```
[F,err] = mvncdf([0 0],[1 1],mu,Sigma)
F =
      0.20974
err =
       1e-008
```

See Also

"Multivariate Distributions" on page 5-8

Multivariate t Distribution

In this section...

Definition

The probability density function of the d-dimensional multivariate Student's t distribution is given by

$$f(x,\Sigma,\nu) = \frac{1}{|\Sigma|^{1/2}} \frac{1}{\sqrt{(\nu\pi)^d}} \frac{\Gamma((\nu+d)/2)}{\Gamma(\nu/2)} \left(1 + \frac{x' \Sigma^{-1} x}{\nu}\right)^{-(\nu+d)/2}.$$

where x is a 1-by-d vector, Σ is a d-by-d symmetric, positive definite matrix, and ν is a positive scalar. While it is possible to define the multivariate Student's t for singular Σ, the density cannot be written as above. For the singular case, only random number generation is supported. Note that while most textbooks define the multivariate Student's t with x oriented as a column vector, for the purposes of data analysis software, it is more convenient to orient x as a row vector, and Statistics Toolbox software uses that orientation.

Background

The multivariate Student's t distribution is a generalization of the univariate Student's t to two or more variables. It is a distribution for random vectors of correlated variables, each element of which has a univariate Student's t distribution. In the same way as the univariate Student's t distribution can be constructed by dividing a standard univariate normal random variable by the square root of a univariate chi-square random variable, the multivariate Student's t distribution can be constructed by dividing a multivariate normal random vector having zero mean and unit variances by a univariate chi-square random variable.

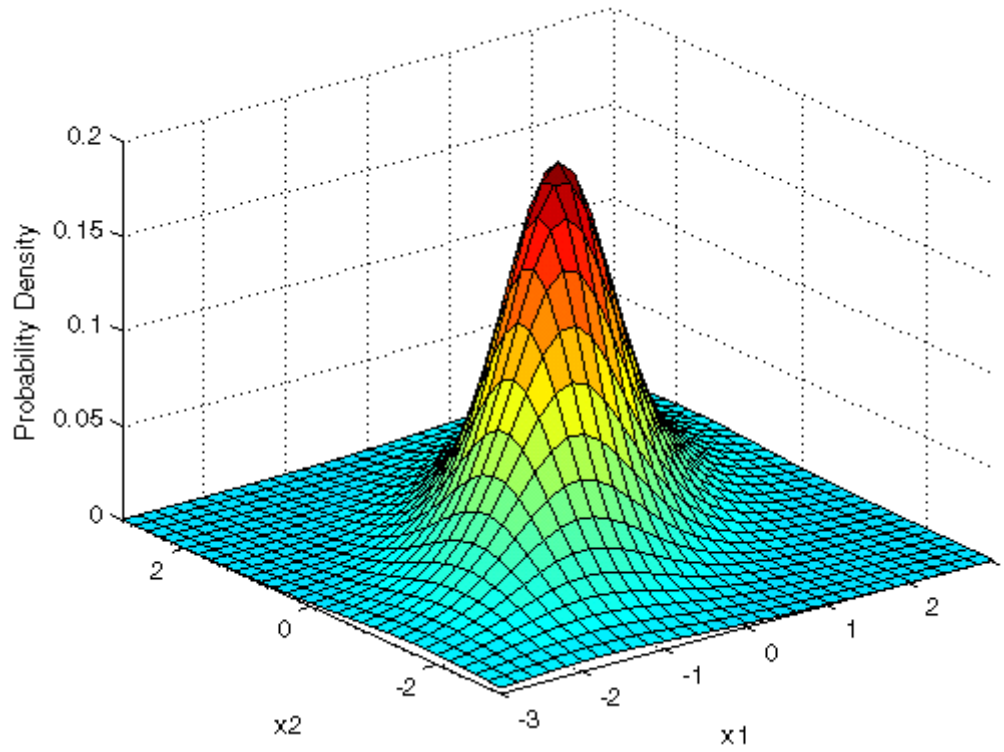
The multivariate Student's t distribution is parameterized with a correlation matrix, Σ, and a positive scalar degrees of freedom parameter, ν. ν is analogous to the degrees of freedom parameter of a univariate Student's t distribution. The off-diagonal elements of Σ contain the correlations between variables. Note that when Σ is the identity matrix, variables are uncorrelated; however, they are not independent.

The multivariate Student's t distribution is often used as a substitute for the multivariate normal distribution in situations where it is known that the marginal distributions of the individual variables have fatter tails than the normal.

