## Image Processing Toolbox ${ }^{\text {TM }}$

 ReferenceR2012b

MATLAB ${ }^{\circ}$

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508-647-7000 (Phone)

508-647-7001 (Fax)
The MathWorks, Inc.
3 Apple Hill Drive
Natick, MA 01760-2098
For contact information about worldwide offices, see the MathWorks Web site.

## Image Processing Toolbox ${ }^{\text {TM }}$ Reference

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## Function Reference

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ROI-Based, Neighborhood, and Block Processing (p. 1-20)

Colormaps and Color Space (p. 1-22)
Utilities (p. 1-24)

Display, import, and export images

Modular interactive tools and associated utility functions.

Spatial transformation and image registration
Image analysis, texture analysis, view pixel values, and calculate image statistics
Add, subtract, multiply, and divide images

Enhance and restore images

Linear filters, filter design, and image transforms

Morphological image processing ROI-based, neighborhood, and block operations

Manipulate image color
Array operations, examples, preferences and other toolbox utility functions

## Image Display and Exploration

| Image Display and Exploration | Display and explore images |
| :--- | :--- |
| (p. 1-2) |  |$\quad$| Image File I/O (p. 1-2) | Import and export images |
| :--- | :--- |
| Image Types and Type Conversions | Convert between the various image <br> types |

## Image Display and Exploration

immovie
implay
imshow
imtool
montage
subimage
warp

Make movie from multiframe image
Play movies, videos, or image sequences
Display image
Image Tool
Display multiple image frames as rectangular montage
Display multiple images in single figure
Display image as texture-mapped surface

## Image File I/O

| analyze75info | Read metadata from header file of <br> Analyze 7.5 data set |
| :--- | :--- |
| analyze75read | Read image data from image file of <br> Analyze 7.5 data set |
| dicomanon | Anonymize DICOM file |
| dicomdict | Get or set active DICOM data <br> dictionary |

dicominfo
dicomlookup
dicomread
dicomuid
dicomwrite
hdrread
hdrwrite
interfileinfo
interfileread
isrset
makehdr
nitfinfo
nitfread
openrset
rsetwrite
tonemap

Read metadata from DICOM message

Find attribute in DICOM data dictionary

Read DICOM image
Generate DICOM unique identifier
Write images as DICOM files
Read high dynamic range (HDR) image

Write Radiance high dynamic range (HDR) image file

Read metadata from Interfile file
Read images in Interfile format
Check if file is R -Set
Create high dynamic range image
Read metadata from National Imagery Transmission Format (NITF) file

Read image from NITF file
Open R-Set file
Create reduced resolution data set from image file

Render high dynamic range image for viewing

## Image Types and Type Conversions

demosaic<br>gray2ind

Convert Bayer pattern encoded image to truecolor image

Convert grayscale or binary image to indexed image
grayslice
graythresh
im2bw
im2double
im2int16
im2java2d
im2single
im2uint16
im2uint8
ind2gray
ind2rgb
label2rgb
mat2gray
rgb2gray
ima
ima
ima
ima
grayslice graythresh
im2bw
im2double
im2int16
im2java2d
im2single
im2uint16
im2uint8
ind2gray
ind 2 rgb
label2rgb
mat2gray
rgb2gray

Convert grayscale image to indexed image using multilevel thresholding
Global image threshold using Otsu's method

Convert image to binary image, based on threshold

Convert image to double precision
Convert image to 16 -bit signed integers

Convert image to Java buffered image
Convert image to single precision
Convert image to 16 -bit unsigned integers
Convert image to 8 -bit unsigned integers

Convert indexed image to grayscale image
Convert indexed image to RGB image

Convert label matrix into RGB image
Convert matrix to grayscale image
Convert RGB image or colormap to grayscale

## GUI Tools

| Modular Interactive Tools (p. 1-5) | Modular interactive tool creation <br> functions |
| :--- | :--- |
| Navigational Tools for Image Scroll | Modular interactive navigational <br> tools |
| Panel (p. 1-5) | Modular interactive tool utility <br> functions |
| Utilities for Interactive Tools (p. 1-6) |  |

## Modular Interactive Tools

| imageinfo | Image Information tool |
| :--- | :--- |
| imcontrast | Adjust Contrast tool |
| imdisplayrange | Display Range tool |
| imdistline | Distance tool |
| impixelinfo | Pixel Information tool |
| impixelinfoval | Pixel Information tool without text |
| label |  |
| impixelregion | Pixel Region tool |
| impixelregionpanel | Pixel Region tool panel |

## Navigational Tools for Image Scroll Panel

| immagbox | Magnification box for scroll panel |
| :--- | :--- |
| imoverview | Overview tool for image displayed in <br> scroll panel |
| imoverviewpanel | Overview tool panel for image <br> displayed in scroll panel |
| imscrollpanel | Scroll panel for interactive image <br> navigation |

## Utilities for Interactive Tools

| axes2pix | Convert axes coordinates to pixel <br> coordinates |
| :--- | :--- |
| getimage | Image data from axes |
| getimagemodel | Image model object from image <br> object |
| imattributes | Information about image attributes |
| imellipse | Create draggable ellipse |
| imfreehand | Create draggable freehand region |
| imgca | Get handle to current axes |
| containing image |  |
| imgcf | Get handle to current figure |
| imgetfile | Containing image |
| imhandles | Get Image dialog box |
| imline | Create draggable, resizable line |
| impoint | Create draggable point |
| impoly | Create draggable, resizable polygon |
| imrect | Create draggable rectangle |
| imroi | Region-of-interest (ROI) base class |
| iptaddcallback | Add function handle to callback list |
| iptcheckhandle | Check validity of handle |
| iptgetapi | Get Application Programmer |
| iptGetPointerBehavior | Interface (API) for handle |
| ipticondir | Retrieve pointer behavior from HG <br> object |
| iptPointerManager | Directories containing IPT and |
| MATLAB ${ }^{\circledR}$ icons |  |

iptremovecallback<br>iptSetPointerBehavior<br>iptwindowalign<br>makeConstrainToRectFen<br>truesize

Delete function handle from callback list

Store pointer behavior structure in Handle Graphics object

Align figure windows
Create rectangularly bounded drag constraint function

Adjust display size of image

# Spatial Transformation and Image Registration 

Spatial Transformations (p. 1-8)<br>Image Registration (p. 1-9)<br>Spatial transformation of images and multidimensional arrays<br>Align two images using control points

## Spatial Transformations

| checkerboard | Create checkerboard image |
| :--- | :--- |
| findbounds | Find output bounds for spatial <br> transformation |
| fliptform | Flip input and output roles of TFORM <br> structure |
| imcrop | Crop image |
| impyramid | Image pyramid reduction and <br> expansion |
| imresize | Resize image |
| imrotate | Rotate image <br> imtransform |
| Apply 2-D spatial transformation to <br> image |  |
| makeresampler | Create resampling structure <br> maketform |
| Create spatial transformation |  |
| structure (TFORM) |  |$\quad$| Apply spatial transformation to N-D |
| :--- |
| tformarray |$\quad$| array |
| :--- |
| Apply forward spatial |
| transformation |$\quad$| Apply inverse spatial transformation |
| :--- |

## Image Registration

$\left.\left.\begin{array}{ll}\text { cp2tform } & \begin{array}{l}\text { Infer spatial transformation from } \\ \text { control point pairs }\end{array} \\ \text { cpcorr } & \begin{array}{l}\text { Tune control-point locations using } \\ \text { cross correlation }\end{array} \\ \text { cpselect } & \begin{array}{l}\text { Control Point Selection Tool } \\ \text { cpstruct2pairs }\end{array} \\ \text { Convert CPSTRUCT to valid pairs of } \\ \text { control points }\end{array}\right\} \begin{array}{ll}\text { Composite of two images }\end{array}\right\}$

## Image Analysis and Statistics

Image Analysis (p. 1-10)

Texture Analysis (p. 1-11)

Pixel Values and Statistics (p. 1-11) Create histograms, contour plots, and get statistics on image regions

## Image Analysis

| bwboundaries | Trace region boundaries in binary <br> image |
| :--- | :--- |
| bwtraceboundary | Trace object in binary image |
| corner | Find corner points in image |
| cornermetric | Create corner metric matrix from <br> image |
| edge | Find edges in grayscale image |
| hough | Hough transform |
| houghlines | Extract line segments based on <br> Hough transform |
| houghpeaks | Identify peaks in Hough transform <br> imfindcircles |
| qind circles using circular Hough |  |
| qtdecomp | Quadtree decomposition <br> qtgetblk |
| qlock values in quadtree |  |
| decomposition |  |

## Texture Analysis

entropy
entropyfilt
graycomatrix
graycoprops
rangefilt
stdfilt

Entropy of grayscale image
Local entropy of grayscale image
Create gray-level co-occurrence matrix from image

Properties of gray-level co-occurrence matrix

Local range of image
Local standard deviation of image

## Pixel Values and Statistics

| corr2 | 2-D correlation coefficient |
| :--- | :--- |
| imcontour | Create contour plot of image data |
| imhist | Display histogram of image data |
| imhistmatch | Adjust histogram of image to match |
| impixel | N-bin histogram of reference image |
| improfile | Pixel color values |
| mean2 | Pixel-value cross-sections along line <br> segments |
| regionprops | Average or mean of matrix elements |
| std2 | Measure properties of image regions |
|  | Standard deviation of matrix <br> elements |

## Image Arithmetic

| imabsdiff | Absolute difference of two images |
| :--- | :--- |
| imadd | Add two images or add constant to <br> image |
| imapplymatrix | Linear combination of color channels |
| imcomplement | Complement image |
| imdivide | Divide one image into another or <br> divide image by constant |
| imlincomb | Linear combination of images <br> immultiply |
| Multiply two images or multiply |  |
| imsubtract | image by constant |
|  | Subtract one image from another or <br> subtract constant from image |

## Image Enhancement and Restoration

Image Enhancement (p. 1-13)<br>Image Restoration (Deblurring) (p. 1-13)

Histogram equalization, decorrelation stretching, and 2-D filtering

Deconvolution for deblurring

## Image Enhancement

| adapthisteq | Contrast-limited adaptive histogram <br> equalization (CLAHE) |
| :--- | :--- |
| decorrstretch | Apply decorrelation stretch to <br> multichannel image |
| histeq | Enhance contrast using histogram <br> equalization |
| imadjust | Adjust image intensity values or <br> colormap |
| imnoise | Add noise to image |
| intlut | Convert integer values using lookup |
| medfilt2 | table |
| ordfilt2 | 2-D median filtering |
| stretchlim | 2-D order-statistic filtering |
| wiener2 | Find limits to contrast stretch image |
|  | 2-D adaptive noise-removal filtering |

## Image Restoration (Deblurring)

| deconvblind | Deblur image using blind <br> deconvolution |
| :--- | :--- |
| deconvlucy | Deblur image using Lucy-Richardson <br> method |


| deconvreg | Deblur image using regularized filter |
| :--- | :--- |
| deconvwnr | Deblur image using Wiener filter |
| edgetaper | Taper discontinuities along image <br> edges |
| otf2psf | Convert optical transfer function to <br> point-spread function |
| psf2otf | Convert point-spread function to <br> optical transfer function |

# Linear Filtering and Transforms 

Linear Filtering (p. 1-15)

Linear 2-D Filter Design (p. 1-15)
Image Transforms (p. 1-15)

## Linear Filtering

Convolution, N-D filtering, and predefined 2-D filters

2-D FIR filters
Fourier, Discrete Cosine, Radon, and Fan-beam transforms

2-D convolution matrix
Create predefined 2-D filter
N -D filtering of multidimensional images

2-D frequency response
2-D FIR filter using frequency sampling
2-D FIR filter using frequency transformation

2-D FIR filter using 1-D window method

2-D FIR filter using 2-D window method

2-D discrete cosine transform
Discrete cosine transform matrix

| fan2para | Convert fan-beam projections to <br> parallel-beam |
| :--- | :--- |
| fanbeam | Fan-beam transform |
| idct2 | 2-D inverse discrete cosine transform |
| ifanbeam | Inverse fan-beam transform |
| iradon | Inverse Radon transform |
| para2fan | Convert parallel-beam projections to |
| phantom | fan-beam |
| radon | Create head phantom image |
|  | Radon transform |

## Morphological Operations

Intensity and Binary Images (p. 1-17)

Binary Images (p. 1-18)

Structuring Element Creation and Manipulation (p. 1-19)

Dilate, erode, reconstruct, and perform other morphological operations

Label, pack, and perform morphological operations on binary images

Create and manipulate structuring elements for morphological operations

## Intensity and Binary Images

| conndef | Create connectivity array |
| :--- | :--- |
| imbothat | Bottom-hat filtering |
| imclearborder | Suppress light structures connected <br> to image border |
| imclose | Morphologically close image |
| imdilate | Dilate image |
| imerode | Erode image |
| imextendedmax | Extended-maxima transform |
| imextendedmin | Extended-minima transform |
| imfill | Fill image regions and holes |
| imhmax | H-maxima transform |
| imhmin | H-minima transform |
| imimposemin | Impose minima |
| imopen | Morphologically open image |
| imreconstruct | Morphological reconstruction |
| imregionalmax | Regional maxima |

imregionalmin<br>imtophat<br>watershed

Regional minima
Top-hat filtering
Watershed transform

## Binary Images

| applylut | Neighborhood operations on binary images using lookup tables |
| :---: | :---: |
| bwarea | Area of objects in binary image |
| bwareaopen | Remove small objects from binary image |
| bwconncomp | Find connected components in binary image |
| bwconvhull | Generate convex hull image from binary image |
| bwdist | Distance transform of binary image |
| bwdistgeodesic | Geodesic distance transform of binary image |
| bweuler | Euler number of binary image |
| bwhitmiss | Binary hit-miss operation |
| bwlabel | Label connected components in 2-D binary image |
| bwlabeln | Label connected components in binary image |
| bwmorph | Morphological operations on binary images |
| bwpack | Pack binary image |
| bwperim | Find perimeter of objects in binary image |
| bwselect | Select objects in binary image |


| bwulterode | Ultimate erosion |
| :--- | :--- |
| bwunpack | Unpack binary image |
| graydist | Gray-weighted distance transform <br> of grayscale image |
| imtophat | Top-hat filtering <br> makelut |
| Create lookup table for use with <br> bwlookup |  |

## Structuring Element Creation and Manipulation

getheight
getneighbors
getnhood
getsequence
isflat
reflect
strel
translate

Height of structuring element
Structuring element neighbor locations and heights

Structuring element neighborhood
Sequence of decomposed structuring elements

True for flat structuring element
Reflect structuring element
Create morphological structuring element (STREL)
Translate structuring element (STREL)

## ROI-Based, Neighborhood, and Block Processing

ROI-Based Processing (p. 1-20)<br>Neighborhood and Block Processing (p. 1-20)

## ROI-Based Processing

```
poly2mask
roicolor
roifill
roifilt2
roipoly
```

Define regions of interest (ROI) and perform operations on them

Define neighborhoods and blocks and process them

Convert region of interest (ROI) polygon to region mask

Select region of interest (ROI) based on color

Fill in specified region of interest (ROI) polygon in grayscale image
Filter region of interest (ROI) in image

Specify polygonal region of interest (ROI)

## Neighborhood and Block Processing

bestblk<br>blockproc<br>close (ImageAdapter)<br>col2im<br>colfilt<br>im2col<br>ImageAdapter

Determine optimal block size for block processing

Distinct block processing for image
Close ImageAdapter object
Rearrange matrix columns into blocks

Columnwise neighborhood operations

Rearrange image blocks into columns
Interface for image I/O

| nlfilter | General sliding-neighborhood <br> operations |
| :--- | :--- |
| readRegion (ImageAdapter) | Read region of image |
| writeRegion (ImageAdapter) | Write block of data to region of image |

## Colormaps and Color Space

Color Space Conversions (p. 1-22)

## Color Space Conversions

| applycform | Apply device-independent color space transformation |
| :---: | :---: |
| iccfind | Search for ICC profiles |
| iccread | Read ICC profile |
| iccroot | Find system default ICC profile repository |
| iccwrite | Write ICC color profile to disk file |
| isicc | True for valid ICC color profile |
| lab2double | Convert $L^{*} a^{*} b^{*}$ data to double |
| lab2uint16 | Convert $L * a^{*} b^{*}$ data to uint16 |
| lab2uint8 | Convert $L^{*} a^{*} b^{*}$ data to uint8 |
| makecform | Create color transformation structure |
| ntsc2rgb | Convert NTSC values to RGB color space |
| rgb2ntsc | Convert RGB color values to NTSC color space |
| rgb2ycber | Convert RGB color values to YCbCr color space |
| whitepoint | $X Y Z$ color values of standard illuminants |
| xyz2double | Convert XYZ color values to double |

xyz2uint16
ycbcr2rgb

Convert $X Y Z$ color values to uint16
Convert YCbCr color values to RGB color space

## Utilities

Preferences (p. 1-24)

Validation (p. 1-24)

Mouse (p. 1-25)

Array Operations (p. 1-25)

Examples (p. 1-25)
Performance (p. 1-25)

Set and determine value of toolbox preferences
Check input arguments and perform other common programming tasks

Retrieve values of lines, points, and rectangles defined interactively using mouse
Circularly shift pixel values and pad arrays
Launch Image Processing Toolbox ${ }^{\text {TM }}$ examples
Check for presence of Intel ${ }^{\circledR}$ Integrated Performance Primitives (Intel IPP) library

Get values of Image Processing Toolbox preferences

Display Image Processing Preferences dialog box

Set Image Processing Toolbox preferences or display valid values

Default display range of image based on its class
Check validity of connectivity argument
Check validity of array

iptcheckmap<br>iptchecknargin<br>iptcheckstrs<br>iptnum2ordinal

## Mouse

getline
getpts
getrect

## Array Operations

padarray

## Examples

iptdemos

## Performance

ippl

Check validity of colormap
Check number of input arguments
Check validity of option string
Convert positive integer to ordinal string

Select polyline with mouse
Specify points with mouse
Specify rectangle with mouse

Pad array

Index of Image Processing Toolbox examples

Check for presence of Intel Integrated Performance Primitives (Intel IPP) library

## Class Reference

- "Image Input and Output" on page 2-2
- "Image Registration" on page 2-3


## Image Input and Output

## ImageAdapter

| close | Close ImageAdapter object |
| :--- | :--- |
| ImageAdapter | Interface for image I/O |
| readRegion | Read region of image |
| writeRegion | Write block of data to region of image |

## Image Registration

## registration.metric.MattesMutualInformation

registration.metric.MattesMutualInforMatices mutual information metric configuration object

## registration.metric.MeanSquares,

registration.metric.MeanSquares Mean square error metric configuration object

## registration.optimizer.RegularStepGradientDescent

registration.optimizer.RegularStepGradiegitIRessemt gradient descent optimizer configuration object

## registration.optimizer.OnePlusOneEvolutionary

registration.optimizer.OnePlusOneEvonnieplury-one evolutionary optimizer configuration object

2 Class Reference

Functions - Alphabetical
List

Purpose Contrast-limited adaptive histogram equalization (CLAHE)
Syntax $\quad J=\operatorname{adapthisteq}(I)$
J = adapthisteq(I,param1, val1,param2,val2...)
Description
$J=$ adapthisteq(I) enhances the contrast of the grayscale image I by transforming the values using contrast-limited adaptive histogram equalization (CLAHE).