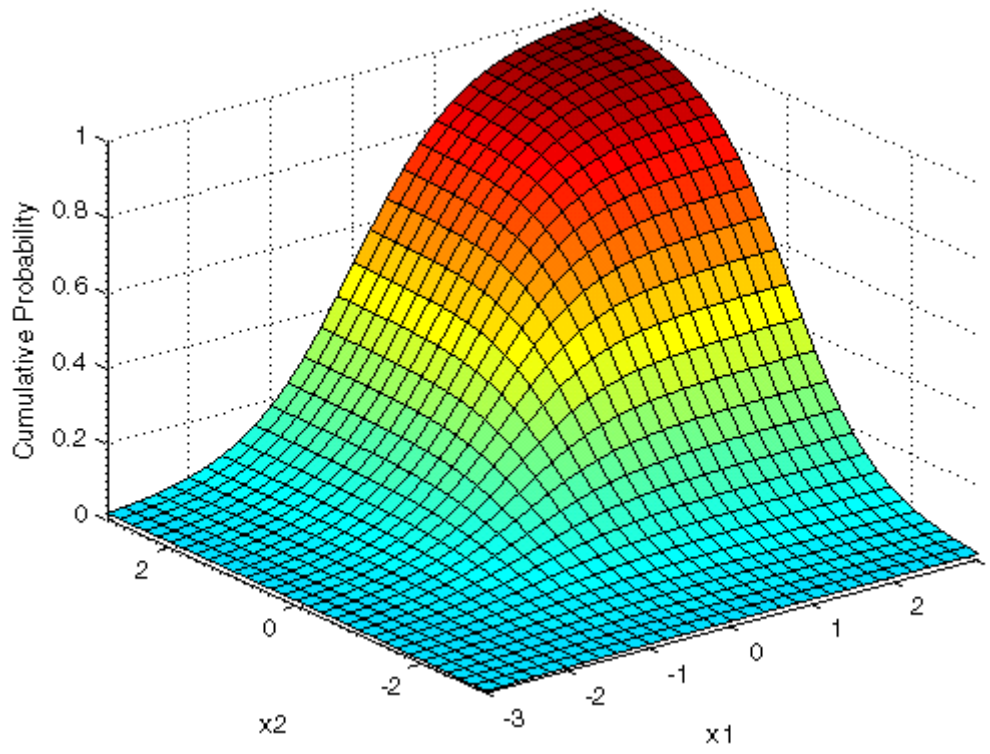
Example

This example shows the probability density function (pdf) and cumulative distribution function (cdf) for a bivariate Student's t distribution. You can use the multivariate Student's t distribution in a higher number of dimensions as well, although visualization is not easy.

```
Rho = [1 .6; .6 1];
nu = 5;
x1 = -3:.2:3; x2 = -3:.2:3;
[X1,X2] = meshgrid(x1,x2);
F = mvtpdf([X1(:) X2(:)],Rho,nu);
F = reshape(F,length(x2),length(x1));
surf(x1,x2,F);
caxis([min(F(:))-.5*range(F(:)),max(F(:))]);
axis([-3 3 -3 3 0 .2])
xlabel('x1'); ylabel('x2'); zlabel('Probability Density');
```

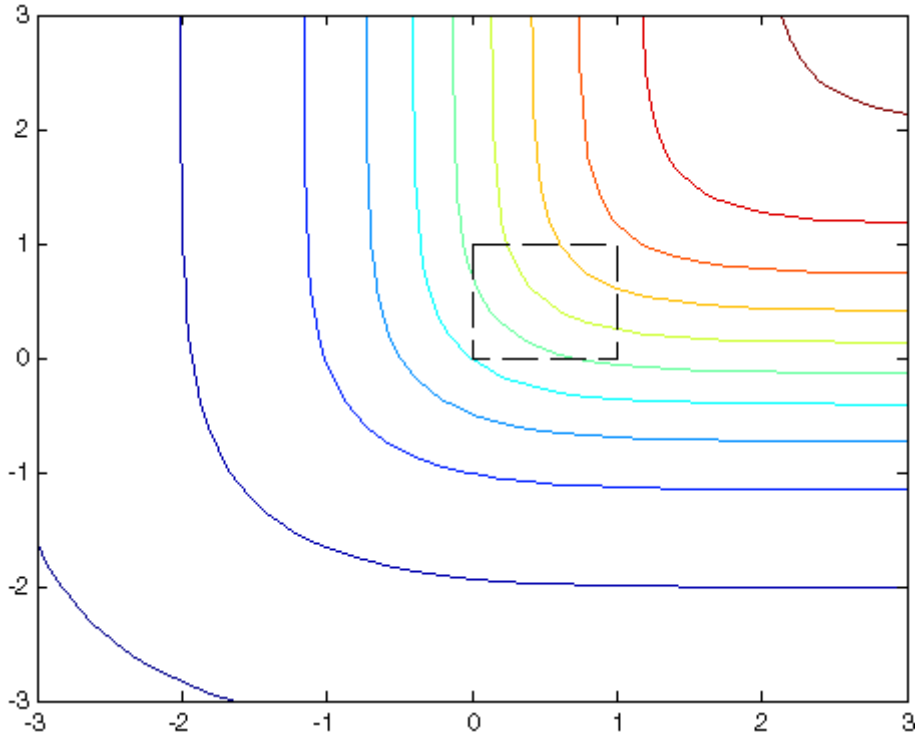



```
F = mvtcdf([X1(:) X2(:)],Rho,nu);
F = reshape(F,length(x2),length(x1));
surf(x1,x2,F);
caxis([min(F(:))-.5*range(F(:)),max(F(:))]);
axis([-3 3 -3 3 0 1])
xlabel('x1'); ylabel('x2'); zlabel('Cumulative Probability');
```



Since the bivariate Student's *t* distribution is defined on the plane, you can also compute cumulative probabilities over rectangular regions. For example, this contour plot illustrates the computation that follows, of the probability contained within the unit square.

```
contour(x1,x2,F,[.0001 .001 .01 .05:.1:.95 .99 .999 .9999]);
xlabel('x'); ylabel('y');
line([0 0 1 1 0],[1 0 0 1 1],'linestyle','--','color','k');
```




```
mvtcdf([0 0],[1 1],Rho,nu)
ans =
      0.14013
```

Computing a multivariate cumulative probability requires significantly more work than computing a univariate probability. By default, the `mvtcdf` function computes values to less than full machine precision, and returns an estimate of the error as an optional second output:

```
[F,err] = mvtcdf([0 0],[1 1],Rho,nu)
F =
      0.14013
err =
       1e-008
```

See Also

"Multivariate Distributions" on page 5-8

Nakagami Distribution

In this section...

Definition

The Nakagami distribution has the density function

$$2\left(\frac{\mu}{\omega}\right)^{\mu}\frac{1}{\Gamma(\mu)}x^{(2\mu-1)}e^{\frac{-\mu}{\omega}x^2}$$

with shape parameter μ and scale parameter $\omega > 0$, for $x > 0$. If x has a Nakagami distribution with parameters μ and ω, then x^2 has a gamma distribution with shape parameter μ and scale parameter ω/μ.

Background

In communications theory, Nakagami distributions, Rician distributions, and Rayleigh distributions are used to model scattered signals that reach a receiver by multiple paths. Depending on the density of the scatter, the signal will display different fading characteristics. Rayleigh and Nakagami distributions are used to model dense scatters, while Rician distributions model fading with a stronger line-of-sight. Nakagami distributions can be reduced to Rayleigh distributions, but give more control over the extent of the fading.

Parameters

See `mle`, `dfittool`.

See Also

"Continuous Distributions (Data)" on page 5-4

Negative Binomial Distribution

In this section...

Definition

When the r parameter is an integer, the negative binomial pdf is

$$y = f(x \mid r, p) = \binom{r + x - 1}{x} p^r q^x I_{(0,1,\ldots)}(x)$$

where $q = 1 - p$. When r is not an integer, the binomial coefficient in the definition of the pdf is replaced by the equivalent expression

$$\frac{\Gamma(r + x)}{\Gamma(r)\Gamma(x + 1)}$$

Background

In its simplest form (when r is an integer), the negative binomial distribution models the number of failures x before a specified number of successes is reached in a series of independent, identical trials. Its parameters are the probability of success in a single trial, p, and the number of successes, r. A special case of the negative binomial distribution, when $r = 1$, is the geometric distribution, which models the number of failures before the first success.

More generally, r can take on non-integer values. This form of the negative binomial distribution has no interpretation in terms of repeated trials, but, like the Poisson distribution, it is useful in modeling count data. The negative binomial distribution is more general than the Poisson distribution because it has a variance that is greater than its mean, making it suitable for count data

that do not meet the assumptions of the Poisson distribution. In the limit, as r increases to infinity, the negative binomial distribution approaches the Poisson distribution.

Parameters

Suppose you are collecting data on the number of auto accidents on a busy highway, and would like to be able to model the number of accidents per day. Because these are count data, and because there are a very large number of cars and a small probability of an accident for any specific car, you might think to use the Poisson distribution. However, the probability of having an accident is likely to vary from day to day as the weather and amount of traffic change, and so the assumptions needed for the Poisson distribution are not met. In particular, the variance of this type of count data sometimes exceeds the mean by a large amount. The data below exhibit this effect: most days have few or no accidents, and a few days have a large number.

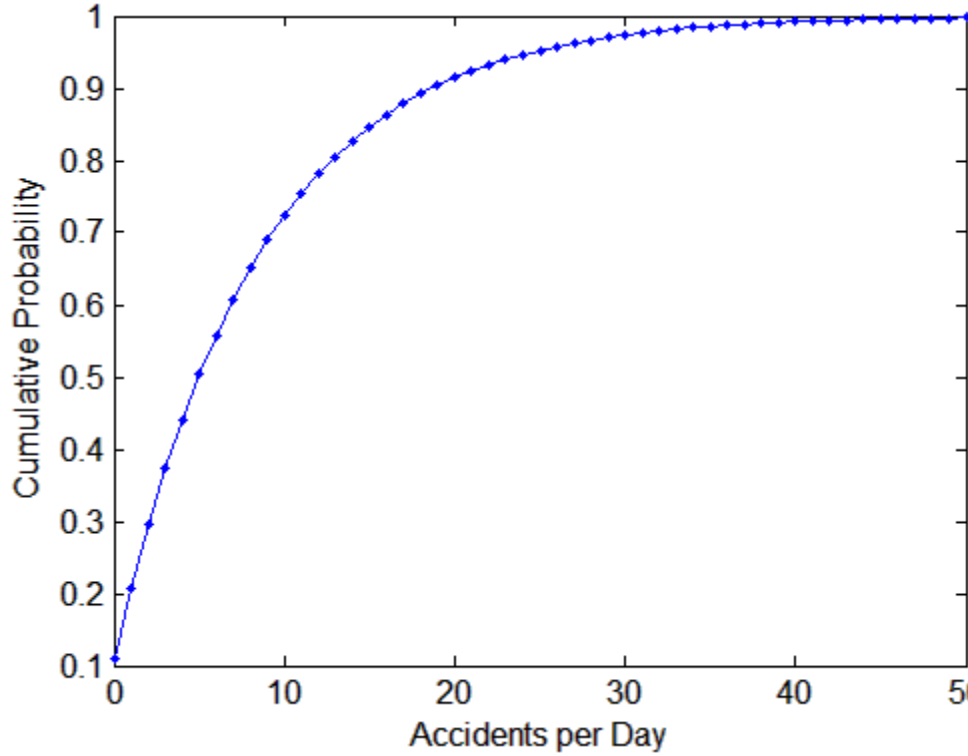
```
accident = [2  3  4  2  3  1  12  8  14  31  23  1  10  7  0];
mean(accident)
ans =
       8.0667

var(accident)
ans =
       79.352
```

The negative binomial distribution is more general than the Poisson, and is often suitable for count data when the Poisson is not. The function `nbinfit` returns the maximum likelihood estimates (MLEs) and confidence intervals for the parameters of the negative binomial distribution. Here are the results from fitting the `accident` data:

```
[phat,pci] = nbinfit(accident)
phat =
    1.0060    0.1109
pci =
    0.2152    0.0171
    1.7968    0.2046
```

It is difficult to give a physical interpretation in this case to the individual parameters. However, the estimated parameters can be used in a model for the number of daily accidents. For example, a plot of the estimated cumulative probability function shows that while there is an estimated 10% chance of no accidents on a given day, there is also about a 10% chance that there will be 20 or more accidents.