CLAHE operates on small regions in the image, called tiles, rather than the entire image. Each tile's contrast is enhanced, so that the histogram of the output region approximately matches the histogram specified by the 'Distribution' parameter. The neighboring tiles are then combined using bilinear interpolation to eliminate artificially induced boundaries. The contrast, especially in homogeneous areas, can be limited to avoid amplifying any noise that might be present in the image.
$J=$ adapthisteq(I, param1, val1, param2, val2...) specifies any of the additional parameter/value pairs listed in the following table. Parameter names can be abbreviated, and case does not matter.

| Parameter | Value |
| :--- | :--- |
| 'NumTiles' | $\left.\begin{array}{l}\text { Two-element vector of positive integers specifying } \\ \text { the number of tiles by row and column, [M N]. } \\ \text { Both } M \text { and } N \text { must be at least 2. The total number } \\ \text { of tiles is equal to } \mathrm{M}^{*} \mathrm{~N} . \\ \text { Default: }[8 \quad 8\end{array}\right]$ |
| 'ClipLimit' | Real scalar in the range [0 1] that specifies a <br> contrast enhancement limit. Higher numbers <br> result in more contrast. <br> Default: 0.01 |


| Parameter | Value |
| :---: | :---: |
| 'NBins' | Positive integer scalar specifying the number of bins for the histogram used in building a contrast enhancing transformation. Higher values result in greater dynamic range at the cost of slower processing speed. <br> Default: 256 |
| 'Range ' | String specifying the range of the output image data. <br> 'original' - Range is limited to the range of the original image, $[\min (I(:)) \quad \max (I(:))]$. <br> 'full' - Full range of the output image class is used. For example, for uint8 data, range is [0 255]. <br> Default: 'full' |
| 'Distribution' | String specifying the desired histogram shape for the image tiles. <br> 'uniform' — Flat histogram <br> 'rayleigh' — Bell-shaped histogram <br> 'exponential' - Curved histogram <br> Default: 'uniform' |
| 'Alpha' | Nonnegative real scalar specifying a distribution parameter. <br> Default: 0.4 |
|  | Note Only used when 'Distribution' is set to either 'rayleigh' or 'exponential'. |

Tips

- 'NumTiles' specifies the number of rectangular contextual regions (tiles) into which adapthisteq divides the image. adapthisteq calculates the contrast transform function for each of these regions individually. The optimal number of tiles depends on the type of the input image, and it is best determined through experimentation.
- 'ClipLimit' is a contrast factor that prevents over-saturation of the image specifically in homogeneous areas. These areas are characterized by a high peak in the histogram of the particular image tile due to many pixels falling inside the same gray level range. Without the clip limit, the adaptive histogram equalization technique could produce results that, in some cases, are worse than the original image.
- 'Distribution' specifies the distribution that adapthisteq uses as the basis for creating the contrast transform function. The distribution you select should depend on the type of the input image. For example, underwater imagery appears to look more natural when the Rayleigh distribution is used.

Class

## Examples

Grayscale image I can be of class uint8, uint16, int16, single, or double. The output image $J$ has the same class as I.

Apply Contrast-limited Adaptive Histogram Equalization (CLAHE) to an image and display the results.

```
I = imread('tire.tif');
A = adapthisteq(I,'clipLimit',0.02,'Distribution','rayleigh');
figure, imshow(I);
figure, imshow(A);
```

Apply CLAHE to a color image.

```
[X MAP] = imread('shadow.tif');
% Convert indexed image to true-color (RGB) format
RGB = ind2rgb(X,MAP);
```

```
% Convert image to L*a*b* color space
cform2lab = makecform('srgb2lab');
LAB = applycform(RGB, cform2lab);
% Scale values to range from 0 to 1
L = LAB(:,:,1)/100;
% Perform CLAHE
LAB(:,:,1) = adapthisteq(L,'NumTiles',...
    [8 8],'ClipLimit',0.005)*100;
% Convert back to RGB color space
cform2srgb = makecform('lab2srgb');
J = applycform(LAB, cform2srgb);
% Display the results
figure, imshow(RGB);
figure, imshow(J);
\begin{tabular}{ll} 
References & [1] Zuiderveld, Karel. "Contrast Limited Adaptive Histograph \\
& Equalization." Graphic Gems IV. San Diego: Academic Press \\
& Professional, 1994.474-485.
\end{tabular}
```

See Also

histeq

## analyze75info

## Purpose <br> Read metadata from header file of Analyze 7.5 data set

## Syntax

Description

Examples

See Also
info = analyze75info(filename)
info = analyze75info(filename,'ByteOrder', endian)
info $=$ analyze75info(filename) reads the header file of the Analyze 7.5 data set specified by the string filename. The function returns info, a structure whose fields contain information about the data set.

Analyze 7.5 is a 3-D biomedical image visualization and analysis product developed by the Biomedical Imaging Resource of the Mayo Clinic. An Analyze 7.5 data set is made of two files, a header file and an image file. The files have the same name with different file extensions. The header file has the file extension .hdr and the image file has the file extension .img.
info = analyze75info(filename,'ByteOrder', endian) reads the Analyze 7.5 header file using the byte ordering specified by endian, where endian can have either of the following values:

| Value | Meaning |
| :--- | :--- |
| 'ieee-le' | Byte ordering is Little Endian |
| 'ieee-be' | Byte ordering is Big Endian |

If the specified endian value results in a read error, analyze75info issues a warning message and attempts to read the header file with the opposite ByteOrder format.

Read an Analyze 7.5 header file.

```
info = analyze75info('brainMRI.hdr');
```

Specify the byte ordering of the data set.

```
info = analyze75info('brainMRI', 'ByteOrder', 'ieee-le');
```

analyze75read

## Purpose

Read image data from image file of Analyze 7.5 data set
Syntax
X = analyze75read(filename)
X = analyze75read(info)

Description
$X=$ analyze75read(filename) reads the image data from the image file of an Analyze 7.5 format data set specified by the string filename. The function returns the image data in $X$. For single-frame, grayscale images, X is an $m$-by- $n$ array. analyze 75 read uses a data type for X that is consistent with the data type specified in the data set header file.

Analyze 7.5 is a $3-\mathrm{D}$ biomedical image visualization and analysis product developed by the Biomedical Imaging Resource of the Mayo Clinic. An Analyze 7.5 data set is made of two files, a header file and an image file. The files have the same name with different file extensions. The header file has the file extension .hdr and the image file has the file extension .img.
$\mathrm{X}=$ analyze75read(info) reads the image data from the image file specified in the metadata structure info. info must be a valid metadata structure returned by the analyze75info function.

Note analyze75read returns image data in radiological orientation (LAS). This is the default used by the Analyze 7.5 format.

## Example 1

Read image data from an Analyze 7.5 image file.
X = analyze75read('brainMRI');
Because Analyze 7.5 format uses radiological orientation (LAS), flip the data for correct image display in MATLAB.

X = flipdim(X,1);
Select frames 12 to 17 and use reshape to create an array for montage.
$Y=\operatorname{reshape}(X(:,:, 12: 17),[\operatorname{size}(X, 1) \operatorname{size}(X, 2) 16]) ;$
montage( Y );

## Example 2

Call analyze75read with the metadata obtained from the header file using analyze75info.
info = analyze75info('brainMRI.hdr');
X = analyze75read(info);

Class Support

See Also analyze75info

## Purpose Apply device-independent color space transformation

Syntax
Description
$B=$ applycform(A,C)
$B=$ applycform $(A, C)$ converts the color values in $A$ to the color space specified in the color transformation structure C. The color transformation structure specifies various parameters of the transformation. See makecform for details.

If A is two-dimensional, each row is interpreted as a color unless the color transformation structure contains a grayscale ICC profile. (See Note for this case.) A can have 1 or more columns, depending on the input color space. B has the same number of rows and 1 or more columns, depending on the output color space. (The ICC spec currently supports up to 15 -channel device spaces.)
If A is three-dimensional, each row-column location is interpreted as a color, and size $(\mathrm{A}, 3)$ is typically 1 or more, depending on the input color space. B has the same number of rows and columns as A, and size $(B, 3)$ is 1 or more, depending on the output color space.

Class Support

A is a real, nonsparse array of class uint8, uint16, or double or a string. A is only a string if C was created with the following syntax:

C = makecform('named', profile, space)
The output array B has the same class as A, unless the output space is $X Y Z$. If the input is $X Y Z$ data of class uint8, the output is of class uint16, because there is no standard 8-bit encoding defined for $X Y Z$ color values.

Note If the color transformation structure C contains a grayscale ICC profile, applycform interprets each pixel in A as a color. A can have any number of columns. $B$ has the same size as $A$.

```
Examples Read in a color image that uses the sRGB color space.
rgb = imread('peppers.png');
Create a color transformation structure that defines an sRGB to \(L^{*} a^{*} b^{*}\) conversion.
C = makecform('srgb2lab');
Perform the transformation with applycform.
lab \(=\) applycform(rgb,C);
See Also lab2double | lab2uint8 | lab2uint16 | makecform | whitepoint | xyz2double | xyz2uint16
How To . "Converting Color Data Between Color Spaces"
```

Purpose
Syntax
Description

Support

## Algorithms

Neighborhood operations on binary images using lookup tables
A = applylut(BW,LUT)
A = applylut (BW, LUT) performs a 2 -by-2 or 3-by-3 neighborhood operation on binary image BW by using a lookup table (LUT). LUT is either a 16 -element or 512 -element vector returned by makelut. The vector consists of the output values for all possible 2 -by- 2 or 3 -by- 3 neighborhoods.

BW can be numeric or logical, and it must be real, two-dimensional, and nonsparse. LUT can be numeric or logical, and it must be a real vector with 16 or 512 elements. If all the elements of LUT are 0 or 1 , then $A$ is logical. If all the elements of LUT are integers between 0 and 255 , then $A$ is uint8. For all other cases, A is double.
applylut performs a neighborhood operation on a binary image by producing a matrix of indices into lut, and then replacing the indices with the actual values in lut. The specific algorithm used depends on whether you use 2 -by- 2 or 3 -by- 3 neighborhoods.

## 2-by-2 Neighborhoods

For 2-by-2 neighborhoods, length(lut) is 16 . There are four pixels in each neighborhood, and two possible states for each pixel, so the total number of permutations is $2^{4}=16$.
To produce the matrix of indices, applylut convolves the binary image BW with this matrix.

| 8 | 2 |
| :--- | :--- |
| 4 | 1 |

The resulting convolution contains integer values in the range $[0,15]$. applylut uses the central part of the convolution, of the same size as $B W$, and adds 1 to each value to shift the range to $[1,16]$. It then constructs A by replacing the values in the cells of the index matrix with the values in lut that the indices point to.

## applylut

## 3-by-3 Neighborhoods

For 3-by-3 neighborhoods, length (lut) is 512 . There are nine pixels in each neighborhood, and two possible states for each pixel, so the total number of permutations is $2^{9}=512$.

To produce the matrix of indices, applylut convolves the binary image BW with this matrix.

| 256 | 32 | 4 |
| ---: | ---: | ---: |
| 128 | 16 | 2 |
| 64 | 8 | 1 |

The resulting convolution contains integer values in the range [ 0,511$]$. applylut uses the central part of the convolution, of the same size as $B W$, and adds 1 to each value to shift the range to $[1,512]$. It then constructs A by replacing the values in the cells of the index matrix with the values in lut that the indices point to.

## Examples

Perform erosion using a 2-by-2 neighborhood. An output pixel is on only if all four of the input pixel's neighborhood pixels are on.

```
lut = makelut('sum(x(:)) == 4',2);
BW = imread('text.png');
BW2 = applylut(BW,lut);
imshow(BW), figure, imshow(BW2)
```

The term watershed refers to a ridge that ...

The term watershed


See Also
makelut

## Purpose Convert axes coordinates to pixel coordinates

```
Syntax pixelx = axes2pix(dim, XDATA, AXESX)
```

Description

Class
Support

## Note

## Examples

Example with default XData and YData.

```
h = imshow('pout.tif');
[nrows,ncols] = size(get(h,'CData'));
xdata = get(h,'XData')
ydata = get(h,'YData')
px = axes2pix(ncols,xdata,30)
py = axes2pix(nrows,ydata,30)
```

Example with non-default XData and YData.

```
xdata = [10 100]
```

ydata $=[20$ 90]
px = axes2pix(ncols, xdata, 30)
py = axes2pix(nrows,ydata,30)

See Also impixelinfo | bwselect | imfill | impixel | improfile | roipoly
Purpose Determine optimal block size for block processing
Syntax
siz = bestblk([m n],k)
[mb,nb] = bestblk([m n],k)
Description
Algorithmsbestblk returns the optimal block size given $\mathrm{m}, \mathrm{n}$, and k . The algorithmfor determining siz is

- If $m$ is less than or equal to $k$, return $m$.
- If $m$ is greater than $k$, consider all values between min(m/10,k/2)and $k$. Return the value that minimizes the padding required.
The same algorithm is then repeated for $n$.
Examples $\quad$ siz $=$ bestblk([640 800],72)siz =
6450
See Also ..... blockproc


## blockproc

| Purpose | Distinct block processing for image |
| :--- | :--- |
| Syntax | $B=\operatorname{blockproc}(A,[M N]$, fun $)$ |
|  | $B=\operatorname{blockproc}($ src_filename, $[\mathrm{M} \mathrm{N}]$, fun $)$ |
|  | $B=\operatorname{blockproc}($ adapter, $[\mathrm{M} N]$, fun $)$ |
| blockproc $(\ldots$, Name, Value,$\ldots)$ |  |

## Description

$B=$ blockproc(A,[MN],fun) processes the image $A$ by applying the function fun to each distinct $M$-by - $N$ block of $A$ and concatenating the results into B , the output matrix. fun is a function handle to a function that accepts a block struct as input and returns a matrix, vector, or scalar Y. For example, Y = fun(block_struct). (For more information about a block struct, see the Definition section below.) For each block of data in the input image, A , blockproc passes the block in a block struct to the user function, fun, to produce Y , the corresponding block in the output image. If $Y$ is empty, blockproc does not generate any output and returns empty after processing all blocks. Choosing an appropriate block size can significantly improve performance. For more information, see "Choosing Block Size" in the Image Processing Toolbox documentation.

B = blockproc(src_filename, [M N],fun) processes the image src_filename, reading and processing one block at a time. This syntax is useful for processing very large images since only one block of the image is read into memory at a time. If the output matrix $B$ is too large to fit into memory, omit the output argument and instead use the 'Destination ' parameter/value pair to write the output to a file.
$B=$ blockproc(adapter, [M N],fun) processes the source image specified by adapter, an ImageAdapter object. An ImageAdapter is a user-defined class that provides blockproc with a common API for reading and writing to a particular image file format. For more information, see "Working with Data in Unsupported Formats" in the Image Processing Toolbox documentation.
blockproc(..., Name, Value, ...) processes the input image, specifying parameters and corresponding values that control various aspects of the block behavior. Parameter names are not case sensitive.

## Input Arguments

## A

Input image.

## [M N]

Block size of A.

## fun

Function handle to a function that accepts a block struct as input and returns a matrix, vector, or scalar.

## src_filename

Input image.

## adapter

A user-defined class that provides blockproc with a common API for reading and writing to a particular image file format.

## Name-Value Pair Arguments

Specify 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 and value pair arguments in any order as Name1, Value1, . . . , NameN, ValueN.

## BorderSize

A two-element vector, [V H], specifying the amount of border pixels to add to each block. The function adds V rows above and below each block and H columns left and right of each block. The size of each resulting block will be:

$$
[M+2 * V, N+2 * H]
$$

By default, the function automatically removes the border from the result of fun. See the 'TrimBorder ' parameter for more information.

## blockproc

The function pads blocks with borders extending beyond the image edges with zeros.

Default: [0 0] (no border)

## Destination

The destination for the output of blockproc. When you specify the 'Destination' parameter, blockproc does not return the processed image as an output argument, but instead writes the output to the 'Destination'. (You cannot request an output argument when the 'Destination' parameter is specified.)
Valid 'Destination' parameters are:

- TIFF filename: A string filename ending with '.tif'. If a file with this name already exists, it will be overwritten.
- ImageAdapter object: An instance of an ImageAdapter class. ImageAdapters provide an interface for reading and writing to arbitrary image file formats.
The 'Destination' parameter is useful when you expect your output to be too large to practically fit into memory. It provides a workflow for file-to-file image processing for arbitrarily large images.


## PadPartialBlocks

A logical scalar. When set to true, blockproc pads partial blocks to make them full-sized ( $M-$ by-N) blocks. Partial blocks arise when the image size is not exactly divisible by the block size. If they exist, partial blocks lie along the right and bottom edge of the image. The default is false, meaning that the function does not pad the partial blocks, but processes them as-is. blockproc uses zeros to pad partial blocks when necessary.

> Default: false

## PadMethod

## blockproc

The 'PadMethod' determines how blockproc will pad the image boundary. Options are:

- $X$ : Pads the image with a scalar $(X)$ pad value. By default $X==0$.
- 'replicate': Repeats border elements of image A.
- 'symmetric': Pads image A with mirror reflections of itself.


## TrimBorder

A logical scalar. When set to true, the blockproc function trims off border pixels from the output of the user function, fun. The function removes $V$ rows from the top and bottom of the output of fun, and $H$ columns from the left and right edges. The 'BorderSize' parameter defines $V$ and $H$. The default is true, meaning that the blockproc function automatically removes borders from the fun output.

Default: true

## UseParallel

A logical scalar. Enabling this mode of image processing requires the Parallel Computing Toolbox ${ }^{\text {TM }}$. When set to true, blockproc will attempt to run in parallel mode, distributing the processing across multiple workers (MATLAB sessions) in an open MATLAB pool. In parallel mode, the input image cannot be an ImageAdapter object. See the documentation for matlabpool for information on configuring your parallel environment.

> Default: false

File Format Support: Input and output files for blockproc (as specified by src_filename and the 'Destination' parameter) must have one of the following file types and must be named with one of the listed file extensions:

- Read/Write File Formats: TIFF (*.tif, *.tiff), JPEG2000 (*.jp2, *.j2c, *.j2k)


## blockproc

- Read-Only File Formats: JPEG2000 (*.jpf, *.jpx)


## Output <br> Arguments

## Definitions

## B

Output matrix.
A block struct is a MATLAB structure that contains the block data as well as other information about the block. Fields in the block struct are:

- block_struct.border: A two-element vector, [V H], that specifies the size of the vertical and horizontal padding around the block of data. (See the 'BorderSize' parameter in the Inputs section.)
- block_struct.blockSize: A two-element vector, [rows cols], that specifies the size of the block data. If a border has been specified, the size does not include the border pixels.
- block_struct.data: M-by-N or M-by-N-by-P matrix of block data
- block_struct.imageSize: A two-element vector, [rows cols], that specifies the full size of the input image.
- block_struct.location: A two-element vector, [row col], that specifies the position of the first pixel (minimum-row, minimum-column) of the block data in the input image. If a border has been specified, the location refers to the first pixel of the discrete block data, not the added border pixels.


## Examples Generate an image thumbnail:

```
fun = @(block_struct) imresize(block_struct.data,0.15);
I = imread('pears.png');
I2 = blockproc(I,[100 100],fun);
figure;
imshow(I);
figure;
imshow(I2);
```



Set the pixels in each 32 -by- 32 block to the standard deviation of the elements in that block:

```
fun = @(block_struct) ...
    std2(block_struct.data) * ones(size(block_struct.data));
I2 = blockproc('moon.tif',[32 32],fun);
figure;
imshow('moon.tif');
figure;
imshow(I2,[]);
```



Original Image


Standard Deviation Image

Switch the red and green bands of an RGB image and write the results to a new TIFF file:

## blockproc

```
I = imread('peppers.png');
fun = @(block_struct) block_struct.data(:,:,[2 1 3]);
blockproc(I,[200 200],fun,'Destination','grb_peppers.tif');
figure;
imshow('peppers.png');
figure;
imshow('grb_peppers.tif');
```



Original Image of Peppers


Recolored Image of Peppers

Convert a TIFF image into a new JPEG2000 image. Replace
'largeImage.tif' in the example below with the name of your file:

```
fun = @(block_struct) block_struct.data;
blockproc('largeImage.tif',[1024 1024],fun,...
    'Destination', 'New.jp2');
```

See Also colfilt | function_handle | "ImageAdapter" on page 2-2 | nlfilter
How To . "Anonymous Functions"

- "Parameterizing Functions"
- "Performing Distinct Block Operations"

Purpose Area of objects in binary image
Syntax total = bwarea (BW)
Description
total = bwarea(BW) estimates the area of the objects in binary image BW. total is a scalar whose value corresponds roughly to the total number of on pixels in the image, but might not be exactly the same because different patterns of pixels are weighted differently.