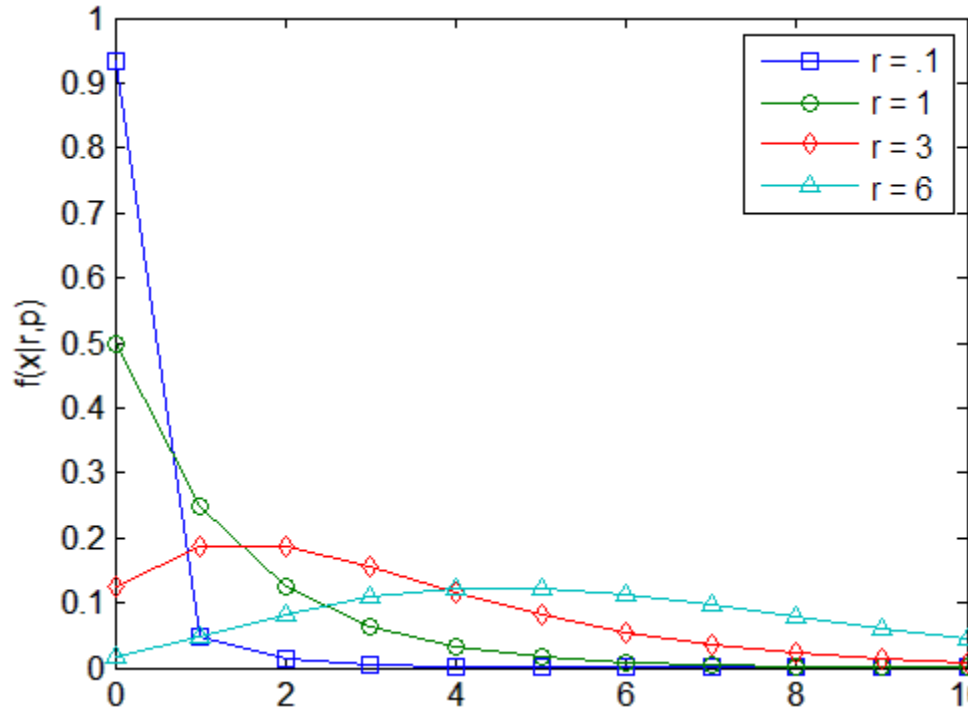
```
plot(0:50,nbincdf(0:50,phat(1),phat(2)),'.-');
xlabel('Accidents per Day')
ylabel('Cumulative Probability')
```



Example

The negative binomial distribution can take on a variety of shapes ranging from very skewed to nearly symmetric. This example plots the probability function for different values of `r`, the desired number of successes: `.1`, `1`, `3`, `6`.

```
x = 0:10;
plot(x,nbinpdf(x,.1,.5),'s-', ...
     x,nbinpdf(x,1,.5),'o-', ...
     x,nbinpdf(x,3,.5),'d-', ...
     x,nbinpdf(x,6,.5),'^-');
legend({'r = .1' 'r = 1' 'r = 3' 'r = 6'})
xlabel('x')
ylabel('f(x|r,p)')
```



See Also

"Discrete Distributions" on page 5-7

Noncentral Chi-Square Distribution

In this section...

Definition

There are many equivalent formulas for the noncentral chi-square distribution function. One formulation uses a modified Bessel function of the first kind. Another uses the generalized Laguerre polynomials. The cumulative distribution function is computed using a weighted sum of χ^2 probabilities with the weights equal to the probabilities of a Poisson distribution. The Poisson parameter is one-half of the noncentrality parameter of the noncentral chi-square

$$F(x \mid \nu, \delta) = \sum_{j=0}^{\infty} \left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!} e^{\frac{-\delta}{2}} \right) \Pr\left[\chi^2_{\nu+2j} \le x \right]$$

where δ is the noncentrality parameter.

Background

The χ^2 distribution is actually a simple special case of the noncentral chi-square distribution. One way to generate random numbers with a χ^2 distribution (with ν degrees of freedom) is to sum the squares of ν standard normal random numbers (mean equal to zero.)

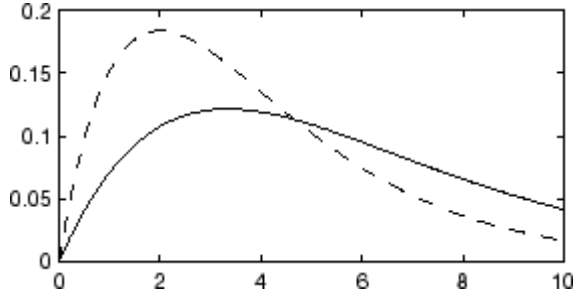
What if the normally distributed quantities have a mean other than zero? The sum of squares of these numbers yields the noncentral chi-square distribution. The noncentral chi-square distribution requires two parameters: the degrees of freedom and the noncentrality parameter. The noncentrality parameter is the sum of the squared means of the normally distributed quantities.

The noncentral chi-square has scientific application in thermodynamics and signal processing. The literature in these areas may refer to it as the "Rician Distribution" on page B-93 or generalized "Rayleigh Distribution" on page B-91.

Example

The following commands generate a plot of the noncentral chi-square pdf.

```
x = (0:0.1:10)';
p1 = ncx2pdf(x,4,2);
p = chi2pdf(x,4);
plot(x,p,'-',x,p1,'-')
```



Noncentral F Distribution

In this section...

Definition

Similar to the noncentral χ^2 distribution, the toolbox calculates noncentral F distribution probabilities as a weighted sum of incomplete beta functions using Poisson probabilities as the weights.

$$F(x \mid \nu_1,\nu_2,\delta) = \sum_{j=0}^{\infty} \left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!} e^{\frac{-\delta}{2}} \right) I\left(\frac{\nu_1 \cdot x}{\nu_2 + \nu_1 \cdot x} \middle| \frac{\nu_1}{2} + j, \frac{\nu_2}{2} \right)$$

$I(x \mid a,b)$ is the incomplete beta function with parameters a and b, and δ is the noncentrality parameter.

Background

As with the χ^2 distribution, the F distribution is a special case of the noncentral F distribution. The F distribution is the result of taking the ratio of χ^2 random variables each divided by its degrees of freedom.