## Class <br> Support

BW can be numeric or logical. For numeric input, any nonzero pixels are considered to be on. The return value total is of class double.
bwarea estimates the area of all of the on pixels in an image by summing the areas of each pixel in the image. The area of an individual pixel is determined by looking at its 2 -by- 2 neighborhood. There are six different patterns, each representing a different area:

- Patterns with zero on pixels $($ area $=0)$
- Patterns with one on pixel (area $=1 / 4)$
- Patterns with two adjacent on pixels (area = 1/2)
- Patterns with two diagonal on pixels (area $=3 / 4$ )
- Patterns with three on pixels (area $=7 / 8$ )
- Patterns with all four on pixels $($ area $=1)$

Keep in mind that each pixel is part of four different 2 -by-2 neighborhoods. This means, for example, that a single on pixel surrounded by off pixels has a total area of 1 .

Examples Compute the area in the objects of a 256 -by- 256 binary image.

```
BW = imread('circles.png');
imshow(BW);
```



References [1] Pratt, William K., Digital Image Processing, New York, John Wiley
See Also bweuler | bwperim

## bwareaopen

## Purpose Remove small objects from binary image

```
Syntax
BW2 = bwareaopen(BW, P)
BW2 = bwareaopen(BW, P, conn)
```

BW2 = bwareaopen (BW, P) removes from a binary image all connected components (objects) that have fewer than $P$ pixels, producing another binary image, BW2. This operation is known as an area opening. The default connectivity is 8 for two dimensions, 26 for three dimensions, and conndef(ndims (BW), 'maximal') for higher dimensions.

BW2 = bwareaopen(BW, P, conn) specifies the desired connectivity. conn can have any of the following scalar values.

| Value | Meaning |
| :--- | :--- |
| Two-dimensional connectivities |  |
| 4 | 4-connected neighborhood |
| 8 | 8 -connected neighborhood |
| Three-dimensional connectivities |  |
| 6 | 6 -connected neighborhood |
| 18 | 18 -connected neighborhood |
| 26 | 26 -connected neighborhood |

Connectivity can be defined in a more general way for any dimension by using for conn a 3 -by- 3 -by-...-by- 3 matrix of 0 s and 1 s . The 1 -valued elements define neighborhood locations relative to the central element of conn. Note that conn must be symmetric about its central element.

BW can be a logical or numeric array of any dimension, and it must be nonsparse. The return value BW2 is of class logical.

## Algorithms The basic steps are

1 Determine the connected components:
$C C=$ bwconncomp(BW, conn);

2 Compute the area of each component:

S = regionprops(CC, 'Area');
3 Remove small objects:

```
L = labelmatrix(CC);
BW2 = ismember(L, find([S.Area] >= P));
```


## Examples

Remove all objects in the image text.png containing fewer than 50 pixels:

```
BW = imread('text.png');
BW2 = bwareaopen(BW, 50);
imshow(BW);
```


figure, imshow(BW2)

## bwareaopen



See Also
bwconncomp | conndef

## Purpose Trace region boundaries in binary image

Syntax
$B=$ bwboundaries(BW)
$B=$ bwboundaries(BW,conn)
$B=$ bwboundaries(BW, conn,options)
[B,L] = bwboundaries(...)
[B,L,N,A] = bwboundaries(...)
Description
$B=$ bwboundaries (BW) traces the exterior boundaries of objects, as well as boundaries of holes inside these objects, in the binary image BW. bwboundaries also descends into the outermost objects (parents) and traces their children (objects completely enclosed by the parents). BW must be a binary image where nonzero pixels belong to an object and 0 pixels constitute the background. The following figure illustrates these components.

bwboundaries returns B, a P-by- 1 cell array, where P is the number of objects and holes. Each cell in the cell array contains a Q-by-2 matrix. Each row in the matrix contains the row and column coordinates of a boundary pixel. Q is the number of boundary pixels for the corresponding region.
$B=$ bwboundaries (BW, conn) specifies the connectivity to use when tracing parent and child boundaries. conn can have either of the following scalar values.

## bwboundaries

| Value | Meaning |
| :--- | :--- |
| 4 | 4 -connected neighborhood |
| 8 | 8 -connected neighborhood. This is the default. |

$B=$ bwboundaries(BW,conn,options) specifies an optional argument, where options can have either of the following values:

| Value | Meaning |
| :--- | :--- |
| 'holes ' | Search for both object and hole boundaries. This is the <br> default. |
| 'noholes ' | Search only for object (parent and child) boundaries. This <br> can provide better performance. |

$[B, L]=$ bwboundaries(...) returns the label matrix $L$ as the second output argument. Objects and holes are labeled. L is a two-dimensional array of nonnegative integers that represent contiguous regions. The $k$ th region includes all elements in $L$ that have value $k$. The number of objects and holes represented by $L$ is equal to $\max (\mathrm{L}(:))$. The zero-valued elements of $L$ make up the background.
$[B, L, N, A]=$ bwboundaries (...) returns $N$, the number of objects found, and $A$, an adjacency matrix. The first $N$ cells in $B$ are object boundaries. A represents the parent-child-hole dependencies. A is a square, sparse, logical matrix with side of length $\max (\mathrm{L}(:))$, whose rows and columns correspond to the positions of boundaries stored in B.

The boundaries enclosed by a $\mathrm{B}\{\mathrm{m}\}$ as well as the boundary enclosing $B\{m\}$ can both be found using $A$ as follows:

```
enclosing_boundary = find(A(m,:));
enclosed_boundaries = find(A(:,m));
```

Class Support

BW can be logical or numeric and it must be real, two-dimensional, and nonsparse. $L$ and $N$ are double. $A$ is sparse logical.

## Examples Example 1

Read in and threshold an intensity image. Display the labeled objects using the jet colormap, on a gray background, with region boundaries outlined in white.

```
I = imread('rice.png');
BW = im2bw(I, graythresh(I));
[B,L] = bwboundaries(BW,'noholes');
imshow(label2rgb(L, @jet, [.5 .5 .5]))
hold on
for k = 1:length(B)
    boundary = B{k};
    plot(boundary(:,2), boundary(:,1), 'w', 'LineWidth', 2)
end
```


## Example 2

Read in and display a binary image. Overlay the region boundaries on the image. Display text showing the region number (based on the label matrix) next to every boundary. Additionally, display the adjacency matrix using the MATLAB spy function.
After the image is displayed, use the zoom tool to read individual labels.

```
BW = imread('blobs.png');
[B,L,N,A] = bwboundaries(BW);
figure, imshow(BW); hold on;
colors=['b' 'g' 'r' 'c' 'm' 'y'];
for k=1:length(B)
    boundary = B{k};
    cidx = mod(k,length(colors))+1;
    plot(boundary(:,2), boundary(:,1),...
            colors(cidx),'LineWidth',2);
    %randomize text position for better visibility
    rndRow = ceil(length(boundary)/(mod(rand*k,7)+1));
    col = boundary(rndRow,2); row = boundary(rndRow,1);
    h = text(col+1, row-1, num2str(L(row,col)));
    set(h,'Color',colors(cidx),...
            'FontSize',14,'FontWeight','bold');
```


## bwboundaries

```
end
figure; spy(A);
```


## Example 3

Display object boundaries in red and hole boundaries in green.
BW = imread('blobs.png');
[B,L,N] = bwboundaries(BW);
figure; imshow(BW); hold on;
for $k=1: l$ length $(B)$,
boundary = $\mathrm{B}\{\mathrm{k}\}$;
if(k > N)
plot(boundary (:,2),...
boundary(:,1),'g','LineWidth',2);
else
plot (boundary (:,2),...
boundary(:,1), 'r','LineWidth',2);
end
end

## Example 4

Display parent boundaries in red (any empty row of the adjacency matrix belongs to a parent) and their holes in green.

```
BW = imread('blobs.png');
[B,L,N,A] = bwboundaries(BW);
figure; imshow(BW); hold on;
for k=1:length(B),
    if(~sum(A(k,:)))
        boundary = B{k};
        plot(boundary(:,2),...
            boundary(:,1),'r','LineWidth',2);
        for l=find(A(:,k))'
            boundary = B{l};
            plot(boundary(:,2),...
                boundary(:,1),'g','LineWidth',2);
            end
```


# end end 

Algorithms The bwboundaries function implements the Moore-Neighbor tracing algorithm modified by Jacob's stopping criteria. This function is based on the boundaries function presented in the first edition of Digital Image Processing Using MATLAB[1].<br>References [1] Gonzalez, R. C., R. E. Woods, and S. L. Eddins, Digital Image Processing Using MATLAB, New Jersey, Pearson Prentice Hall, 2004.

See Also<br>bwlabel | bwlabeln | bwperim | bwtraceboundary

## bwconncomp

## Purpose Find connected components in binary image

Syntax $\quad \begin{aligned} & C C=\text { bwconncomp }(B W) \\ & C C=\text { bwconncomp }(B W, \text { conn })\end{aligned}$
Description
$C C=$ bwconncomp(BW) returns the connected components CC found in $B W$. The binary image BW can have any dimension. CC is a structure with four fields.

| Field | Description |
| :--- | :--- |
| Connectivity | Connectivity of the connected components (objects) |
| ImageSize | Size of BW |
| NumObjects | Number of connected components (objects) in BW |
| PixelIdxList | 1 -by-NumObjects cell array where the $k$ th element <br> in the cell array is a vector containing the linear <br> indices of the pixels in the $k$ th object. |

bwconncomp uses a default connectivity of 8 for two dimensions, 26 for three dimensions, and conndef(ndims(BW), 'maximal') for higher dimensions.
$C C=$ bwconncomp(BW, conn) specifies the desired connectivity for the connected components. conn can have the following scalar values.

| Value | Meaning |
| :--- | :--- |
| Two-dimensional connectivities |  |
| 4 | 4 -connected neighborhood |
| 8 | 8 -connected neighborhood |
| Three-dimensional connectivities |  |
| 6 | 6 -connected neighborhood |
| 18 | 18 -connected neighborhood |
| 26 | 26 -connected neighborhood |

Connectivity can be defined in a more general way for any dimension using a 3 -by- 3 -by- ... -by- 3 matrix of 0 s and 1 s . conn must be symmetric about its center element. The 1 -valued elements define neighborhood locations relative to conn.

The functions bwlabel, bwlabeln, and bwconncomp all compute connected components for binary images. bwconncomp replaces the use of bwlabel and bwlabeln. It uses significantly less memory and is sometimes faster than the other functions.

| Function | Input <br> Dimension | Output Form | Memory <br> Use | Connectivity |
| :--- | :--- | :--- | :--- | :--- |
| bwlabel | 2-D | Label matrix with <br> double-precision | High | 4 or 8 |
| bwlabeln | N-D | Double-precision <br> label matrix | High | Any |
| bwconncomp | N-D | CC struct | Low | Any |

## Tips

Class Support

## Examples

To extract features from a binary image using regionprops with default connectivity, just pass BW directly into regionprops (i.e., regionprops(BW)).

To compute a label matrix having more memory-efficient data type (e.g., uint8 versus double), use the labelmatrix function on the output of bwconncomp. See the documentation for each function for more information.

BW can be a logical or numeric array of any dimension, and it must be real and nonsparse. CC is a structure.

## Example 1

Calculate the centroids of the 3-D objects.

```
BW = cat(3, [1 1 0; 0 0 0; 1 0 0],...
    [0 1 0; 0 0 0; 0 1 0],...
```


## bwconncomp

[0 1 1 1; 0 0 0; 0 0 1]);
$C C=$ bwconncomp(BW);
S = regionprops(CC,'Centroid');

## Example 2

Erase the largest letter from the image.

```
BW = imread('text.png');
imshow(BW);
```

> The term watershed refers to a ridge that ...

$C C=$ bwconncomp (BW);
numPixels = cellfun(@numel,CC.PixelIdxList);
[biggest,idx] $=\max ($ numPixels $)$;
BW(CC.PixelIdxList\{idx\}) $=0$;
figure, imshow(BW);

The term watershed refers to a ridge that ...


Algorithms

See Also

The basic steps in finding the connected components are:
1 Search for the next unlabeled pixel, p.
2 Use a flood-fill algorithm to label all the pixels in the connected component containing $p$.

3 Repeat steps 1 and 2 until all the pixels are labelled.
bwlabel | bwlabeln | labelmatrix | regionprops

## bwconvhull

Purpose Generate convex hull image from binary image
Syntax CH = bwconvhull(BW)
CH = bwconvhull(BW, method) CH = bwconvhull(BW, 'objects', conn)
Description
Input ..... BW
Arguments$\mathrm{CH}=$ bwconvhull(BW) computes the convex hull of all objects in BW andreturns CH , a binary convex hull image.$\mathrm{CH}=$ bwconvhull(BW, method) specifies the desired method forcomputing the convex hull image.
CH = bwconvhull(BW, 'objects', conn) specifies the desiredconnectivity used when defining individual foreground objects. Theconn parameter is only valid when the method is 'objects'.
A logical 2-D image

## method

A string that can have the following values:

- 'union': Compute the convex hull of all foreground objects, treating them as a single object.
- 'objects': Compute the convex hull of each connected component of BW individually. CH contains the convex hulls of each connected component.

> Default: 'union'

## conn

Connectivity. Can have the following scalar values:

- 4: Two-dimensional, four-connected neighborhood.
- 8: Two-dimensional, eight-connected neighborhood.

Additionally, conn may be defined in a more general way, using a 3 -by- 3 matrix of 0 s and 1 s . The 1 -valued elements define neighborhood locations relative to conn's center element. conn must be symmetric about its center element.

## Default: 8

## Output Arguments

Examples

## CH

A logical, convex hull image, containing the binary mask of the convex hull of all foreground objects in BW.

Display the binary convex hull of an image:

```
subplot(2,2,1);
I = imread('coins.png');
imshow(I);
title('Original');
subplot(2,2,2);
BW = I > 100;
imshow(BW);
title('Binary');
subplot(2,2,3);
CH = bwconvhull(BW);
imshow(CH);
title('Union Convex Hull');
subplot(2,2,4);
CH_objects = bwconvhull(BW,'objects');
imshow(CH_objects);
title('Objects Convex Hull');
```


## bwconvhull



See Also
bwconncomp | bwlabel | labelmatrix | regionprops

## Purpose

Distance transform of binary image
Syntax
D = bwdist(BW)
[D,IDX] = bwdist(BW)
[D, IDX] = bwdist(BW,method)

## Description

D = bwdist(BW) computes the Euclidean distance transform of the binary image BW. For each pixel in BW, the distance transform assigns a number that is the distance between that pixel and the nearest nonzero pixel of BW. bwdist uses the Euclidean distance metric by default. BW can have any dimension. $D$ is the same size as BW.
[D, IDX] = bwdist(BW) also computes the closest-pixel map in the form of an index array, IDX. (The closest-pixel map is also called the feature map, feature transform, or nearest-neighbor transform.) IDX has the same size as BW and D. Each element of IDX contains the linear index of the nearest nonzero pixel of BW.
[D, IDX] = bwdist(BW,method) computes the distance transform, where method specifies an alternate distance metric. method can take any of the following values. The method string can be abbreviated.

| Method | Description |
| :--- | :--- |
| 'chessboard' | In 2-D, the chessboard distance between $\left(x_{1}, y_{1}\right)$ <br> and $\left(x_{2}, y_{2}\right)$ is $\max \left(\left\|x_{1}-x_{2}\right\|,\left\|y_{1}-y_{2}\right\|\right)$. |
| 'cityblock' | In 2-D, the cityblock distance between $\left(x_{1}, y_{1}\right)$ <br> and $\left(x_{2}, y_{2}\right)$ is $\left\|x_{1}-x_{2}\right\|+\left\|y_{1}-y_{2}\right\|$. |

## bwdist

| Method | Description |
| :--- | :--- |
| 'euclidean' | In 2-D, the Euclidean distance between $\left(x_{1}, y_{1}\right)$ <br> and $\left(x_{2}, y_{2}\right)$ is |
| $\quad \sqrt{\left(x_{1}-x_{2}\right)^{2}+\left(y_{1}-y_{2}\right)^{2}}$. |  |
| This is the default method. |  |

bwdist uses fast algorithms to compute the true Euclidean distance transform, especially in the 2-D case. The other methods are provided primarily for pedagogical reasons. However, the alternative distance transforms are sometimes significantly faster for multidimensional input images, particularly those that have many nonzero elements.

The function bwdist changed in version 6.4 (R2009b). Previous versions of the Image Processing Toolbox used different algorithms for computing the Euclidean distance transform and the associated label matrix. If you need the same results produced by the previous implementation, use the function bwdist_old.

BW can be numeric or logical, and it must be nonsparse. D is a single matrix with the same size as BW. The class of IDX depends on the number of elements in the input image, and is determined using the following table.

| Class | Range |
| :--- | :--- |
| 'uint32' | numel $(\mathrm{BW})<=2^{32}-1$ |
| 'uint64' | numel $(\mathrm{BW})>=2^{32}$ |

## Examples

Compute the Euclidean distance transform.

```
bw = zeros(5,5); bw(2,2) = 1; bw(4,4) = 1
bw =
\begin{tabular}{lllll}
0 & 0 & 0 & 0 & 0 \\
0 & 1 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 0
\end{tabular}
[D,IDX] = bwdist(bw)
D =
\begin{tabular}{rrrrr}
1.4142 & 1.0000 & 1.4142 & 2.2361 & 3.1623 \\
1.0000 & 0 & 1.0000 & 2.0000 & 2.2361 \\
1.4142 & 1.0000 & 1.4142 & 1.0000 & 1.4142 \\
2.2361 & 2.0000 & 1.0000 & 0 & 1.0000 \\
3.1623 & 2.2361 & 1.4142 & 1.0000 & 1.4142
\end{tabular}
IDX =
\begin{tabular}{rrrrr}
7 & 7 & 7 & 7 & 7 \\
7 & 7 & 7 & 7 & 19 \\
7 & 7 & 7 & 19 & 19 \\
7 & 7 & 19 & 19 & 19 \\
7 & 19 & 19 & 19 & 19
\end{tabular}
```

In the nearest-neighbor matrix IDX the values 7 and 19 represent the position of the nonzero elements using linear matrix indexing. If a pixel contains a 7, its closest nonzero neighbor is at linear position 7 .

Compare the 2-D distance transforms for each of the supported distance methods. In the figure, note how the quasi-Euclidean distance

## bwdist

transform best approximates the circular shape achieved by the Euclidean distance method.

```
bw = zeros(200,200); bw(50,50) = 1; bw(50,150) = 1;
bw(150,100) = 1;
D1 = bwdist(bw,'euclidean');
D2 = bwdist(bw,'cityblock');
D3 = bwdist(bw,'chessboard');
D4 = bwdist(bw,'quasi-euclidean');
figure
subplot(2,2,1), subimage(mat2gray(D1)), title('Euclidean')
hold on, imcontour(D1)
subplot(2,2,2), subimage(mat2gray(D2)), title('City block')
hold on, imcontour(D2)
subplot(2,2,3), subimage(mat2gray(D3)), title('Chessboard')
hold on, imcontour(D3)
subplot(2,2,4), subimage(mat2gray(D4)), title('Quasi-Euclidean')
hold on, imcontour(D4)
```



Compare isosurface plots for the distance transforms of a 3-D image containing a single nonzero pixel in the center.

```
bw = zeros(50,50,50); bw(25,25,25) = 1;
D1 = bwdist(bw);
D2 = bwdist(bw,'cityblock');
D3 = bwdist(bw,'chessboard');
D4 = bwdist(bw,'quasi-euclidean');
figure
subplot(2,2,1), isosurface(D1,15), axis equal, view(3)
camlight, lighting gouraud, title('Euclidean')
subplot(2,2,2), isosurface(D2,15), axis equal, view(3)
camlight, lighting gouraud, title('City block')
subplot(2,2,3), isosurface(D3,15), axis equal, view(3)
camlight, lighting gouraud, title('Chessboard')
subplot(2,2,4), isosurface(D4,15), axis equal, view(3)
camlight, lighting gouraud, title('Quasi-Euclidean')
```



## Algorithms

For Euclidean distance transforms, bwdist uses the fast algorithm described in
[1] Maurer, Calvin, Rensheng Qi, and Vijay Raghavan, "A Linear Time Algorithm for Computing Exact Euclidean Distance Transforms

## bwdist

of Binary Images in Arbitrary Dimensions," IEEE Transactions on Pattern Analysis and Machine Intelligence, Vol. 25, No. 2, February 2003, pp. 265-270.

For cityblock, chessboard, and quasi-Euclidean distance transforms, bwdist uses the two-pass, sequential scanning algorithm described in
[2] Rosenfeld, Azriel and John Pfaltz, "Sequential operations in digital picture processing," Journal of the Association for Computing Machinery, Vol. 13, No. 4, 1966, pp. 471-494.

The different distance measures are achieved by using different sets of weights in the scans, as described in
[3] Paglieroni, David, "Distance Transforms: Properties and Machine Vision Applications," Computer Vision, Graphics, and Image Processing: Graphical Models and Image Processing, Vol. 54, No. 1, January 1992, pp. 57-58.

See Also bwulterode | watershed
How To . "Distance Transform"

| Purpose | Geodesic distance transform of binary image |
| :---: | :---: |
| Syntax | $\begin{aligned} & \mathrm{D}=\text { bwdistgeodesic(BW,mask) } \\ & \mathrm{D}=\text { bwdistgeodesic(BW,C,R) } \\ & \mathrm{D}=\text { bwdistgeodesic(BW,ind) } \\ & \mathrm{D}=\text { bwdistgeodesic(...,method) } \end{aligned}$ |
| Description | D = bwdistgeodesic(BW,mask) computes the geodesic distance transform, given the binary image BW and the seed locations specified by mask. Regions where BW is true represent valid regions that can be traversed in the computation of the distance transform. Regions where BW is false represent constrained regions that cannot be traversed in the distance computation. For each true pixel in BW, the geodesic distance transform assigns a number that is the constrained distance between that pixel and the nearest true pixel in mask. Output matrix D contains geodesic distances. <br> D = bwdistgeodesic(BW,C,R) computes the geodesic distance transform of the binary image BW. Vectors $C$ and $R$ contain the column and row coordinates of the seed locations. <br> $\mathrm{D}=$ bwdistgeodesic(BW,ind) computes the geodesic distance transform of the binary image $B W$. ind is a vector of linear indices of seed locations. <br> D = bwdistgeodesic(..., method) specifies an alternate distance metric. |
| Input Arguments | BW <br> Binary image. <br> mask |

Logical image the same size as BW that specifies seed locations.

## C,R

## bwdistgeodesic

Numeric vectors that contain the positive integer column and row coordinates of the seed locations. Coordinate values are valid C,R subscripts in BW.

## ind

Numeric vector of positive integer, linear indices of seed locations.

## method

Type of distance metric. method can have any of these values.

| Method | Description |
| :--- | :--- |
| 'cityblock' | In 2-D, the cityblock distance between $\left(x_{1}, y_{1}\right)$ and <br> $\left(x_{2}, y_{2}\right)$ is $\left\|x_{1}-x_{2}\right\|+\left\|y_{1}-y_{2}\right\|$. |
| 'chessboard' | The chessboard distance is <br> $\max \left(\left\|x_{1}-x_{2}\right\|,\left\|y_{1}-y_{2}\right\|\right)$. |
| 'quasi- <br> euclidean' | The quasi-Euclidean distance is <br> $\left\|x_{1}-x_{2}\right\|+(\sqrt{2}-1)\left\|y_{1}-y_{2}\right\|,\left\|x_{1}-x_{2}\right\|>\left\|y_{1}-y_{2}\right\|$ <br> $(\sqrt{2}-1)\left\|x_{1}-x_{2}\right\|+\left\|y_{1}-y_{2}\right\|$, otherwise. |

## Default: 'chessboard'

## Output Arguments

## Class Support

## D

Numeric array of class single, with the same size as input BW, that contains geodesic distances.
$B W$ is a logical matrix. $C, R$, and ind are numeric vectors that contain positive integer values. $D$ is a numeric array of class single that has the same size as the input BW.

```
Examples the output \(D(10,5)\) has a value of Inf.
```

```
BW = [\begin{array}{llllllllllll}{1}&{1}&{1}&{1}&{1}&{1}&{1}&{1}&{1}&{1;}&{\ldots}\end{array}]
```

BW = [$$
\begin{array}{llllllllllll}{1}&{1}&{1}&{1}&{1}&{1}&{1}&{1}&{1}&{1;}&{\ldots}\end{array}
$$]
1 1 1 1 1 1 1 0 0 0 1 1;...
1 1 1 1 1 1 1 0 0 0 1 1;...
1 1 1 1 1 1 0 0 1 1;...
1 1 1 1 1 1 0 0 1 1;...
1 1 1 1 1 1 1 0 0 1 1;...
1 1 1 1 1 1 1 0 0 1 1;...
0 0 0 0 0 1 0 0 1 0;...
0 0 0 0 0 1 0 0 1 0;...
0 0 0 0 1 1 0 1 1 0;...
0 0 0 0 1 1 0 1 1 0;...
0 1 0 0 1 1 0 0 0 0;...

```
    0 1 0 0 1 1 0 0 0 0;...
```




```
    0 111 0 0 0 1 1 1 0;...
```

    0 111 0 0 0 1 1 1 0;...
    0 0 0 0 1 0 0 0 0 0];
    0 0 0 0 1 0 0 0 0 0];
    BW = logical(BW);
BW = logical(BW);
C = [11 2 3 3 3];
C = [11 2 3 3 3];
R = [3 3 3 1 2];
R = [3 3 3 1 2];
D = bwdistgeodesic(BW,C,R);

```
D = bwdistgeodesic(BW,C,R);
```

Compute the geodesic distance transformation of BW based on the seed locations specified by vectors C and R. Output pixels for which BW is false have undefined geodesic distance and contain NaN values. Because there is no connected path from the seed locations to element BW $(10,5)$,

# Algorithms bwdistgeodesic uses the geodesic distance algorithm described in Soille, P., Morphological Image Analysis: Principles and Applications, 2nd Edition, Secaucus, NJ, Springer-Verlag, 2003, pp. 219-221. 

## See Also

bwdist | graydist

## bweuler

Purpose Euler number of binary image
Syntax eul = bweuler (BW, n)
Description
eul = bweuler (BW, $n$ ) returns the Euler number for the binary image BW. The return value eul is a scalar whose value is the total number of objects in the image minus the total number of holes in those objects. The argument $n$ can have a value of either 4 or 8 , where 4 specifies 4 -connected objects and 8 specifies 8 -connected objects; if the argument is omitted, it defaults to 8 .

Class Support

BW can be numeric or logical and it must be real, nonsparse, and two-dimensional. The return value eul is of class double.

```
Examples BW = imread('circles.png');
imshow(BW);
```


bweuler (BW)
ans $=$

Algorithms<br>References [1] Horn, Berthold P. K., Robot Vision, New York, McGraw-Hill, 1986, pp. 73-77.<br>[2] Pratt, William K., Digital Image Processing, New York, John Wiley \& Sons, Inc., 1991, p. 633.<br>See Also bwmorph | bwperim

## bwhitmiss

Purpose Binary hit-miss operation

```
Syntax BW2 = bwhitmiss(BW1,SE1,SE2)
BW2 = bwhitmiss(BW1,INTERVAL)
```


## Examples

Perform the hit-miss operation on a binary image using an interval.

$$
\left.\mathrm{bw}=\begin{array}{llllll}
{[0} & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 1 & 1 & 0 & 0 \\
0 & 1 & 1 & 1 & 1 & 0 \\
0 & 1 & 1 & 1 & 1 & 0 \\
0 & 0 & 1 & 1 & 0 & 0 \\
0 & 0 & 1 & 0 & 0 & 0
\end{array}\right]
$$

```
interval = [\begin{array}{lll}{0}&{-1}&{-1}\end{array}]
        clc
```

bw2 = bwhitmiss(bw,interval)
bw2 =

| 0 | 0 | 0 | 0 | 0 | 0 |
| :--- | :--- | :--- | :--- | :--- | :--- |
| 0 | 0 | 0 | 1 | 0 | 0 |
| 0 | 0 | 0 | 0 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 |

See Also imdilate | imerode | strel

## bwlabel

## Purpose Label connected components in 2-D binary image

Syntax $\quad L=\operatorname{bwlabel}(B W, n)$
[L, num] = bwlabel(BW, n)
Description $L=\operatorname{bwlabel}(B W, n)$ returns a matrix $L$, of the same size as $B W$, containing labels for the connected objects in BW. The variable $n$ can have a value of either 4 or 8 , where 4 specifies 4 -connected objects and 8 specifies 8 -connected objects. If the argument is omitted, it defaults to 8 .

The elements of $L$ are integer values greater than or equal to 0 . The pixels labeled 0 are the background. The pixels labeled 1 make up one object; the pixels labeled 2 make up a second object; and so on.
[ $L$, num] $=$ bwlabel $(B W, n)$ returns in num the number of connected objects found in BW.
The functions bwlabel, bwlabeln, and bwconncomp all compute connected components for binary images. bwconncomp replaces the use of bwlabel and bwlabeln. It uses significantly less memory and is sometimes faster than the other functions.

|  | Input <br> Dimension | Output Form | Memory <br> Use | Connectivity |
| :--- | :--- | :--- | :--- | :--- |
| bwlabel | 2-D | Double-precision <br> label matrix | High | 4 or 8 |
| bwlabeln | N-D | Double-precision <br> label matrix | High | Any |
| bwconncomp | N-D | CC struct | Low | Any |

## Tips

## Using find with bwlabel

You can use the MATLAB find function in conjunction with bwlabel to return vectors of indices for the pixels that make up a specific object. For example, to return the coordinates for the pixels in object 2, enter the following:

$$
[r, c]=\text { find }(b w l a b e l(B W)==2)
$$

You can display the output matrix as a pseudocolor indexed image. Each object appears in a different color, so the objects are easier to distinguish than in the original image. For more information, see label2rgb.

## Using labelmatrix and regionprops

To compute a label matrix having a more memory-efficient data type (e.g., uint8 versus double), use the labelmatrix function on the output of bwconncomp. For more information, see the reference page for each function.

To extract features from a binary image using regionprops with default connectivity, just pass BW directly into regionprops, i.e., regionprops(BW).

## Class Support

BW can be logical or numeric, and it must be real, two-dimensional, and nonsparse. L is of class double.

## Examples

Label components using 4 -connected objects. Notice objects 2 and 3 ; with 8 -connected labeling, bwlabel would consider these a single object rather than two separate objects.


## bwlabel

| 1 | 1 | 1 | 0 | 2 | 2 | 0 | 0 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | 1 | 1 | 0 | 2 | 2 | 0 | 0 |
| 1 | 1 | 1 | 0 | 0 | 0 | 3 | 0 |
| 1 | 1 | 1 | 0 | 0 | 0 | 3 | 0 |
| 1 | 1 | 1 | 0 | 0 | 0 | 3 | 0 |
| 1 | 1 | 1 | 0 | 0 | 3 | 3 | 0 |
| 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| [ $\mathrm{r}, \mathrm{c}]=\mathrm{find}(\mathrm{L}==2)$; |  |  |  |  |  |  |  |
| $\mathrm{rc}=$ |  |  |  |  |  |  |  |
| 2 | 5 |  |  |  |  |  |  |
| 3 | 5 |  |  |  |  |  |  |
| 2 | 6 |  |  |  |  |  |  |
| 3 | 6 |  |  |  |  |  |  |

[^0]
## Purpose

Label connected components in binary image
Syntax
L = bwlabeln(BW)
[L, NUM] = bwlabeln(BW)
[L, NUM] = bwlabeln(BW, conn)

## Description

$L=$ bwlabeln(BW) returns a label matrix, $L$, containing labels for the connected components in BW. The input image BW can have any dimension; $L$ is the same size as $B W$. The elements of $L$ are integer values greater than or equal to 0 . The pixels labeled 0 are the background. The pixels labeled 1 make up one object; the pixels labeled 2 make up a second object; and so on. The default connectivity is 8 for two dimensions, 26 for three dimensions, and conndef(ndims(BW), 'maximal') for higher dimensions.
[L, NUM] = bwlabeln(BW) returns in NUM the number of connected objects found in BW.
[L, NUM] = bwlabeln(BW, conn) specifies the desired connectivity. conn can have any of the following scalar values.

| Value | Meaning |
| :--- | :--- |
| Two-dimensional connectivities |  |
| 4 | 4 -connected neighborhood |
| 8 | 8 -connected neighborhood |
| Three-dimensional connectivities |  |
| 6 | 6 -connected neighborhood |
| 18 | 18 -connected neighborhood |
| 26 | 26 -connected neighborhood |

Connectivity can also be defined in a more general way for any dimension by using for conn a 3 -by- 3 -by- ...-by- 3 matrix of 0 s and 1 s . The 1 -valued elements define neighborhood locations relative to the

## bwlabeln

central element of conn. Note that conn must be symmetric about its central element.

The functions bwlabel, bwlabeln, and bwconncomp all compute connected components for binary images. bwconncomp replaces the use of bwlabel and bwlabeln. It uses significantly less memory and is sometimes faster than the older functions.

| Function | Input <br> Dimension | Output Form | Memory <br> Use | Connectivity |
| :--- | :--- | :--- | :--- | :--- |
| bwlabel | 2-D | Double-precision <br> label matrix | High | 4 or 8 |
| bwlabeln | N-D | Double-precision <br> label matrix | High | Any |
| bwconncomp | N-D | CC struct | Low | Any |

## Tips

To extract features from a binary image using regionprops with default connectivity, just pass BW directly into regionprops, i.e., regionprops(BW).

To compute a label matrix having a more memory-efficient data type (e.g., uint8 versus double), use the labelmatrix function on the output of bwconncomp:

C = bwconncomp(BW);
L = labelmatrix(CC);
CC = bwconncomp(BW, conn);
S = regionprops(CC);

## Class

Support
BW can be numeric or logical, and it must be real and nonsparse. L is of class double.

Examples Calculate the centroids of the 3-D objects.

```
BW = cat(3, [1 1 0; 0 0 0; 1 0 0],...
```

```
    [0 1 0; 0 0 0; 0 1 0],...
    [0 1 1; 0 0 0; 0 0 1])
bwlabeln(BW)
ans(:,:,1) =
    1 1 0
    0 0
    2 0 0
ans(:,:,2) =
    0}1
    0 0 0
    0 0
ans(:,:,3) =
    0 1 1
    0 0 0
    0 0 2
```


## Algorithms

## References

bwlabeln uses the following general procedure:
1 Scan all image pixels, assigning preliminary labels to nonzero pixels and recording label equivalences in a union-find table.

2 Resolve the equivalence classes using the union-find algorithm [1].
3 Relabel the pixels based on the resolved equivalence classes.
[1] Sedgewick, Robert, Algorithms in C, 3rd Ed., Addison-Wesley, 1998, pp. 11-20.

## bwlabeln

See Also bwconncomp | bwlabel | labelmatrix | label2rgb | regionprops

Purpose Nonlinear filtering using lookup tables
Syntax $\quad A=$ bwlookup (BW, lut)
Description

## Input Arguments

 A at the targeted position.- A is the same size as BW
- A is the same data type as lut generation, see "Supported Functions".


## BW - Input image

binary image | grayscale image

A = bwlookup(BW,lut) performs a $2-$ by -2 or 3 -by -3 nonlinear neighborhood filtering operation on binary or grayscale image BW and returns the results in output image A. The neighborhood processing determines an integer index value used to access values in lookup table lut. The fetched lut value becomes the pixel value in output image
bwlookup supports the generation of efficient, production-quality C/C++ code from MATLAB. For best results, specify an input image of class logical. To see a complete list of toolbox functions that support code

Input image transformed by nonlinear neighborhood filtering operation, specified as either a grayscale or binary (logical) image. In the case of numeric values, non-zero pixels are considered true which is equivalent to logical 1.

## Data Types

single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32 | uint64 | logical

## lut - Lookup table of output pixel values

16- or 256 -element vector
Lookup table of output pixel values, specified as a 16 - or 256 -element vector. The size of lut determines which of the two neighborhood operations is performed.

## bwlookup

- If lut contains 16 data elements, then the neighborhood matrix is 2-by-2.
- If lut contains 256 data elements, then the neighborhood matrix is $3-$ by -3 .


## Data Types

single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32
| uint64 | logical

## Output Arguments

## A - Output image

binary image | grayscale image
Output image, returned as a grayscale or binary image whose size matches BW, and whose distribution of pixel values are determined by the content of lut.

- A is the same size as BW
- A is the same data type as lut


## Data Types

single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32 | uint64 | logical

## Examples

## 2-by-2 Neighborhood Erosion of Binary Image

This example performs an erosion along the edges of a binary image.
Vector lut is constructed such that the filtering operation places a 1 at the targeted pixel location in image A only when all 4 pixels in the 2 -by- 2 neighborhood of BW are set to 1 . For all other 2 -by- 2 neighborhood combinations in BW, the targeted pixel location in image A receives a 0.

```
% Construct lut so it is 'true' only
% when all 4 2-by2 locations equal 1
lutfun = @(x)(sum(x(:))==4);
lut = makelut(lutfun,2);
% load binary image
BW1 = imread('text.png');
```

```
% Perform 2x2 Neighborhood processing
% with 16 element vector lut
BW2 = bwlookup(BW1,lut);
% show Zoomed before and after images
figure;
h1 = subplot(1,2,1); imshow(BW1), axis off; title('BW1')
h2 = subplot(1,2,2); imshow(BW2); axis off; title('BW2')
% do a 16X Zoom to see effects of erosion on text
set(h1,'Ylim',[.5 64.5]); set(h1,'Xlim',[.5 64.5]);
set(h2,'Ylim',[.5 64.5]); set(h2,'Xlim',[.5 64.5]);
lut =
0
0
0
0
0
O
O
O
O
0
0
0
0
0
O
1
```



The first step in each iteration of the filtering operation performed by bwlookup entails computing the index into vector lut based on the binary pixel pattern of the neighborhood matrix on image BW. The value in lut accessed at index, lut (index), is inserted into output image A at the targeted pixel location. This results in image A being the same data type as vector lut.

Since there is a 1-to- 1 correspondence in targeted pixel locations, image $A$ is the same size as image BW. If the targeted pixel location is on an edge of image BW and if any part of the $2 \times 2$ or $3 \times 3$ neighborhood matrix extends beyond the image edge, then these non-image locations are padded with 0 in order to perform the filtering operation.