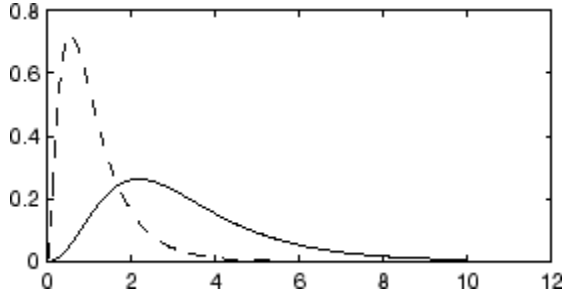
If the numerator of the ratio is a noncentral chi-square random variable divided by its degrees of freedom, the resulting distribution is the noncentral F distribution.

The main application of the noncentral F distribution is to calculate the power of a hypothesis test relative to a particular alternative.

Example

The following commands generate a plot of the noncentral *F* pdf.

```
x = (0.01:0.1:10.01)';
p1 = ncfpdf(x,5,20,10);
p  = fpdf(x,5,20);
plot(x,p,'-',x,p1,'-')
```



See Also

"Continuous Distributions (Statistics)" on page 5-6

Noncentral t Distribution

In this section...

Definition

The most general representation of the noncentral t distribution is quite complicated. Johnson and Kotz [60] give a formula for the probability that a noncentral t variate falls in the range $[-u, u]$.

$$P(-u < x < u \mid \nu, \delta) = \sum_{j=0}^{\infty} \left(\frac{\left(\frac{1}{2}\delta^2\right)^j}{j!} e^{\frac{-\delta^2}{2}} \right) I\left(\frac{u^2}{\nu + u^2} \middle| \frac{1}{2} + j, \frac{\nu}{2} \right)$$

$I(x \mid \nu,\delta)$ is the incomplete beta function with parameters ν and δ. δ is the noncentrality parameter, and ν is the number of degrees of freedom.

Background

The noncentral t distribution is a generalization of Student's t distribution.

Student's t distribution with $n - 1$ degrees of freedom models the t-statistic

$$t = \frac{\bar{x} - \mu}{s / \sqrt{n}}$$

where $\bar{x}$ is the sample mean and s is the sample standard deviation of a random sample of size n from a normal population with mean μ. If the population mean is actually μ_0, then the t-statistic has a noncentral t distribution with noncentrality parameter

$$\delta = \frac{\mu_0 - \mu}{\sigma / \sqrt{n}}$$

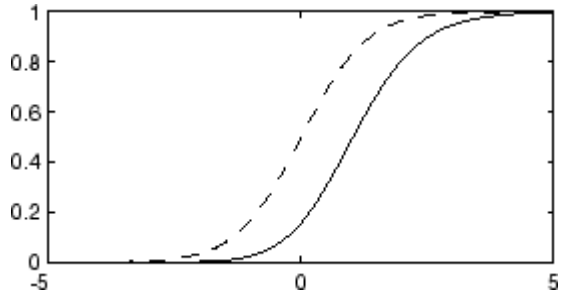
The noncentrality parameter is the normalized difference between μ_0 and μ.

The noncentral t distribution gives the probability that a t test will correctly reject a false null hypothesis of mean μ when the population mean is actually μ_0; that is, it gives the power of the t test. The power increases as the difference $\mu_0 - \mu$ increases, and also as the sample size n increases.

Example

The following commands generate a plot of the noncentral t pdf.

```
x = (-5:0.1:5)';
p1 = nctcdf(x,10,1);
p = tcdf(x,10);
plot(x,p,'-',x,p1,'-')
```



See Also

"Continuous Distributions (Statistics)" on page 5-6

Nonparametric Distributions

See the discussion of `ksdensity` in "Estimating PDFs without Parameters" on page 5-55.

Normal Distribution

In this section...

Definition

The normal pdf is

$$y = f(x \mid \mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{\frac{-(x-\mu)^2}{2\sigma^2}}$$

Background

The normal distribution is a two-parameter family of curves. The first parameter, μ, is the mean. The second, σ, is the standard deviation. The standard normal distribution (written $\Phi(x)$) sets μ to 0 and σ to 1.

$\Phi(x)$ is functionally related to the error function, *erf*.

$$erf\left(x\right) = 2\Phi\left(x\sqrt{2}\right) - 1$$

The first use of the normal distribution was as a continuous approximation to the binomial.

The usual justification for using the normal distribution for modeling is the Central Limit Theorem, which states (roughly) that the sum of independent samples from any distribution with finite mean and variance converges to the normal distribution as the sample size goes to infinity.

Parameters

To use statistical parameters such as mean and standard deviation reliably, you need to have a good estimator for them. The maximum likelihood estimates (MLEs) provide one such estimator. However, an MLE might be biased, which means that its expected value of the parameter might not equal the parameter being estimated. For example, an MLE is biased for estimating the variance of a normal distribution. An unbiased estimator that is commonly used to estimate the parameters of the normal distribution is the *minimum variance unbiased estimator* (*MVUE*). The MVUE has the minimum variance of all unbiased estimators of a parameter.

The MVUEs of parameters μ and σ^2 for the normal distribution are the sample mean and variance. The sample mean is also the MLE for μ. The following are two common formulas for the variance.

$$s^2 = \frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^2 \qquad \textbf{(B-1)}$$

$$s^2 = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})^2 \qquad \textbf{(B-2)}$$

where

$$\bar{x} = \sum_{i=1}^{n}\frac{x_i}{n}$$

Equation 1 is the maximum likelihood estimator for σ^2, and equation 2 is the MVUE.