## Mapping from Neighborhood Matrices to Binary Notation

The following figures show the mapping from binary 0 and 1 patterns in the neighborhood matrices to its binary representation. Adding 1 to the binary representation yields index which is used to access lut.

For 2-by-2 neighborhoods, length(lut) is 16 . There are four pixels in each neighborhood, and two possible states for each pixel, so the total number of permutations is $2^{4}=16$.


Targeted Pixel Position for 2×2 Neighborhood


Color coded mapping from Pixel Patterns to Binary Representation for $2 \times 2$ Matrix

## bwlookup

Example: This example demonstrates how the pixel pattern in a $2 \times 2$ matrix determines which entry in lut is placed in the targeted pixel location.

Create random 16 element lut vector containing uint8 data

```
scurr = rng; % save current seed state
rng('default') % always generate same set of random numbers
lut = uint8( round( 255*rand(16,1) ) ) % generate 16 uint8
rng(scurr); % restore
```

lut =
208
231
32
233
161
25
71
139
244
246
40
248
244
124
204
36

Create a small 2 x 2 image; targeted pixel location will be at location BW $(1,1)$.

```
BW = [1 0; 0 1]
```

$B W=$

```
1 0
```

By referring to the color coded mapping figure above, the binary representation for this $2 \times 2$ neighborhood can be computed as shown in the code snippet below. The logical 1 at $\mathrm{BW}(1,1)$ corresponds to blue in the figure which maps to the Least Signficant Bit (LSB) at position 0 in the 4 -bit binary representation $\left(, 2^{0}=1\right)$. The logical 1 at $\mathrm{BW}(2,2)$ is red which maps to the Most Significant Bit (MSB) at position 3 in the 4 -bit binary representation $\left(2^{3}=8\right)$.

```
% BW(1,1): blue square; sets bit position O on right
% BW(2,2): red square; sets bit position 3 on left
binNot = '1 0 0 1'; % binary representation of 2x2 neighborhood matr
X = bin2dec( binNot ); % convert from binary to decimal
index = X + 1 % add 1 to compute index value for uint8 vector lut
A11 = lut(index) % value at A(1,1)
index =
```

    10
    A11 =
246

The above calculation predicts that output image A should contain the value 246 at targeted position $A(1,1)$.

```
A = bwlookup(BW,lut) % perform filtering
```

$A=$
24632
161231

A(1,1) does in fact equal 246 .

## bwlookup

Note For a more robust way to perform image erosion, see function imerode.

For 3-by-3 neighborhoods, length(lut) is 512. There are nine pixels in each neighborhood, and two possible states for each pixel, so the total number of permutations is $2^{9}=512$.

The process for computing the binary representation of 3 x 3 neighborhood processing is the same as shown above for 2 x 2 neighborhoods.


Figure 1: Color coded mapping from Pixel Patterns to

## bwmorph

Purpose
Morphological operations on binary images
Syntax
BW2 = bwmorph(BW,operation)
BW2 = bwmorph(BW,operation,n)
Description
BW2 = bwmorph(BW,operation) applies a specific morphological operation to the binary image BW .
BW2 $=$ bwmorph(BW,operation, $n$ ) applies the operation $n$ times. $n$ can be Inf, in which case the operation is repeated until the image no longer changes.
operation is a string that can have one of the values listed below.

| Operation | Description |
| :---: | :---: |
| 'bothat' | Performs the morphological "bottom hat" operation, returning the image minus the morphological closing of the image (dilation followed by erosion). |
| 'branchpoints' | Find branch points of skeleton. For example: $\begin{array}{lllllllllll} 0 & 0 & 1 & 0 & 0 & & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & \text { becomes } & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 1 & 1 & 1 & & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{array}$ |
| 'bridge' | Bridges unconnected pixels, that is, sets 0 -valued pixels to 1 if they have two nonzero neighbors that are not connected. For example: |


| Operation | Description |
| :---: | :---: |
| 'clean' | Removes isolated pixels (individual 1s that are surrounded by 0 s ), such as the center pixel in this pattern. |
| 'close' | Performs morphological closing (dilation followed by erosion). |
| 'diag' | Uses diagonal fill to eliminate 8 -connectivity of the background. For example: |
| 'dilate' | Performs dilation using the structuring element ones (3). |
| 'endpoints' | Finds end points of skeleton. For example: $\begin{array}{lllllllll} 1 & 0 & 0 & 0 & & 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & \text { becomes } & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & & 0 & 0 & 0 & 0 \end{array}$ |
| 'erode ' | Performs erosion using the structuring element ones (3). |


| Operation | Description |
| :---: | :---: |
| 'fill' | Fills isolated interior pixels (individual 0s that are surrounded by 1s), such as the center pixel in this pattern. |
| 'hbreak' | Removes H-connected pixels. For example: |
| 'majority' | Sets a pixel to 1 if five or more pixels in its 3-by-3 neighborhood are 1 s ; otherwise, it sets the pixel to 0 . |
| 'open' | Performs morphological opening (erosion followed by dilation). |
| 'remove' | Removes interior pixels. This option sets a pixel to 0 if all its 4 -connected neighbors are 1 , thus leaving only the boundary pixels on. |
| 'shrink' | With $\mathrm{n}=$ Inf, shrinks objects to points. It removes pixels so that objects without holes shrink to a point, and objects with holes shrink to a connected ring halfway between each hole and the outer boundary. This option preserves the Euler number. |
| 'skel' | With $\mathrm{n}=$ Inf, removes pixels on the boundaries of objects but does not allow objects to break apart. The pixels remaining make up the image skeleton. This option preserves the Euler number. |


| Operation | Description |
| :---: | :---: |
| 'spur' | Removes spur pixels. For example: |
| 'thicken' | With $\mathrm{n}=$ Inf, thickens objects by adding pixels to the exterior of objects until doing so would result in previously unconnected objects being 8 -connected. This option preserves the Euler number. |
| 'thin' | With $n=$ Inf, thins objects to lines. It removes pixels so that an object without holes shrinks to a minimally connected stroke, and an object with holes shrinks to a connected ring halfway between each hole and the outer boundary. This option preserves the Euler number. See "Algorithms" on page 3-75 for more detail. |
| 'tophat' | Performs morphological "top hat" operation, returning the image minus the morphological opening of the image (erosion followed by dilation). |

bwmorph supports the generation of efficient, production-quality C/C++ code from MATLAB. The text string specifying the operation must be a constant and, for best results, specify an input image of class logical. To see a complete list of toolbox functions that support code generation, see "Supported Functions".

[^1]The input image BW can be numeric or logical. It must be 2 -D, real and nonsparse. The output image BW2 is of class logical.

## bwmorph



BW2 = bwmorph(BW,'remove'); figure, imshow(BW2)


BW3 = bwmorph(BW,'skel', Inf); figure, imshow(BW3)


## References

## Algorithms

[1] Haralick, Robert M., and Linda G. Shapiro, Computer and Robot Vision, Vol. 1, Addison-Wesley, 1992.
[2] Kong, T. Yung and Azriel Rosenfeld, Topological Algorithms for Digital Image Processing, Elsevier Science, Inc., 1996.
[3] Lam, L., Seong-Whan Lee, and Ching Y. Suen, "Thinning Methodologies-A Comprehensive Survey," IEEE Transactions on Pattern Analysis and Machine Intelligence, Vol 14, No. 9, September 1992, page 879, bottom of first column through top of second column.
[4] Pratt, William K., Digital Image Processing, John Wiley \& Sons, Inc., 1991.

When used with the 'thin' option, bwmorph uses the following algorithm (References [3]):

1 Divide the image into two distinct subfields in a checkerboard pattern.

2 In the first subiteration, delete pixel $p$ from the first subfield if and only if the conditions $G_{1}, G_{2}$, and $G_{3}$ are all satisfied.

3 In the second subiteration, delete pixel $p$ from the second subfield if and only if the conditions $G_{1}, G_{2}$, and $G_{3}{ }^{\prime}$ are all satisfied.

## bwmorph

## Condition G1:

$$
X_{H}(p)=1
$$

where

$$
\begin{aligned}
& X_{H}(p)=\sum_{i=1}^{4} b_{i} \\
& b_{i}=\left\{\begin{array}{l}
1, \text { if } x_{2 i-1}=0 \text { and }\left(x_{2 i}=1 \text { or } x_{2 i+1}=1\right) \\
0, \text { otherwise }
\end{array}\right.
\end{aligned}
$$

$x_{1}, x_{2}, \ldots, x_{8}$ are the values of the eight neighbors of $p$, starting with the east neighbor and numbered in counter-clockwise order.

## Condition G2:

$$
2 \leq \min \left\{n_{1}(p), n_{2}(p)\right\} \leq 3
$$

where

$$
\begin{aligned}
& n_{1}(p)=\sum_{k=1}^{4} x_{2 k-1} \vee x_{2 k} \\
& n_{2}(p)=\sum_{k=1}^{4} x_{2 k} \vee x_{2 k+1}
\end{aligned}
$$

## Condition G3:

$$
\left(x_{2} \vee x_{3} \vee \bar{x}_{8}\right) \wedge x_{1}=0
$$

## Condition G3':

$$
\left(x_{6} \vee x_{7} \vee \bar{x}_{4}\right) \wedge x_{5}=0
$$

The two subiterations together make up one iteration of the thinning algorithm. When the user specifies an infinite number of iterations ( $n=$ Inf), the iterations are repeated until the image stops changing. The conditions are all tested using applylut with precomputed lookup tables.

See Also bweuler | bwperim | imdilate | imerode
Purpose Pack binary image

## Syntax BWP = bwpack (BW)

Description
BWP = bwpack(BW) packs the uint8 binary image BW into the uint32 array BWP, which is known as a packed binary image. Because each 8-bit pixel value in the binary image has only two possible values, 1 and 0 , bwpack can map each pixel to a single bit in the packed output image.
bwpack processes the image pixels by column, mapping groups of 32 pixels into the bits of a uint 32 value. The first pixel in the first row corresponds to the least significant bit of the first uint32 element of the output array. The first pixel in the 32nd input row corresponds to the most significant bit of this same element. The first pixel of the 33rd row corresponds to the least significant bit of the second output element, and so on. If BW is M-by-N, then BWP is ceil (M/32) - by-N. This figure illustrates how bwpack maps the pixels in a binary image to the bits in a packed binary image.


Binary image packing is used to accelerate some binary morphological operations, such as dilation and erosion. If the input to imdilate or imerode is a packed binary image, the functions use a specialized routine to perform the operation faster.
bwunpack is used to unpack packed binary images.

## Class Support

BW can be logical or numeric, and it must be 2-D, real, and nonsparse. BWP is of class uint32.

## Examples

Pack, dilate, and unpack a binary image:

```
BW = imread('text.png');
BWp = bwpack(BW);
BWp_dilated = imdilate(BWp,ones(3,3),'ispacked');
BW_dilated = bwunpack(BWp_dilated, size(BW,1));
```


## bwpack

See Also bwunpack | imdilate | imerode

## Purpose

Find perimeter of objects in binary image
Syntax
BW2 = bwperim(BW1)
BW2 = bwperim(BW1, conn)

BW2 = bwperim(BW1) returns a binary image containing only the perimeter pixels of objects in the input image BW1. A pixel is part of the perimeter if it is nonzero and it is connected to at least one zero-valued pixel. The default connectivity is 4 for two dimensions, 6 for three dimensions, and conndef (ndims (BW), 'minimal') for higher dimensions.

BW2 = bwperim(BW1, conn) specifies the desired connectivity. conn can have any of the following scalar values.

| Value | Meaning |
| :--- | :--- |
| Two-dimensional connectivities |  |
| 4 | 4 -connected neighborhood |
| 8 | 8 -connected neighborhood |
| Three-dimensional connectivities |  |
| 6 | 6 -connected neighborhood |
| 18 | 18 -connected neighborhood |
| 26 | 26 -connected neighborhood |

Connectivity can also be defined in a more general way for any dimension by using for conn a 3 -by-3-by-...-by-3 matrix of 0's and 1's. The 1 -valued elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

Class
Support
BW1 must be logical or numeric, and it must be nonsparse. BW2 is of class logical.

## bwperim

Examples Find the perimeter of objects in an image mask.

```
BW1 = imread('circbw.tif');
BW2 = bwperim(BW1,8);
imshow(BW1)
figure, imshow(BW2)
```



See Also
bwarea | bwboundaries | bweuler | bwtraceboundary | conndef | imfill

Purpose
Select objects in binary image
Syntax
BW2 $=$ bwselect ( $B W, c, r, n$ )
BW2 = bwselect(BW, n)
[BW2,idx] = bwselect(...)
BW2 = bwselect( $x, y, B W, x i, y i, n)$
[ $x, y$, BW2,idx, xi,yi] = bwselect(...)
Description
BW2 $=$ bwselect $(B W, c, r, n)$ returns a binary image containing the objects that overlap the pixel ( $r, c$ ). $r$ and $c$ can be scalars or equal-length vectors. If $r$ and $c$ are vectors, BW2 contains the sets of objects overlapping with any of the pixels $(r(k), c(k))$. $n$ can have a value of either 4 or 8 (the default), where 4 specifies 4 -connected objects and 8 specifies 8 -connected objects. Objects are connected sets of on pixels (i.e., pixels having a value of 1 ).
BW2 = bwselect (BW, n) displays the image BW on the screen and lets you select the ( $r, c$ ) coordinates using the mouse. If you omit BW, bwselect operates on the image in the current axes. Use normal button clicks to add points. Pressing Backspace or Delete removes the previously selected point. A shift-click, right-click, or double-click selects the final point; pressing Return finishes the selection without adding a point.
[BW2,idx] = bwselect(...) returns the linear indices of the pixels belonging to the selected objects.

BW2 = bwselect ( $\mathrm{x}, \mathrm{y}, \mathrm{BW}, \mathrm{xi}, \mathrm{yi}, \mathrm{n}$ ) uses the vectors x and y to establish a nondefault spatial coordinate system for BW1. xi and yi are scalars or equal-length vectors that specify locations in this coordinate system.
[ $x, y, B W 2, i d x, x i, y i]=$ bwselect(...) returns the XData and YData in $x$ and $y$, the output image in BW2, linear indices of all the pixels belonging to the selected objects in idx, and the specified spatial coordinates in xi and yi.

If bwselect is called with no output arguments, the resulting image is displayed in a new figure.

## bwselect

Class Support

Examples

The input image BW can be logical or numeric and must be 2-D and nonsparse. The output image BW2 is of class logical.

```
BW1 = imread('text.png');
c = [43 185 212];
r = [38 68 181];
BW2 = bwselect(BW1,c,r,4);
imshow(BW1), figure, imshow(BW2)
```



```
bwlabel | imfill | impixel | roipoly | roifill
```


## Purpose Trace object in binary image

Syntax $\quad B=$ bwtraceboundary (BW, $P$, fstep $)$
$B=$ bwtraceboundary (BW,P,fstep,conn)
B = bwtraceboundary(...,N,dir)

## Description

$B=$ bwtraceboundary (BW, P, fstep) traces the outline of an object in binary image bw. Nonzero pixels belong to an object and 0 pixels constitute the background. P is a two-element vector specifying the row and column coordinates of the point on the object boundary where you want the tracing to begin.
fstep is a string specifying the initial search direction for the next object pixel connected to $P$. You use strings such as ' $N$ ' for north, ' $N E$ ' for northeast, to specify the direction. The following figure illustrates all the possible values for fstep.

bwtraceboundary returns B , a Q -by-2 matrix, where Q is the number of boundary pixels for the region. B holds the row and column coordinates of the boundary pixels.
$B=$ bwtraceboundary (bw, P, fstep, conn) specifies the connectivity to use when tracing the boundary. conn can have either of the following scalar values.

## bwtraceboundary

| Value | Meaning |
| :--- | :--- |
| 4 | 4 -connected neighborhood |
|  | Note With this connectivity, fstep is limited to the <br> following values: ' $N$ ', ' E ', 'S', and 'W'. |
| 8 | 8 -connected neighborhood. This is the default. |

$\mathrm{B}=$ bwtraceboundary(..., N, dir) specifies n , the maximum number of boundary pixels to extract, and dir, the direction in which to trace the boundary. When $N$ is set to Inf, the default value, the algorithm identifies all the pixels on the boundary. dir can have either of the following values:

| Value | Meaning |
| :--- | :--- |
| 'clockwise' | Search in a clockwise direction. This is the <br> default. |
| 'counterclockwise' | Search in counterclockwise direction. |

BW can be logical or numeric and it must be real, 2-D, and nonsparse. B, $P$, conn, and $N$ are of class double. dir and fstep are strings.

Examples Read in and display a binary image. Starting from the top left, project a beam across the image searching for the first nonzero pixel. Use the location of that pixel as the starting point for the boundary tracing. Including the starting point, extract 50 pixels of the boundary and overlay them on the image. Mark the starting points with a green x. Mark beams that missed their targets with a red x .

```
BW = imread('blobs.png');
imshow(BW,[]);
s=size(BW);
for row = 2:55:s(1)
    for col=1:s(2)
```

```
        if BW(row,col),
        break;
        end
    end
    contour = bwtraceboundary(BW, [row, col], 'W', 8, 50,\ldots
                                    'counterclockwise');
    if(~isempty(contour))
        hold on;
        plot(contour(:,2),contour(:,1),'g','LineWidth', 2);
        hold on;
        plot(col, row,'gx','LineWidth',2);
    else
        hold on; plot(col, row,'rx','LineWidth',2);
    end
end
bwboundaries, bwperim
```


## bwulterode

## Purpose Ultimate erosion

```
Syntax BW2 = bwulterode(BW)
BW2 = bwulterode(BW,method,conn)
```

BW2 = bwulterode (BW) computes the ultimate erosion of the binary image BW. The ultimate erosion of BW consists of the regional maxima of the Euclidean distance transform of the complement of BW. The default connectivity for computing the regional maxima is 8 for two dimensions, 26 for three dimensions, and conndef(ndims(BW), 'maximal') for higher dimensions.

BW2 = bwulterode(BW,method,conn) specifies the distance transform method and the regional maxima connectivity. method can be one of the strings 'euclidean', 'cityblock', 'chessboard', and 'quasi-euclidean'.
conn can have any of the following scalar values.

| Value | Meaning |
| :--- | :--- |
| Two-dimensional connectivities |  |
| 4 | 4-connected neighborhood |
| 8 | 8-connected neighborhood |
| Three-dimensional connectivities |  |
| 6 | 6-connected neighborhood |
| 18 | 18-connected neighborhood |
| 26 | 26 -connected neighborhood |

Connectivity can be defined in a more general way for any dimension by using for conn a 3 -by- 3 -by... - by- 3 matrix of 0's and 1's. The 1 -valued elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

| Class | BW can be numeric or logical and it must be nonsparse. It can have any |
| :--- | :--- |
| Support | dimension. The return value BW2 is always a logical array. |
| Examples | originalBW = imread('circles.png'); ; <br> imshow(originalBW) <br> ultimateErosion $=$ bwulterode(originalBW) ; <br> figure, imshow(ultimateErosion) |
| See Also | bwdist \| conndef | imregionalmax |

Purpose Unpack binary image
Syntax $\quad B W=$ bwunpack $(B W P, m)$
Description
BW = bwunpack(BWP,m) unpacks the packed binary image BWP. BWP is a uint32 array. When it unpacks BWP, bwunpack maps the least significant bit of the first row of BWP to the first pixel in the first row of BW. The most significant bit of the first element of BWP maps to the first pixel in the 32 nd row of BW , and so on. BW is $\mathrm{M}-\mathrm{by}-\mathrm{N}$, where $N$ is the number of columns of BWP. If $m$ is omitted, its default value is 32*size (BWP, 1).