As an example, suppose you want to estimate the mean, μ, and the variance, σ^2, of the heights of all fourth grade children in the United States. The function `normfit` returns the MVUE for μ, the square root of the MVUE for σ^2, and confidence intervals for μ and σ^2. Here is a playful example modeling the heights in inches of a randomly chosen fourth grade class.

```
height = normrnd(50,2,30,1);              % Simulate heights.
[mu,s,muci,sci] = normfit(height)
```

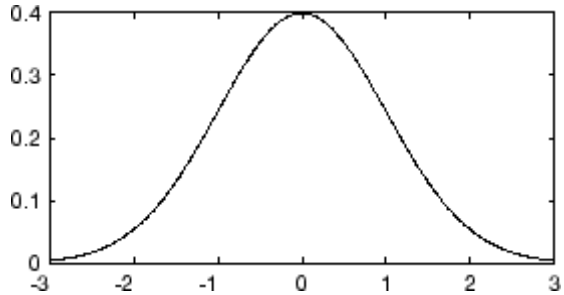
```
mu =
   50.2025

s =
    1.7946

muci =
   49.5210
   50.8841

sci =
    1.4292
    2.4125
```

Note that `s^2` is the MVUE of the variance.

```
s^2

ans =
    3.2206
```

Example

The plot shows the bell curve of the standard normal pdf, with $\mu = 0$ and $\sigma = 1$.



See Also

"Continuous Distributions (Data)" on page 5-4

Pareto Distribution

See “Generalized Pareto Distribution” on page B-37.

Pearson System

See “Pearson and Johnson Systems” on page 6-25.

Piecewise Distributions

See the discussion of the `@piecewisedistribution` class in “Fitting Piecewise Distributions” on page 5-72.

Poisson Distribution

In this section...

Definition

The Poisson pdf is

$$y = f(x \mid \lambda) = \frac{\lambda^x}{x!} e^{-\lambda} I_{(0,1,\ldots)}(x)$$

Background

The Poisson distribution is appropriate for applications that involve counting the number of times a random event occurs in a given amount of time, distance, area, etc. Sample applications that involve Poisson distributions include the number of Geiger counter clicks per second, the number of people walking into a store in an hour, and the number of flaws per 1000 feet of video tape.

The Poisson distribution is a one-parameter discrete distribution that takes nonnegative integer values. The parameter, λ, is both the mean and the variance of the distribution. Thus, as the size of the numbers in a particular sample of Poisson random numbers gets larger, so does the variability of the numbers.

The Poisson distribution is the limiting case of a binomial distribution where N approaches infinity and p goes to zero while $Np = \lambda$.

The Poisson and exponential distributions are related. If the number of counts follows the Poisson distribution, then the interval between individual counts follows the exponential distribution.

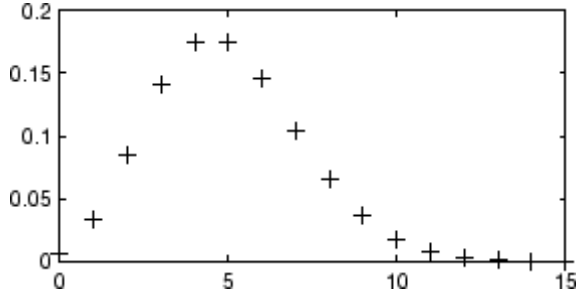
Parameters

The MLE and the MVUE of the Poisson parameter, λ, is the sample mean. The sum of independent Poisson random variables is also Poisson distributed with the parameter equal to the sum of the individual parameters. This is used to calculate confidence intervals λ. As λ gets large the Poisson distribution can be approximated by a normal distribution with $\mu = \lambda$ and $\sigma^2 = \lambda$. This approximation is used to calculate confidence intervals for values of λ greater than 100.

Example

The plot shows the probability for each nonnegative integer when $\lambda = 5$.

```
x = 0:15;
y = poisspdf(x,5);
plot(x,y,'+')
```



See Also

"Discrete Distributions" on page 5-7

Rayleigh Distribution

In this section...

Definition

The Rayleigh pdf is

$$y = f(x \mid b) = \frac{x}{b^2} e^{\left(\frac{-x^2}{2b^2}\right)}$$

Background

The Rayleigh distribution is a special case of the Weibull distribution. If A and B are the parameters of the Weibull distribution, then the Rayleigh distribution with parameter b is equivalent to the Weibull distribution with parameters $A = \sqrt{2}b$ and $B = 2$.

If the component velocities of a particle in the x and y directions are two independent normal random variables with zero means and equal variances, then the distance the particle travels per unit time is distributed Rayleigh.

In communications theory, Nakagami distributions, Rician distributions, and Rayleigh distributions are used to model scattered signals that reach a receiver by multiple paths. Depending on the density of the scatter, the signal will display different fading characteristics. Rayleigh and Nakagami distributions are used to model dense scatters, while Rician distributions model fading with a stronger line-of-sight. Nakagami distributions can be reduced to Rayleigh distributions, but give more control over the extent of the fading.

Parameters

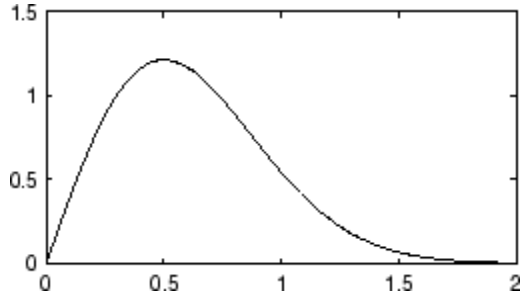
The `raylfit` function returns the MLE of the Rayleigh parameter. This estimate is

$$b = \sqrt{\frac{1}{2n}\sum_{i=1}^{n} x_i^2}$$

Example

The following commands generate a plot of the Rayleigh pdf.

```
x = [0:0.01:2];
p = raylpdf(x,0.5);
plot(x,p)
```



See Also

"Continuous Distributions (Data)" on page 5-4

Rician Distribution

In this section...

Definition

The Rician distribution has the density function

$$I_0\left(\frac{xs}{\sigma^2}\right)\frac{x}{\sigma^2}e^{-\left(\frac{x^2+s^2}{2\sigma^2}\right)}$$

with noncentrality parameter $s \geq 0$ and scale parameter $\sigma > 0$, for $x > 0$. I_0 is the zero-order modified Bessel function of the first kind. If x has a Rician distribution with parameters s and σ, then $(x/\sigma)^2$ has a noncentral chi-square distribution with two degrees of freedom and noncentrality parameter $(s/\sigma)^2$.