Binary image packing is used to accelerate some binary morphological operations, such as dilation and erosion. If the input to imdilate or imerode is a packed binary image, the functions use a specialized routine to perform the operation faster.
bwpack is used to create packed binary images.

## Class <br> Support

Examples Pack, dilate, and unpack a binary image.

```
bw = imread('text.png');
bwp = bwpack(bw);
bwp_dilated = imdilate(bwp,ones(3,3),'ispacked');
bw_dilated = bwunpack(bwp_dilated, size(bw,1));
```

See Also bwpack | imdilate | imerode

## Purpose Create checkerboard image

Syntax I = checkerboard
I = checkerboard(n)
I = checkerboard( $n, p, q$ )

## Description

Examples
Create a checkerboard where the side of every square is 20 pixels in length.

I = checkerboard(20);imshow(I)


Create a rectangular checkerboard that is 2 tiles in height and 3 tiles wide.

J = checkerboard(10,2,3);
figure, imshow(J)


Create a black and white checkerboard.
K = (checkerboard > 0.5);
figure, imshow(K)


See Also cp2tform | imtransform | maketform

| Purpose | Rearrange matrix columns into blocks |
| :---: | :---: |
| Syntax | $A=\operatorname{col2im}(B,[m \mathrm{n}],[\mathrm{mm} n \mathrm{n}], \mathrm{distinct'})$ |
|  | $A=\operatorname{col2im}\left(B,[m \mathrm{n}],[\mathrm{mm} \mathrm{nn}], \mathrm{sliding}{ }^{\text {( }}\right.$ ) |

Description
$A=\operatorname{col2im}(B,[m n],[m m n n], ' d i s t i n c t ')$ rearranges each column of $B$ into a distinct $m$-by- $n$ block to create the matrix $A$ of size mm-by-nn. If $B=[A 11(:) \quad A 21(:) \quad A 12(:) \quad A 22(:)]$, where each column has length $m * n$, then $A=[A 11$ A12; A21 A22] where each Aij is m-by-n.
$A=\operatorname{col} 2 i m(B,[m n],[m m n n], ' s l i d i n g ')$ rearranges the row vector $B$ into a matrix of size $(m m-m+1)-$ by- $(n n-n+1)$. B must be a vector of size 1-by- $(m m-m+1)$ * $(n n-n+1)$. B is usually the result of processing the output of im2col(...,'sliding') using a column compression function (such as sum).
$\operatorname{col} 2 \mathrm{im}(B,[m \mathrm{n}],[\mathrm{mm} n \mathrm{n}])$ is the same as col2im(B, [mn], [mm nn],'sliding').

Class B can be logical or numeric. The return value A is of the same class as B.
Support
Examples $\quad B=\operatorname{reshape}(\text { uint8(1:25),[5 5] })^{\prime}$
$C=\operatorname{im2col}\left(B,\left[\begin{array}{ll}1 & 5\end{array}\right)\right.$
$A=\operatorname{col2im}(C,[15],[55], ' d i s t i n c t ')$
See Also blockproc | colfilt | im2col | nlfilter

| Purpose | Columnwise neighborhood operations |
| :--- | :--- |
| Syntax | $B=\operatorname{colfilt}(A,[m \quad n]$, block_type, fun $)$ |
|  | $B=\operatorname{colfilt}(A,[m \quad n],[m b l o c k$ nblock $]$, block_type,fun $)$ |
|  | $B=\operatorname{colfilt}(A, ' i n d e x e d ', \ldots)$ |

$B=$ colfilt(A, [m n],block_type,fun) processes the image $A$ by rearranging each m-by-n block of A into a column of a temporary matrix, and then applying the function fun to this matrix. fun must be a function handle. Parameterizing Functions, in the MATLAB Mathematics documentation, explains how to provide additional parameters to the function fun. The function colfilt zero-pads A, if necessary.

Before calling fun, colfilt calls im2col to create the temporary matrix. After calling fun, colfilt rearranges the columns of the matrix back into m-by-n blocks using col2im.
block_type is a string that can have one of the values listed in this table.

Note colfilt can perform operations similar to blockproc and nlfilter, but often executes much faster.

| Value | Description |
| :--- | :--- |
| 'distinct' | Rearranges each m-by-n distinct block of A into a column <br> in a temporary matrix, and then applies the function <br> fun to this matrix. fun must return a matrix the same <br> size as the temporary matrix. colfilt then rearranges <br> the columns of the matrix returned by fun into m-by-n <br> distinct blocks. |
| 'sliding' | Rearranges each m-by-n sliding neighborhood of A into <br> a column in a temporary matrix, and then applies the <br> function fun to this matrix. fun must return a row <br> vector containing a single value for each column in the |


| Value | Description |
| :--- | :--- |

temporary matrix. (Column compression functions such as sum return the appropriate type of output.) colfilt then rearranges the vector returned by fun into a matrix the same size as A.
$B=$ colfilt(A,[m n],[mblock nblock],block_type,fun) processes the matrix $A$ as above, but in blocks of size mblock-by-nblock to save memory. Note that using the [mblock nblock] argument does not change the result of the operation.
$B=$ colfilt(A,'indexed',...) processes A as an indexed image, padding with 0's if the class of A is uint8 or uint16, or 1's if the class of $A$ is double or single.

Note To save memory, the colfilt function might divide A into subimages and process one subimage at a time. This implies that fun may be called multiple times, and that the first argument to fun may have a different number of columns each time.

## Class <br> Support <br> Examples

The input image A can be of any class supported by fun. The class of B depends on the class of the output from fun.

Set each output pixel to the mean value of the input pixel's 5-by- 5 neighborhood.

```
I = imread('tire.tif');
imshow(I)
I2 = uint8(colfilt(I,[5 5],'sliding',@mean));
figure, imshow(I2)
```

See Also blockproc | col2im | function_handle | im2col| nlfilter

## How To

- "Anonymous Functions"
- "Parameterizing Functions"


## Purpose Create connectivity array

```
Syntax
conn = conndef(num_dims,type)
```


## Description

conn = conndef(num_dims, type) returns the connectivity array defined by type for num_dims dimensions. type can have either of the values listed in this table.

| Value | Description |
| :--- | :--- |
| 'minimal' | Defines a neighborhood whose neighbors are touching <br> the central element on an (N-1)-dimensional surface, <br> for the N-dimensional case. |
| 'maximal' | Defines a neighborhood including neighbors <br> that touch the central element in any way; it is <br> ones(repmat (3,1,NUM_DIMS)). |

Several Image Processing Toolbox functions use conndef to create the default connectivity input argument.

Examples
The minimal connectivity array for two dimensions includes the neighbors touching the central element along a line.

```
conn1 = conndef(2,'minimal')
conn1 =
\begin{tabular}{lll}
0 & 1 & 0 \\
1 & 1 & 1 \\
0 & 1 & 0
\end{tabular}
```

The minimal connectivity array for three dimensions includes all the neighbors touching the central element along a face.

```
conndef(3,'minimal')
ans(:,:,1) =
    0 0 0
```

| 0 | 1 | 0 |
| :---: | :---: | :---: |
| 0 | 0 | 0 |
| ans $(:,:, 2)$ | $=$ |  |
| 0 | 1 | 0 |
| 1 | 1 | 1 |
| 0 | 1 | 0 |
|  |  |  |
| ans $(:,:, 3)$ | $=$ |  |
| 0 | 0 | 0 |
| 0 | 1 | 0 |
| 0 | 0 | 0 |

The maximal connectivity array for two dimensions includes all the neighbors touching the central element in any way.

```
conn2 = conndef(2,'maximal')
conn2 =
    1 1 1
    1 1 1
    1 1 1
```

Purpose 2-D convolution matrix
Syntax T = convmtx2(H,m,n)
T = convmtx2(H,[m n])
Description $\mathrm{T}=$ convmtx2 $(\mathrm{H}, \mathrm{m}, \mathrm{n})$ returns the convolution matrix T for the matrix$H$. If $X$ is an m-by-n matrix, then reshape ( $T * X(:)$, $\operatorname{size}(H)+[m n]-1)$ isthe same as conv2 $(\mathrm{X}, \mathrm{H})$.$\mathrm{T}=$ convmtx2 $(\mathrm{H},[\mathrm{m} \mathrm{n}])$ returns the convolution matrix, where thedimensions m and n are a two-element vector.
Class Support
See Also
Purpose Find corner points in image

| Syntax | C = corner(I) |
| :---: | :---: |
|  | $C=\operatorname{corner}(\mathrm{I}$, method) |
|  | C = corner (I, N) |
|  | C = corner(I, method, N ) |
|  | C = corner (..., Name, Value) |

Description

Tips

Input
Arguments
$C=$ corner(I) detects corners in image I and returns them in matrix $C$.
C = corner(I, method) detects corners in image I using the specified method.

C = corner(I, N) detects corners in image I and returns a maximum of N corners.
$C=$ corner(I, method, $N$ ) detects corners using the specified method and maximum number of corners.

C = corner(..., Name, Value) specifies parameters and corresponding values that control various aspects of the corner detection algorithm.

The corner and cornermetric functions both detect corners in images. For most applications, use the streamlined corner function to find corners in one step. If you want greater control over corner selection, use the cornermetric function to compute a corner metric matrix and then write your own algorithm to find peak values.

## I

A grayscale or binary image.

## method

The algorithm used to detect corners. Supported methods are:

- 'Harris': The Harris corner detector.
- 'MinimumEigenvalue ': Shi \& Tomasi's minimum eigenvalue method.


## Default: 'Harris'

## N

The maximum number of corners the corner function can return.

Default: 200

## Name-Value Pair Arguments

Specify 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 and value pair arguments in any order as Name1, Value1, ... , NameN, ValueN.

## FilterCoefficients

A vector, V , of filter coefficients for the separable smoothing filter. The outer product, $\mathrm{V}^{*} \mathrm{~V}^{\prime}$, gives the full filter kernel.

Default: fspecial('gaussian',[5 1],1.5)

## QualityLevel

A scalar value, $Q$, where $0<Q<1$, specifying the minimum accepted quality of corners. When candidate corners have corner metric values less than $Q$ * max(corner metric), the toolbox rejects them. Use larger values of $Q$ to remove erroneous corners.

Default: 0.01

## SensitivityFactor

A scalar value, $K$, where $0<K<0.25$, specifying the sensitivity factor used in the Harris detection algorithm. The smaller the value of $K$, the more likely the algorithm is to detect sharp corners. Use this parameter with the 'Harris' method only.

Default: 0.04

## Output <br> Arguments

## Class Support

Examples

```
I = checkerboard(50,2,2);
C = corner(I);
imshow(I);
hold on
plot(C(:,1), C(:,2), 'r*');
```



Algorithms
The corner function performs nonmaxima suppression on candidate corners, and corners are at least two pixels apart.

See Also
cornermetric
How To . "Detecting Corners Using the corner Function"

| Purpose | Create corner metric matrix from image |
| :--- | :--- |
| Description $\quad$CM = cornermetric (I) generates a corner metric matrix for the <br> grayscale or logical image I. The corner metric, CM, is used to detect <br> corner features in I and is the same size as I. Larger values in CM <br> correspond to pixels in I with a higher likelihood of being a corner <br> feature. |  |
| CM = cornermetric (I, method) generates a corner metric matrix <br> for the grayscale or logical image I using the specified method. Valid <br> values for method are: |  |


| Value | Description |
| :--- | :--- |
| 'Harris' | The Harris corner detector. This is the <br> default method. |
| 'MinimumEigenvalue' | Shi and Tomasi's minimum eigenvalue <br> method. |

CM = cornermetric(..., param1, val1, param2, val2, ...) generates a corner metric matrix for $I$, specifying parameters and corresponding values that control various aspects of the corner metric calculation algorithm. Parameters include:

| Parameter | Description |
| :--- | :--- |
| 'FilterCoefficients' | A vector, V, of filter coefficients for <br> the separable smoothing filter. This <br> parameter is valid with the 'Harris' <br> and 'MinimumEigenvalue' methods. <br> The outer product, $V * V$ ', gives the <br> full filter kernel. The default is <br> fspecial('gaussian' , [5 1], 1.5). |
| 'SensitivityFactor' | A scalar k, $0<k<0.25$, specifying the <br> sensitivity factor used in the Harris <br> detection algorithm. For smaller values <br> of $k$, the algorithm is more likely to |

## Parameter $\quad$ Description

detect sharper corners. This parameter is only valid with the 'Harris' method. Default value: 0.04

## Tips

Class
Support

## Examples Find corner features in grayscale image.

First generate a corner metric matrix.

```
I = imread('pout.tif');
I = I(1:150,1:120);
subplot(1,3,1);
imshow(I);
title('Original Image');
CM = cornermetric(I);
```

Adjust corner metric for viewing.

```
CM_adjusted = imadjust(CM);
subplot(1,3,2);
imshow(CM_adjusted);
title('Corner Metric');
```

Find and display some corner features.

```
corner_peaks = imregionalmax(CM);
corner_idx = find(corner_peaks == true);
[r g b] = deal(I);
```

```
r(corner_idx) = 255;
g(corner_idx) = 255;
b(corner_idx) = 0;
RGB = cat(3,r,g,b);
subplot(1,3,3);
imshow(RGB);
title('Corner Points');
```

The following figure shows the output of these operations.


See Also
corner | edge | immovie | imshow

## Purpose

2-D correlation coefficient

## Syntax

$r=\operatorname{corr2}(A, B)$
Description
$r=\operatorname{corr2}(A, B)$ computes the correlation coefficient between $A$ and $B$, where $A$ and $B$ are matrices or vectors of the same size.

Class Support

Examples Compute the correlation coefficient between an image and the same image processed with a median filter.

```
I = imread('pout.tif');
J = medfilt2(I);
R = corr2(I,J)
R =
```

$$
0.9959
$$

Algorithms
corr2 computes the correlation coefficient using

$$
r=\frac{\sum_{m} \sum_{n}\left(A_{m n}-\bar{A}\right)\left(B_{m n}-\bar{B}\right)}{\sqrt{\left(\sum_{m} \sum_{n}\left(A_{m n}-\bar{A}\right)^{2}\right)\left(\sum_{m} \sum_{n}\left(B_{m n}-\bar{B}\right)^{2}\right)}}
$$

where $\bar{A}=$ mean2(A), and $\bar{B}=\operatorname{mean2(B).}$

## See Also

std2 | corrcoef

Purpose
Infer spatial transformation from control point pairs

```
Syntax
```

```
TFORM = cp2tform(input_points, base_points, transformtype)
```

TFORM = cp2tform(input_points, base_points, transformtype)
TFORM = cp2tform(CPSTRUCT, transformtype)
TFORM = cp2tform(CPSTRUCT, transformtype)
[TFORM, input_points, base_points] =
[TFORM, input_points, base_points] =
cp2tform(CPSTRUCT, ...)
cp2tform(CPSTRUCT, ...)
TFORM = cp2tform(input_points, base_points, 'polynomial',
TFORM = cp2tform(input_points, base_points, 'polynomial',
order)
order)
TFORM = cp2tform(CPSTRUCT, 'polynomial',order)
TFORM = cp2tform(CPSTRUCT, 'polynomial',order)
TFORM = cp2tform(input_points, base_points,
TFORM = cp2tform(input_points, base_points,
'piecewise linear')
'piecewise linear')
TFORM = cp2tform(CPSTRUCT, 'piecewise linear')
TFORM = cp2tform(CPSTRUCT, 'piecewise linear')
TFORM = cp2tform(input_points, base_points, 'lwm', N)
TFORM = cp2tform(input_points, base_points, 'lwm', N)
TFORM = cp2tform(CPSTRUCT, 'lwm', N)
TFORM = cp2tform(CPSTRUCT, 'lwm', N)
[TFORM, input_points, base_points, input_points_bad,
[TFORM, input_points, base_points, input_points_bad,
base_points_bad] = cp2tform(input_points, base_points,
base_points_bad] = cp2tform(input_points, base_points,
'piecewise linear')
'piecewise linear')
[TFORM, input_points, base_points, input_points_bad,
[TFORM, input_points, base_points, input_points_bad,
base_points_bad] = cp2tform(CPSTRUCT,
base_points_bad] = cp2tform(CPSTRUCT,
'piecewise linear')

```
'piecewise linear')
```


## Description

TFORM = cp2tform(input_points, base_points, transformtype) infers a spatial transformation from control point pairs and returns this transformation as a TFORM structure.

TFORM $=$ cp2tform(CPSTRUCT, transformtype) works on a CPSTRUCT structure that contains the control point matrices for the input and base images. The Control Point Selection Tool, cpselect, creates the CPSTRUCT.
[TFORM, input_points, base_points] = cp2tform(CPSTRUCT, ...) returns the control points that were used in input_points and base_points. Unmatched and predicted points are not used. See cpstruct2pairs.

TFORM = cp2tform(input_points, base_points, 'polynomial', order) lets you specify the order of the polynomials to use.

TFORM $=$ cp2tform(CPSTRUCT, 'polynomial',order) works on a CPSTRUCT structure.

TFORM = cp2tform(input_points, base_points, 'piecewise linear') creates a Delaunay triangulation of the base control points, and maps corresponding input control points to the base control points. The mapping is linear (affine) for each triangle and continuous across the control points but not continuously differentiable as each triangle has its own mapping.

TFORM = cp2tform(CPSTRUCT, 'piecewise linear') works on a CPSTRUCT structure.

TFORM = cp2tform(input_points, base_points, 'lwm', N) creates a mapping by inferring a polynomial at each control point using neighboring control points. The mapping at any location depends on a weighted average of these polynomials. You can optionally specify the number of points, $N$, used to infer each polynomial. The $N$ closest points are used to infer a polynomial of order 2 for each control point pair. If you omit N , it defaults to 12 . N can be as small as 6 , but making N small risks generating ill-conditioned polynomials.

TFORM $=$ cp2tform(CPSTRUCT, 'lwm', $N$ ) works on a CPSTRUCT structure.
[TFORM, input_points, base_points, input_points_bad, base_points_bad] = cp2tform(input_points, base_points, 'piecewise linear') returns the control points that were used in input_points and base_points and the control points that were eliminated because they were middle vertices of degenerate fold-over triangles in input_points_bad and base_points_bad.
[TFORM, input_points, base_points, input_points_bad, base_points_bad] = cp2tform(CPSTRUCT, 'piecewise linear') works on a CPSTRUCT structure.

- When transformtype is 'nonreflective similarity', 'similarity', 'affine', 'projective', or 'polynomial', and input_points and base_points (or CPSTRUCT) have the minimum
number of control points needed for a particular transformation, cp2tform finds the coefficients exactly.
- If input_points and base_points have more than the minimum number of control points, a least-squares solution is found. See mldivide.
- When either input_points or base_points has a large offset with respect to their origin (relative to range of values that it spans), cp2tform shifts the points to center their bounding box on the origin before fitting a TFORM structure. This enhances numerical stability and is handled transparently by wrapping the origin-centered TFORM within a custom TFORM that automatically applies and undoes the coordinate shift as needed. As a result, fields (T) can give different results for different coordinate inputs, even for the same transformation type.


## Input Arguments

## input_points

$m$-by- 2 , double matrix containing the $x$ - and $y$-coordinates of control points in the image you want to transform.

## base_points

$m$-by-2, double matrix containing the $x$ - and $y$-coordinates of control points in the base image.

## transformtype

Specifies the type of spatial transformation to infer. The cp2tform function requires a minimum number of control point pairs to infer a structure of each transform type. The following table lists all the transformation types supported by cp2tform in order of complexity. The 'lwm' and 'polynomial' transform types can each take an optional, additional parameter.