Background

In communications theory, Nakagami distributions, Rician distributions, and Rayleigh distributions are used to model scattered signals that reach a receiver by multiple paths. Depending on the density of the scatter, the signal will display different fading characteristics. Rayleigh and Nakagami distributions are used to model dense scatters, while Rician distributions model fading with a stronger line-of-sight. Nakagami distributions can be reduced to Rayleigh distributions, but give more control over the extent of the fading.

Parameters

See `mle`, `dfittool`.

See Also

"Continuous Distributions (Data)" on page 5-4

Student's t Distribution

In this section...

Definition

Student's t pdf is

$$y = f(x \mid \nu) = \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{x^2}{\nu}\right)^{\frac{\nu+1}{2}}}$$

where $\Gamma(\cdot)$ is the Gamma function.

Background

The t distribution is a family of curves depending on a single parameter ν (the degrees of freedom). As ν goes to infinity, the t distribution approaches the standard normal distribution.

W. S. Gossett discovered the distribution through his work at the Guinness brewery. At the time, Guinness did not allow its staff to publish, so Gossett used the pseudonym "Student."

If x is a random sample of size n from a normal distribution with mean μ, then the statistic

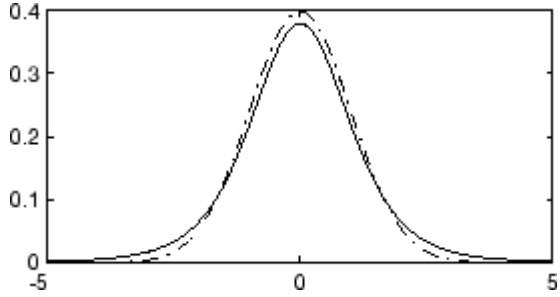
$$t = \frac{\bar{x} - \mu}{s/\sqrt{n}}$$

where $\bar{x}$ is the sample mean and s is the sample standard deviation, has Student's t distribution with $n - 1$ degrees of freedom.

Example

The plot compares the t distribution with $\nu = 5$ (solid line) to the shorter tailed, standard normal distribution (dashed line).

```
x = -5:0.1:5;
y = tpdf(x,5);
z = normpdf(x,0,1);
plot(x,y,'-',x,z,'-.')
```



See Also

"Continuous Distributions (Statistics)" on page 5-6

t Location-Scale Distribution

In this section...

Definition

The t location-scale distribution has the density function

$$\frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\sigma\sqrt{\nu\pi}\,\Gamma\left(\frac{\nu}{2}\right)}\left[\frac{\nu+\left(\frac{x-\mu}{\sigma}\right)^2}{\nu}\right]^{-\left(\frac{\nu+1}{2}\right)}$$

with location parameter μ, scale parameter $\sigma > 0$, and shape parameter $\nu > 0$. If x has a t location-scale distribution, with parameters μ, σ, and ν, then

$$\frac{x-\mu}{\sigma}$$

has a Student's t distribution with ν degrees of freedom.

Background

The t location-scale distribution is useful for modeling data distributions with heavier tails (more prone to outliers) than the normal distribution. It approaches the normal distribution as ν approaches infinity, and smaller values of ν yield heavier tails.

Parameters

See `mle`, `dfittool`.

See Also

"Continuous Distributions (Statistics)" on page 5-6

Uniform Distribution (Continuous)

In this section...

Definition

The uniform cdf is

$$p = F(x \mid a,b) = \frac{x-a}{b-a} I_{[a,b]}(x)$$

Background

The uniform distribution (also called rectangular) has a constant pdf between its two parameters a (the minimum) and b (the maximum). The standard uniform distribution ($a = 0$ and $b = 1$) is a special case of the beta distribution, obtained by setting both of its parameters to 1.

The uniform distribution is appropriate for representing the distribution of round-off errors in values tabulated to a particular number of decimal places.

Parameters

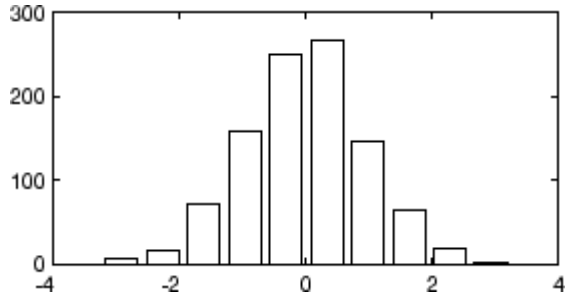
The sample minimum and maximum are the MLEs of a and b respectively.

Example

The example illustrates the inversion method for generating normal random numbers using `rand` and `norminv`. Note that the MATLAB function, `randn`, does not use inversion since it is not efficient for this case.

```
u = rand(1000,1);
```

```
x = norminv(u,0,1);
hist(x)
```



See Also

"Continuous Distributions (Data)" on page 5-4

Uniform Distribution (Discrete)

In this section...

Definition

The discrete uniform pdf is

$$y = f(x \mid N) = \frac{1}{N} I_{(1,\ldots,N)}(x)$$

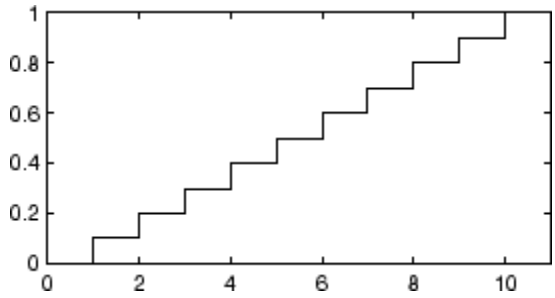
Background

The discrete uniform distribution is a simple distribution that puts equal weight on the integers from one to N.

Example

As for all discrete distributions, the cdf is a step function. The plot shows the discrete uniform cdf for $N = 10$.

```
x = 0:10;
y = unidcdf(x,10);
stairs(x,y)
set(gca,'Xlim',[0 11])
```



Pick a random sample of 10 from a list of 553 items:

```
numbers = unidrnd(553,1,10)
numbers =
   293   372     5   213    37   231   380   326   515   468
```

See Also

"Discrete Distributions" on page 5-7

Weibull Distribution

In this section...