Transformation Types

| Transformation <br> Type | Description | Minimum <br> Number <br> of Control <br> Point Pairs | Example |
| :--- | :--- | :--- | :--- |
| 'nonreflective <br> similarity' | Use this transformation when shapes <br> in the input image are unchanged, <br> but the image is distorted by some <br> combination of translation, rotation, <br> and scaling. Straight lines remain <br> straight, and parallel lines are still <br> parallel. | 2 |  |
| 'similarity' | Same as 'nonreflective <br> similarity ' with the addition <br> of optional reflection. | 3 |  |
| 'affine' | Use this transformation when shapes <br> in the input image exhibit shearing. <br> Straight lines remain straight, and <br> parallel lines remain parallel, but <br> rectangles become parallelograms. | 3 |  |
| 'projective' | Use this transformation when the <br> scene appears tilted. Straight lines <br> remain straight, but parallel lines <br> converge toward vanishing points that <br> might or might not fall within the <br> image. | 4 |  |
| 'polynomial' | Use this transformation when objects <br> in the image are curved. The higher <br> the order of the polynomial, the better <br> the fit, but the result can contain more <br> curves than the base image. | 6 (order 2) <br> (order 3) | 15 (order 4) |

## cp2tform

| Transformation <br> Type | Description | Minimum <br> Number <br> of Control <br> Point Pairs | Example |
| :--- | :--- | :--- | :--- |
| 'piecewise <br> linear' | Use this transformation when parts of <br> the image appear distorted differently. | 4 | 6 (12 |
| 'lwm' | Use this transformation (local <br> weighted mean), when the distortion <br> varies locally and piecewise linear is <br> not sufficient. | recommended) |  |

## CPSTRUCT

Structure containing control point matrices for the input and base images. Use the Control Point Selection Tool (cpselect) to create the CPSTRUCT.

## 'polynomial',order

Specifies the order of polynomials to use. order can be 2,3 , or 4.

## Default: 3

## 'piecewise linear'

Linear for each piece and continuous, not continuously differentiable.

## 'lwm'

Local weighted mean.

## N

Number of points.

## Output Arguments

## TFORM

Structure containing the spatial transformation.

## input_points

Input control points that were used to infer the spatial transformation. Unmatched and predicted points are not used.

## base_points

Base control points that were used to infer the spatial transformation. Unmatched and predicted points are not used.

## input_points_bad

Input control points that were eliminated because they were determined to be outliers.

## base_points_bad

Base control points that were eliminated because they were determined to be outliers.

## Examples

Transform an image, use the cp2tform function to return the transformation, and compare the angle and scale of the TFORM to the angle and scale of the original transformation:

```
I = checkerboard;
J = imrotate(I,30);
base_points = [11 11; 41 71];
input_points = [14 44; 70 81];
cpselect(J,I,input_points,base_points);
t = cp2tform(input_points,base_points,'nonreflective similarity');
% Recover angle and scale by checking how a unit vector
% parallel to the x-axis is rotated and stretched.
u = [0 1];
v = [0 0];
[x, y] = tformfwd(t, u, v);
dx = x(2) - x(1);
dy = y(2) - y(1);
```

```
angle = (180/pi) * atan2(dy, dx)
scale = 1 / sqrt(dx^2 + dy^2)
```


## Algorithms

cp2tform uses the following general procedure:
1 Use valid pairs of control points to infer a spatial transformation or an inverse mapping from output space ( $x, y$ ) to input space $(x, y)$ according to transformtype.

2 Return the TFORM structure containing spatial transformation.
The procedure varies depending on the transformtype.

## Nonreflective Similarity

Nonreflective similarity transformations can include a rotation, a scaling, and a translation. Shapes and angles are preserved. Parallel lines remain parallel. Straight lines remain straight.

Let
sc = scale*cos(angle)
ss = scale*sin(angle)
[u v] = [x y 1] * [ sc -ss
ss sc
tx ty]
Solve for sc, ss, tx, and ty.

## Similarity

Similarity transformations can include rotation, scaling, translation, and reflection. Shapes and angles are preserved. Parallel lines remain parallel. Straight lines remain straight.

Let
$\mathrm{sc}=\mathrm{s}^{*} \cos ($ theta)
ss = s*sin(theta)

$$
\left.\left[\begin{array}{ll}
u & v
\end{array}\right]=\left[\begin{array}{lll}
x & y & 1
\end{array}\right] * \begin{array}{ll}
{\left[\begin{array}{l}
s c \\
s
\end{array}\right.} & -a^{*}-s s \\
s s & a * s c \\
t x & t y
\end{array}\right]
$$

Solve for sc, ss, tx, ty, and a. If a = -1, reflection is included in the transformation. If a $=1$, reflection is not included in the transformation.

## Affine

In an affine transformation, the $x$ and $y$ dimensions can be scaled or sheared independently and there can be a translation. Parallel lines remain parallel. Straight lines remain straight. Nonreflective similarity transformations are a subset of affine transformations.
For an affine transformation,
$\left[\begin{array}{ll}u & v\end{array}\right]=\left[\begin{array}{lll}x & y & 1\end{array}\right]$ * Tinv
Tinv is a 3-by-2 matrix. Solve for the six elements of Tinv:

```
t_affine = cp2tform(input_points,base_points,'affine');
```

The coefficients of the inverse mapping are stored in t_affine.tdata.Tinv.
At least three control-point pairs are needed to solve for the six unknown coefficients.

## Projective

In a projective transformation, quadrilaterals map to quadrilaterals. Straight lines remain straight. Affine transformations are a subset of projective transformations.
For a projective transformation,

```
[up vp wp] = [x y w] * Tinv
```

where

$$
u=u p / w p
$$

$v=v p / w p$

Tinv is a 3-by-3 matrix.
Assuming

```
Tinv = [ A D G;
    B E H;
    C F I ];
u = (Ax + By + C) /(Gx + Hy + I)
v = (Dx + Ey + F)/(Gx + Hy + I)
```

Solve for the nine elements of Tinv:
t_proj = cp2tform(input_points,base_points,'projective');
The coefficients of the inverse mapping are stored in t_proj.tdata.Tinv.
At least four control-point pairs are needed to solve for the nine unknown coefficients.

Note An affine or projective transformation can also be expressed like this, for a 3-by-2 Tinv:
$\left[\begin{array}{ll}u & ]^{\prime}\end{array} \operatorname{Tinv}^{\prime} *\left[\begin{array}{lll}x & y & 1\end{array}{ }^{\prime}\right.\right.$
Or, like this, for a 3-by-3 Tinv:
[u v 1]' = Tinv' * [ $x$ y 1]'

## Polynomial

In a polynomial transformation, polynomial functions of $x$ and $y$ determine the mapping.

## Second-Order Polynomials

For a second-order polynomial transformation,
$\left[\begin{array}{llllll}u & v\end{array}\right]=\left[\begin{array}{llll}1 & x & y & x^{*} y \\ x^{\wedge} 2 & y^{\wedge} 2\end{array}\right]$ * Tinv
Both $u$ and $v$ are second-order polynomials of $x$ and $y$. Each second-order polynomial has six terms. To specify all coefficients, Tinv has size 6 -by- 2 .
t_poly_ord2 = cp2tform(input_points, base_points,'polynomial');

The coefficients of the inverse mapping are stored in t_poly_ord2.tdata.
At least six control-point pairs are needed to solve for the 12 unknown coefficients.

## Third-Order Polynomials

For a third-order polynomial transformation:
$\left[\begin{array}{llllllll} \\ u & v\end{array}\right]=\left[\begin{array}{llllll}1 & x & y & x^{*} y & x^{\wedge} 2 & y^{\wedge} 2 \\ y^{*} x^{\wedge} 2 & x^{*} y^{\wedge} 2 & x^{\wedge} 3 & y^{\wedge} 3\end{array}\right] *$ Tinv

Both $u$ and $v$ are third-order polynomials of $x$ and $y$. Each third-order polynomial has 10 terms. To specify all coefficients, Tinv has size 10-by-2.
t_poly_ord3 = cp2tform(input_points, base_points,'polynomial',3);
The coefficients of the inverse mapping are stored in t_poly_ord3.tdata.
At least ten control-point pairs are needed to solve for the 20 unknown coefficients.

## Fourth-Order Polynomials

For a fourth-order polynomial transformation:
$[u v]=\left[1 x y x x^{*} y x^{\wedge} 2 y^{\wedge} 2 y^{*} x^{\wedge} 2 x x^{\wedge} y^{\wedge} 2 x^{\wedge} 3 y^{\wedge} 3 x^{\wedge} 3^{*} y x^{\wedge} 2^{*} y^{\wedge} 2 x^{*} y^{\wedge} 3 x^{\wedge} 4\right.$ y^4] * Tinv
Both $u$ and $v$ are fourth-order polynomials of $x$ and $y$. Each fourth-order polynomial has 15 terms. To specify all coefficients, Tinv has size 15 -by- 2 .
t_poly_ord4 = cp2tform(input_points, base_points,'polynomial',4);

The coefficients of the inverse mapping are stored in t_poly_ord4.tdata.
At least 15 control-point pairs are needed to solve for the 30 unknown coefficients.

## Piecewise Linear

In a piecewise linear transformation, linear (affine) transformations are applied separately to each triangular region of the image[1].

1 Find a Delaunay triangulation of the base control points.
2 Using the three vertices of each triangle, infer an affine mapping from base to input coordinates.

Note At least four control-point pairs are needed. Four pairs result in two triangles with distinct mappings.

## Local Weighted Mean

For each control point in base_points:
1 Find the N closest control points.
2 Use these $N$ points and their corresponding points in input_points to infer a second-order polynomial.

3 Calculate the radius of influence of this polynomial as the distance from the center control point to the farthest point used to infer the polynomial (using base_points)[2].

Note At least six control-point pairs are needed to solve for the second-order polynomial. Ill-conditioned polynomials might result if too few pairs are used.

References<br>[1] Goshtasby, Ardeshir, "Piecewise linear mapping functions for image registration," Pattern Recognition, Vol. 19, 1986, pp. 459-466.<br>[2] Goshtasby, Ardeshir, "Image registration by local approximation methods," Image and Vision Computing, Vol. 6, 1988, pp. 255-261.<br>See Also<br>cpcorr | cpselect | cpstruct2pairs | imtransform | tformfwd | tforminv

| Purpose | Tune control-point locations using cross correlation |
| :--- | :--- |
| Syntax | input_points = cpcorr_(input_points_in, base_points_in, input, <br> base) |
| Description | input_points = cpcorr_(input_points_in, base_points_in, <br> input, base) uses normalized cross-correlation to adjust each pair of <br> control points specified in input_points_in and base_points_in. |
| input_points_in must be an M-by-2 double matrix containing the <br> coordinates of control points in the input image. base_points_in is <br> an M-by-2 double matrix containing the coordinates of control points <br> in the base image. |  |
| cpcorr returns the adjusted control points in input_points, a double <br> matrix the same size as input_points_in. If cpcorr cannot correlate a <br> pair of control points, input_points contains the same coordinates as <br> input_points_in for that pair. |  |
| cpcorr only moves the position of a control point by up to four pixels. <br> Adjusted coordinates are accurate to one-tenth of a pixel. cpcorr is <br> designed to get subpixel accuracy from the image content and coarse <br> control-point selection. |  |

Note input and base images must have the same scale for cpcorr to be effective.
cpcorr cannot adjust a point if any of the following occur:

- Points are too near the edge of either image.
- Regions of images around points contain Inf or NaN.
- Region around a point in input image has zero standard deviation.
- Regions of images around points are poorly correlated.


## Class Support

Algorithms

## Examples

## See Also

The images input and base can be numeric and must contain finite values. The control-point pairs are of class double.
cpcorr uses the following general procedure.
For each control-point pair,
1 Extract an 11-by-11 template around the input control point and a 21-by-21 region around the base control point.

2 Calculate the normalized cross-correlation of the template with the region.

3 Find the absolute peak of the cross-correlation matrix.
4 Use the position of the peak to adjust the coordinates of the input control point.

Use cpcorr to fine-tune control points selected in an image. Note the difference in the values of the input_points matrix and the input_points_adj matrix.

```
input = imread('onion.png');
base = imread('peppers.png');
input_points = [127 93; 74 59];
base_points = [323 195; 269 161];
input_points_adj = cpcorr(input_points,base_points,...
                                    input(:,:,1),base(:,:,1))
input_points_adj =
    127.0000 93.0000
    71.0000 59.6000
```

cp2tform | cpselect | imtransform | normxcorr2

## Purpose Control Point Selection Tool

```
Syntax cpselect(input, base)
cpselect(input, base, CPSTRUCT_IN)
cpselect(input, base, xyinput_in, xybase_in)
h = cpselect(input, base,...)
cpselect(...,param1, val1,...)
```


## Description

cpselect(input, base) starts the Control Point Selection Tool, a graphical user interface that enables you to select control points in two related images. input is the image that needs to be warped to bring it into the coordinate system of the base image. input and base can be either variables that contain grayscale, truecolor, or binary images, or strings that identify files containing these images. The Control Point Selection Tool returns the control points in a CPSTRUCT structure. (For more information, see "Specifying Control Points Using the Control Point Selection Tool".)
cpselect(input, base, CPSTRUCT_IN) starts cpselect with an initial set of control points that are stored in CPSTRUCT_IN. This syntax allows you to restart cpselect with the state of control points previously saved in CPSTRUCT_IN.
cpselect(input, base, xyinput_in, xybase_in) starts cpselect with a set of initial pairs of control points. xyinput_in and xybase_in are $m$-by- 2 matrices that store the input and base coordinates, respectively.
$\mathrm{h}=\mathrm{cpselect}($ input, base,...) returns a handle h to the tool. You can use the close( $h$ ) syntax to close the tool from the command line.
cpselect(...,param1, val1,...) starts cpselect, specifying parameters and corresponding values that control various aspects of the tool. Parameter names can be abbreviated, and case does not matter. Parameters include:

| Parameter | Description <br> 'Wait' <br> Logical scalar that controls whether cpselect <br> waits for the user to finish the task of selecting <br> points. If set to false (the default, you can run <br> cpselect at the same time as you run other <br> programs in MATLAB. If set to true, you must <br> finish the task of selecting points before doing <br> anything else in MATLAB. <br>  <br> Note When 'Wait' is set to true, cpselect <br> returns the selected pairs of points, not a handle <br> to the tool: <br> [xyinput_out, xybase_out ] $=$ <br> cpselect (..., 'Wait', true) <br> xyinput_out and xybase_out are P-by-2 <br> matrices that store the input and base image <br> coordinates, respectively. |
| :--- | :--- |

## Class Support

## Algorithms

The images can be grayscale, truecolor, or binary. A grayscale image can be uint8, uint16, int16, single, or double. A truecolor image can be uint8, uint16, single, or double. A binary image is of class logical.
cpselect uses the following general procedure for control-point prediction.

1 Find all valid pairs of control points.
2 Infer a spatial transformation between input and base control points using method that depends on the number of valid pairs, as follows:

| 2 pairs | Nonreflective similarity |
| :--- | :--- |
| 3 pairs | Affine |
| 4 or more | Projective |
| pairs |  |

3 Apply spatial transformation to the new point to generate the predicted point.

4 Display predicted point.

## Examples Start Control Point Selection tool with saved images.

cpselect('westconcordaerial.png', 'westconcordorthophoto.png')
Start Control Point Selection tool with images and control points stored in variables in the workspace.

```
I = checkerboard;
J = imrotate(I,30);
base_points = [11 11; 41 71];
input_points = [14 44; 70 81];
cpselect(J, I, input_points, base_points);
```

Use cpselect in a script, specifying the 'wait' parameter to block until control point selection is complete.

```
aerial = imread('westconcordaerial.png');
figure, imshow(aerial)
figure, imshow('westconcordorthophoto.png')
load westconcordpoints % load preselected control points
% Block the tool until you pick some more control points
[aerial_points,ortho_points] = ...
    cpselect(aerial,'westconcordorthophoto.png',...
    input_points,base_points,...
    'Wait',true);
```

```
t_concord = cp2tform(aerial_points,ortho_points,'projective');
info = imfinfo('westconcordorthophoto.png');
aerial_registered = imtransform(aerial, t_concord,...
    'XData',[1 info.Width],...
    'YData',[1 info.Height]);
figure, imshow(aerial_registered)
```


## See Also

cpcorr | cp2tform | cpstruct2pairs | imtransform
How To . "Geometric Transformation and Image Registration"
Purpose Convert CPSTRUCT to valid pairs of control points
Syntax [input_points, base_points] = cpstruct2pairs(CPSTRUCT)
Description [input_points, base_points] = cpstruct2pairs(CPSTRUCT)takes a CPSTRUCT (produced by cpselect) and returns the arraysof coordinates of valid control point pairs in input_points andbase_points. cpstruct2pairs eliminates unmatched points andpredicted points.
Examples Start the Control Point Selection Tool, cpselect.
aerial = imread('westconcordaerial.png');
cpselect(aerial(:,:,1), 'westconcordorthophoto.png')
Using cpselect, pick control points in the images. Select Export Points to Workspace from the File menu to save the points to the workspace. On the Export Points to Workspace dialog box, check the Structure with all points check box and clear Input points of valid pairs and Base points of valid pairs. Click OK. Use cpstruct2pairs to extract the input and base points from the CPSTRUCT.
[input_points,base_points] = cpstruct2pairs(cpstruct);
See Also cp2tform | cpselect | imtransform

## Purpose

2-D discrete cosine transform
Syntax
$B=\operatorname{dct2}(A)$
$B=\operatorname{dct2}(A, m, n)$
$B=\operatorname{dct2}(A,[m n])$
$B=\operatorname{dct2}(A)$ returns the two-dimensional discrete cosine transform of A. The matrix B is the same size as A and contains the discrete cosine transform coefficients $B\left(k_{1}, k_{2}\right)$.
$B=\operatorname{dct2}(A, m, n)$ pads the matrix $A$ with 0 's to size $m$-by-n before transforming. If $m$ or $n$ is smaller than the corresponding dimension of A, dct2 truncates $A$.
$B=\operatorname{dct2}(A,[m n])$ same as above.

## Class

Support
Algorithms
A can be numeric or logical. The returned matrix B is of class double.

The discrete cosine transform (DCT) is closely related to the discrete Fourier transform. It is a separable linear transformation; that is, the two-dimensional transform is equivalent to a one-dimensional DCT performed along a single dimension followed by a one-dimensional DCT in the other dimension. The definition of the two-dimensional DCT for an input image $A$ and output image $B$ is

$$
B_{p q}=\alpha_{p} \alpha_{q} \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} A_{m n} \cos \frac{\pi(2 m+1) p}{2 M} \cos \frac{\pi(2 n+1) q}{2 N}, \quad \begin{aligned}
& 0 \leq p \leq M-1 \\
& 0 \leq q \leq N-1
\end{aligned}
$$

where

$$
\alpha_{p}=\left\{\begin{array}{l}
\frac{1}{\sqrt{M}}, p=0 \\
\sqrt{\frac{2}{M}}, 1 \leq p \leq M-1
\end{array}\right.
$$

and

$$
\alpha_{q}=\left\{\begin{array}{l}
\frac{1}{\sqrt{N}}, q=0 \\
\sqrt{\frac{2}{N}}, 1 \leq \mathrm{q} \leq \mathrm{N}-1
\end{array}\right.
$$

$M$ and $N$ are the row and column size of A, respectively. If you apply the DCT to real data, the result is also real. The DCT tends to concentrate information, making it useful for image compression applications.

This transform can be inverted using idct2.