Definition

The Weibull pdf is

$$y = f(x \mid a,b) = ba^{-b}x^{b-1}e^{-\left(\frac{x}{a}\right)^b} I_{(0,\infty)}(x)$$

Background

Waloddi Weibull offered the distribution that bears his name as an appropriate analytical tool for modeling the breaking strength of materials. Current usage also includes reliability and lifetime modeling. The Weibull distribution is more flexible than the exponential for these purposes.

To see why, consider the hazard rate function (instantaneous failure rate). If $f(t)$ and $F(t)$ are the pdf and cdf of a distribution, then the hazard rate is

$$h(t) = \frac{f(t)}{1 - F(t)}$$

Substituting the pdf and cdf of the exponential distribution for $f(t)$ and $F(t)$ above yields a constant. The example below shows that the hazard rate for the Weibull distribution can vary.

Parameters

Suppose you want to model the tensile strength of a thin filament using the Weibull distribution. The function `wblfit` gives maximum likelihood estimates and confidence intervals for the Weibull parameters.

```
strength = wblrnd(0.5,2,100,1);       % Simulated strengths.
[p,ci] = wblfit(strength)

p =
0.4715    1.9811


ci =

    0.4248    1.7067
    0.5233    2.2996
```

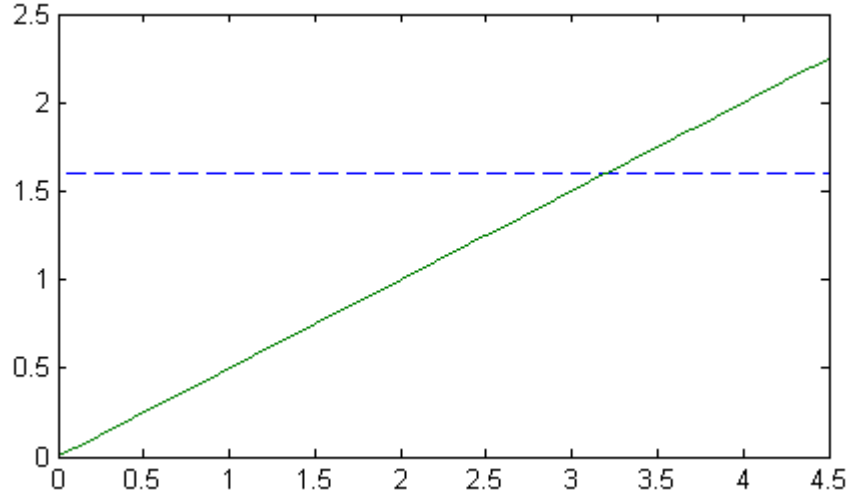
The default 95% confidence interval for each parameter contains the true value.

Example

The exponential distribution has a constant hazard function, which is not generally the case for the Weibull distribution.

The plot shows the hazard functions for exponential (dashed line) and Weibull (solid line) distributions having the same mean life. The Weibull hazard rate here increases with age (a reasonable assumption).

```
t = 0:0.1:4.5;
h1 = exppdf(t,0.6267) ./ (1-expcdf(t,0.6267));
h2 = wblpdf(t,2,2) ./ (1-wblcdf(t,2,2));
plot(t,h1,'--',t,h2,'-')
```



See Also

"Continuous Distributions (Data)" on page 5-4

Wishart Distribution

In this section...

Definition

The probability density function of the d-dimensional Wishart distribution is given by

$$y = f(X, \Sigma, \nu) = \frac{|X|^{((\nu-d-1)/2)} e^{\left(-\frac{1}{2}\mathrm{trace}\left(\Sigma^{-1}X\right)\right)}}{2^{(\nu d)/2}\pi^{(d(d-1))/4}|\Sigma|^{\nu/2}\Gamma(\nu/2)\ldots\Gamma(\nu-(d-1))/2}$$

where X and Σ are d-by-d symmetric positive definite matrices, and ν is a scalar greater than $d - 1$. While it is possible to define the Wishart for singular Σ, the density cannot be written as above.

Only random matrix generation is supported for the Wishart distribution, including both singular and nonsingular Σ.

Background

The Wishart distribution is a generalization of the univariate chi-square distribution to two or more variables. It is a distribution for symmetric positive semidefinite matrices, typically covariance matrices, the diagonal elements of which are each chi-square random variables. In the same way as the chi-square distribution can be constructed by summing the squares of independent, identically distributed, zero-mean univariate normal random variables, the Wishart distribution can be constructed by summing the inner products of independent, identically distributed, zero-mean multivariate normal random vectors.

The Wishart distribution is parameterized with a symmetric, positive semidefinite matrix, Σ, and a positive scalar degrees of freedom parameter, ν. ν is analogous to the degrees of freedom parameter of a univariate chi-square distribution, and Σν is the mean of the distribution.

The Wishart distribution is often used as a model for the distribution of the sample covariance matrix for multivariate normal random data, after scaling by the sample size.

Example

If x is a bivariate normal random vector with mean zero and covariance matrix

$$\Sigma = \begin{pmatrix} 1 & .5 \\ .5 & 2 \end{pmatrix}$$

then you can use the Wishart distribution to generate a sample covariance matrix without explicitly generating x itself. Notice how the sampling variability is quite large when the degrees of freedom is small.

```
Sigma = [1 .5; .5 2];
df = 10; S1 = wishrnd(Sigma,df)/df

S1 =
       1.7959      0.64107
      0.64107       1.5496

df = 1000; S2 = wishrnd(Sigma,df)/df

S2 =
       0.9842      0.50158
      0.50158       2.1682
```

See Also

"Inverse Wishart Distribution" on page B-46, "Multivariate Distributions" on page 5-8

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