## Examples

The commands below compute the discrete cosine transform for the autumn image. Notice that most of the energy is in the upper left corner.

```
RGB = imread('autumn.tif');
I = rgb2gray(RGB);
J = dct2(I);
imshow(log(abs(J)),[]), colormap(jet(64)), colorbar
```



Now set values less than magnitude 10 in the DCT matrix to zero, and then reconstruct the image using the inverse DCT function idct2.

```
J(abs(J) < 10) = 0;
K = idct2(J);
imshow(I)
figure, imshow(K,[0 255])
```



References
[1] Jain, Anil K., Fundamentals of Digital Image Processing, Englewood Cliffs, NJ, Prentice Hall, 1989, pp. 150-153.
[2] Pennebaker, William B., and Joan L. Mitchell, JPEG: Still Image Data Compression Standard, Van Nostrand Reinhold, 1993.

See Also
Purpose Discrete cosine transform matrix
Syntax D = dctmtx (n)
Description $\mathrm{D}=\operatorname{dctmtx}(\mathrm{n})$ returns the n -by-n DCT (discrete cosine transform)matrix. D*A is the DCT of the columns of $A$ and $D^{\prime *} A$ is the inverse DCTof the columns of $A$ (when $A$ is $n-b y-n$ ).
Class
Support
n is an integer scalar of class double. D is returned as a matrix of class double.
Tips If $A$ is square, the two-dimensional DCT of $A$ can be computed as $D * A * D '$. This computation is sometimes faster than using dct2, especially if you are computing a large number of small DCTs, because D needs to be determined only once.

For example, in JPEG compression, the DCT of each 8-by-8 block is
computed. To perform this computation, use dctmtx to determine D, and
then calculate each DCT using $\mathrm{D}^{*} \mathrm{~A}^{*} \mathrm{D}^{\prime}$ (where A is each 8 -by- 8 block).
This is faster than calling dct2 for each individual block.
Examples

A = im2double(imread('rice.png'));

D = dctmtx(size(A,1));

dct = D*A*D';

figure, imshow(dct)
See Also ..... dct2

Purpose
Deblur image using blind deconvolution
Syntax

```
[J,PSF] = deconvblind(I, INITPSF)
[J,PSF] = deconvblind(I, INITPSF, NUMIT)
[J,PSF] = deconvblind(I, INITPSF, NUMIT, DAMPAR)
[J,PSF] = deconvblind(I, INITPSF, NUMIT, DAMPAR, WEIGHT)
[J,PSF] = deconvblind(I, INITPSF, NUMIT, DAMPAR, WEIGHT,
    READOUT)
[J,PSF] = deconvblind(..., FUN, P1, P2,...,PN)
```


## Description

[J,PSF] = deconvblind(I, INITPSF) deconvolves image I using the maximum likelihood algorithm, returning both the deblurred image $J$ and a restored point-spread function PSF. The restored PSF is a positive array that is the same size as INITPSF, normalized so its sum adds up to 1. The PSF restoration is affected strongly by the size of the initial guess INITPSF and less by the values it contains. For this reason, specify an array of 1's as your INITPSF.
I can be a N -dimensional array.
To improve the restoration, deconvblind supports several optional parameters, described below. Use [] as a placeholder if you do not specify an intermediate parameter.
[J, PSF] = deconvblind(I, INITPSF, NUMIT) specifies the number of iterations (default is 10 ).
[J,PSF] = deconvblind(I, INITPSF, NUMIT, DAMPAR) specifies the threshold deviation of the resulting image from the input image I (in terms of the standard deviation of Poisson noise) below which damping occurs. The iterations are suppressed for the pixels that deviate within the DAMPAR value from their original value. This suppresses the noise generation in such pixels, preserving necessary image details elsewhere. The default value is 0 (no damping).
[J,PSF] = deconvblind(I, INITPSF, NUMIT, DAMPAR, WEIGHT) specifies which pixels in the input image $I$ are considered in the restoration. By default, WEIGHT is a unit array, the same size as the input image. You can assign a value between 0.0 and 1.0 to elements
in the WEIGHT array. The value of an element in the WEIGHT array determines how much the pixel at the corresponding position in the input image is considered. For example, to exclude a pixel from consideration, assign it a value of 0 in the WEIGHT array. You can adjust the weight value assigned to each pixel according to the amount of flat-field correction.
[J,PSF] = deconvblind(I, INITPSF, NUMIT, DAMPAR, WEIGHT, READOUT), where READOUT is an array (or a value) corresponding to the additive noise (e.g., background, foreground noise) and the variance of the read-out camera noise. READOUT has to be in the units of the image. The default value is 0 .
[J,PSF] = deconvblind(..., FUN, P1, P2,...,PN), where FUN is a function describing additional constraints on the PSF. FUN must be a function handle.

FUN is called at the end of each iteration. FUN must accept the PSF as its first argument and can accept additional parameters P1, P2, ..., PN. The FUN function should return one argument, PSF, that is the same size as the original PSF and that satisfies the positivity and normalization constraints.

Parameterizing Functions, in the MATLAB Mathematics documentation, explains how to provide additional parameters to the function fun.

Note The output image $J$ could exhibit ringing introduced by the discrete Fourier transform used in the algorithm. To reduce the ringing, use $I=$ edgetaper(I, PSF) before calling deconvblind.

Resuming You can use deconvblind to perform a deconvolution that starts where Deconvolution a previous deconvolution stopped. To use this feature, pass the input image I and the initial guess at the PSF, INITPSF, as cell arrays: \{I \} and \{INITPSF\}. When you do, the deconvblind function returns the output image $J$ and the restored point-spread function, PSF, as cell
arrays, which can then be passed as the input arrays into the next deconvblind call. The output cell array J contains four elements:
$J\{1\}$ contains I, the original image.
$J\{2\}$ contains the result of the last iteration.
$J\{3\}$ contains the result of the next-to-last iteration.
$J\{4\}$ is an array generated by the iterative algorithm.
I and INITPSF can be uint8, uint16, int16, single, or double. DAMPAR and READOUT must have the same class as the input image. Other inputs have to be double. The output image $J$ (or the first array of the output cell) has the same class as the input image I. The output PSF is double.

```
Examples \(\quad I=\) checkerboard (8);
PSF = fspecial('gaussian',7,10);
V = .0001;
BlurredNoisy = imnoise(imfilter(I, PSF), 'gaussian', 0, V);
WT = zeros(size(I));
WT (5: end -4,5:end-4) = 1;
INITPSF = ones(size(PSF));
[J P] = deconvblind(BlurredNoisy,INITPSF,20,10*sqrt(V),WT);
subplot(221);imshow(BlurredNoisy);
title('A = Blurred and Noisy');
subplot(222);imshow(PSF,[]);
title('True PSF');
subplot(223);imshow(J);
title('Deblurred Image');
subplot(224);imshow(P, []);
title('Recovered PSF');
See Also deconvlucy | deconvreg | deconvwn | edgetaper | function_handle | imnoise | otf2psf | padarray | psf2otf
How To . "Anonymous Functions"
- "Parameterizing Functions"
```

| Purpose | Deblur image using Lucy-Richardson method |
| :---: | :---: |
| Syntax | J = deconvlucy (I, PSF) |
|  | J = deconvlucy(I, PSF, NUMIT) |
|  | J = deconvlucy(I, PSF, NUMIT, DAMPAR) |
|  | $J$ = deconvlucy(I, PSF, NUMIT, DAMPAR, WEIGHT) |
|  | J = deconvlucy(I, PSF, NUMIT, DAMPAR, WEIGHT, READOUT) |
|  | J = deconvlucy(I, PSF, NUMIT, DAMPAR, WEIGHT, READOUT, SUBSMPL) |

## Description

$J=$ deconvlucy(I, PSF) restores image I that was degraded by convolution with a point-spread function PSF and possibly by additive noise. The algorithm is based on maximizing the likelihood of the resulting image J's being an instance of the original image I under Poisson statistics.

I can be a N -dimensional array.
To improve the restoration, deconvlucy supports several optional parameters. Use [] as a placeholder if you do not specify an intermediate parameter.
$J=$ deconvlucy(I, PSF, NUMIT) specifies the number of iterations the deconvlucy function performs. If this value is not specified, the default is 10 .
$J=$ deconvlucy(I, PSF, NUMIT, DAMPAR) specifies the threshold deviation of the resulting image from the image I (in terms of the standard deviation of Poisson noise) below which damping occurs. Iterations are suppressed for pixels that deviate beyond the DAMPAR value from their original value. This suppresses the noise generation in such pixels, preserving necessary image details elsewhere. The default value is 0 (no damping).
$J=$ deconvlucy (I, PSF, NUMIT, DAMPAR, WEIGHT) specifies the weight to be assigned to each pixel to reflect its recording quality in the camera. A bad pixel is excluded from the solution by assigning it zero weight value. Instead of giving a weight of unity for good pixels, you
can adjust their weight according to the amount of flat-field correction. The default is a unit array of the same size as input image I.

J = deconvlucy(I, PSF, NUMIT, DAMPAR, WEIGHT, READOUT) specifies a value corresponding to the additive noise (e.g., background, foreground noise) and the variance of the readout camera noise. READOUT has to be in the units of the image. The default value is 0 .

J = deconvlucy(I, PSF, NUMIT, DAMPAR, WEIGHT, READOUT, SUBSMPL), where SUBSMPL denotes subsampling and is used when the PSF is given on a grid that is SUBSMPL times finer than the image. The default value is 1 .

Note The output image $J$ could exhibit ringing introduced by the discrete Fourier transform used in the algorithm. To reduce the ringing, use I = edgetaper(I,PSF) before calling deconvlucy.

## Resuming Deconvolution

If I is a cell array, it can contain a single numerical array (the blurred
image) or it can be the output from a previous run of deconvlucy.
When you pass a cell array to deconvlucy as input, it returns a 1-by-4 cell array J, where
$J\{1\}$ contains I, the original image.
$J\{2\}$ contains the result of the last iteration.
$J\{3\}$ contains the result of the next-to-last iteration.
$J\{4\}$ is an array generated by the iterative algorithm.
I and PSF can be uint8, uint16, int16, double, or single. DAMPAR and READOUT must have the same class as the input image. Other inputs have to be double. The output image $J$ (or the first array of the output cell) has the same class as the input image I.

```
Examples I = checkerboard(8);
PSF = fspecial('gaussian',7,10);
V = .0001;
```

```
BlurredNoisy = imnoise(imfilter(I,PSF),'gaussian',0,V);
WT = zeros(size(I));
WT(5:end-4,5:end-4) = 1;
J1 = deconvlucy(BlurredNoisy,PSF);
J2 = deconvlucy(BlurredNoisy,PSF,20,sqrt(V));
J3 = deconvlucy(BlurredNoisy,PSF,20,sqrt(V),WT);
subplot(221);imshow(BlurredNoisy);
title('A = Blurred and Noisy');
subplot(222);imshow(J1);
title('deconvlucy(A,PSF)');
subplot(223);imshow(J2);
title('deconvlucy(A,PSF,NI,DP)');
subplot(224);imshow(J3);
title('deconvlucy(A,PSF,NI,DP,WT)');
```


## References <br> [1] Biggs, D.S.C. "Acceleration of Iterative Image Restoration Algorithms." Applied Optics. Vol. 36. Number 8, 1997, pp. 1766-1775.

[2] Hanisch, R.J., R.L. White, and R.L. Gilliland. "Deconvolution of Hubble Space Telescope Images and Spectra." Deconvolution of Images and Spectra (P.A. Jansson, ed.). Boston, MA: Academic Press, 1997, pp. 310-356.

## See Also

deconvblind | deconvreg | deconvwnr | otf2psf | padarray | psf2otf
Purpose Deblur image using regularized filter
Syntax

J = deconvreg(I, PSF)

J = deconvreg(I, PSF, NOISEPOWER)

J = deconvreg(I, PSF, NOISEPOWER, LRANGE)

J = deconvreg(I, PSF, NOISEPOWER, LRANGE, REGOP)

[J, LAGRA] = deconvreg(I, PSF,...)

## Description

$J=$ deconvreg(I, PSF) deconvolves image I using the regularized filter algorithm, returning deblurred image J. The assumption is that the image I was created by convolving a true image with a point-spread function PSF and possibly by adding noise. The algorithm is a constrained optimum in the sense of least square error between the estimated and the true images under requirement of preserving image smoothness.
I can be a N -dimensional array.
$J=$ deconvreg(I, PSF, NOISEPOWER) where NOISEPOWER is the additive noise power. The default value is 0 .
$J=$ deconvreg(I, PSF, NOISEPOWER, LRANGE) where LRANGE is a vector specifying range where the search for the optimal solution is performed. The algorithm finds an optimal Lagrange multiplier LAGRA within the LRANGE range. If LRANGE is a scalar, the algorithm assumes that LAGRA is given and equal to LRANGE; the NP value is then ignored. The default range is between [ $1 \mathrm{e}-9$ and 1 e 9 ].
$J=$ deconvreg(I, PSF, NOISEPOWER, LRANGE, REGOP) where REGOP is the regularization operator to constrain the deconvolution. The default regularization operator is the Laplacian operator, to retain the image smoothness. The REGOP array dimensions must not exceed the image dimensions; any nonsingleton dimensions must correspond to the nonsingleton dimensions of PSF.
[J, LAGRA] = deconvreg(I, PSF,...) outputs the value of the Lagrange multiplier LAGRA in addition to the restored image $J$.

Note The output image $J$ could exhibit ringing introduced by the discrete Fourier transform used in the algorithm. To reduce the ringing, process the image with the edgetaper function prior to calling the deconvreg function. For example, I = edgetaper(I,PSF).

```
Class
Support
Examples I = checkerboard(8);
PSF = fspecial('gaussian',7,10);
V = .01;
BlurredNoisy = imnoise(imfilter(I,PSF),'gaussian',0,V);
NOISEPOWER = V*prod(size(I));
[J LAGRA] = deconvreg(BlurredNoisy,PSF,NOISEPOWER);
subplot(221); imshow(BlurredNoisy);
title('A = Blurred and Noisy');
subplot(222); imshow(J);
title('[J LAGRA] = deconvreg(A,PSF,NP)');
subplot(223); imshow(deconvreg(BlurredNoisy,PSF,[],LAGRA/10));
title('deconvreg(A,PSF,[],0.1*LAGRA)');
subplot(224); imshow(deconvreg(BlurredNoisy,PSF,[],LAGRA*10));
title('deconvreg(A,PSF,[],10*LAGRA)');
See Also deconvblind | deconvlucy | deconvwnr | otf2psf | padarray | psf2otf
```

Purpose Deblur image using Wiener filter
Syntax

J = deconvwnr(I,PSF,NSR)
J = deconvwnr(I,PSF,NCORR,ICORR)
Description$J=$ deconvwnr(I, PSF, NSR ) deconvolves image I using the Wienerfilter algorithm, returning deblurred image J. Image I can be anN -dimensional array. PSF is the point-spread function with which I wasconvolved. NSR is the noise-to-signal power ratio of the additive noise.NSR can be a scalar or a spectral-domain array of the same size as I.Specifying 0 for the NSR is equivalent to creating an ideal inverse filter.
The algorithm is optimal in a sense of least mean square error between the estimated and the true images.
$J=$ deconvwnr(I,PSF,NCORR,ICORR) deconvolves image I, where NCORR is the autocorrelation function of the noise and ICORR is the autocorrelation function of the original image. NCORR and ICORR can be of any size or dimension, not exceeding the original image. If NCORR or ICORR are N -dimensional arrays, the values correspond to the autocorrelation within each dimension. If NCORR or ICORR are vectors, and PSF is also a vector, the values represent the autocorrelation function in the first dimension. If PSF is an array, the 1-D autocorrelation function is extrapolated by symmetry to all non-singleton dimensions of PSF. If NCORR or ICORR is a scalar, this value represents the power of the noise of the image.
Note The output image $J$ could exhibit ringing introduced by the discrete Fourier transform used in the algorithm. To reduce the ringing, use

```
I = edgetaper(I,PSF)
```

prior to calling deconvwnr.

Class
Support

## Examples

I can be of class uint8, uint16, int16, single, or double. Other inputs have to be of class double. J has the same class as I.

## Use deconvwnr to Restore an Image

Create a noisy, blurry image and then apply the deconvwnr filter to deblur it.
Display the original image.

```
I = im2double(imread('cameraman.tif'));
imshow(I);
title('Original Image (courtesy of MIT)');
```



Simulate a motion blur.

```
LEN = 21;
THETA = 11;
PSF = fspecial('motion', LEN, THETA);
```

```
blurred = imfilter(I, PSF, 'conv', 'circular');
figure, imshow(blurred)
```

Simulate additive noise.

```
noise_mean = 0;
noise_var = 0.0001;
blurred_noisy = imnoise(blurred, 'gaussian', ...
                                    noise_mean, noise_var);
figure, imshow(blurred_noisy)
title('Simulate Blur and Noise')
```



## deconvwnr

Try restoration assuming no noise.


Try restoration using a better estimate of the noise-to-signal-power ratio.

```
estimated_nsr = noise_var / var(I(:));
wnr3 = deconvwnr(blurred_noisy, PSF, estimated_nsr);
figure, imshow(wnr3)
title('Restoration of Blurred, Noisy Image Using Estimated NSR');
```



## References

See Also
"Digital Image Processing", R. C. Gonzalez \& R. E. Woods, Addison-Wesley Publishing Company, Inc., 1992.

```
deconvblind | deconvlucy | deconvreg | edgetaper | otf2psf |
padarray | psf2otf
```

> Purpose Apply decorrelation stretch to multichannel image
> Syntax $\quad S=$ decorrstretch(I)
> S = decorrstretch(I, TOL)
> S = decorrstretch(I) applies a decorrelation stretch to a multichannel image I and returns the result in S. S has the same size and class as I. The mean and variance in each band are the same as in I.

> S = decorrstretch(I, TOL) applies a contrast following the decorrelation stretch. The contrast stretch is controlled by TOL:
> - TOL = [LOW_FRACT HIGH_FRACT] specifies the fraction of the image to saturate at low and high intensities.
> - If TOL is a scalar, LOW_FRACT = TOL, and HIGH_FRACT = $1-$ TOL, which saturates equal fractions at low and high intensities.

> Notes The decorrelation stretch is normally applied to three band images (ordinary RGB images or RGB multispectral composite images), but decorrstretch works on an arbitrary number of bands.

> The primary purpose of decorrelation stretch is visual enhancement. Small adjustments to TOL can strongly affect the visual appearance of the output.

## Class The input image must be of class uint8, uint16, int16, single, or double.

Examples $[\mathrm{X}$, map] $=$ imread('forest.tif');
S = decorrstretch(ind2rgb(X, map), 'tol', 0.01);
figure, imshow(X,map)
figure, imshow(S)

See Also imadjust | stretchlim
Purpose Convert Bayer pattern encoded image to truecolor image
Syntax RGB = demosaic(I, sensorAlignment)
DescriptionRGB = demosaic( I , sensorAlignment) converts a Bayer patternencoded image to a truecolor image using gradient-corrected linearinterpolation. I is an M-by-N array of intensity values that are Bayerpattern encoded. I must have at least 5 rows and 5 columns.
A Bayer filter mosaic, or color filter array, refers to the arrangement of color filters that let each sensor in a single-sensor digital camera record only red, green, or blue data. The patterns emphasize the number of green sensors to mimic the human eye's greater sensitivity to green light. The demosaic function uses interpolation to convert the two-dimensional Bayer-encoded image into the truecolor image, RGB, which is an M-by-N-by-3 array.
sensorAlignment is one of the following text strings that specifies the Bayer pattern. Each string represents the order of the red, green, and blue sensors by describing the four pixels in the upper-left corner of the image (left-to-right, top-to-bottom).

| Value <br> 'gbrg' | 2-by-2 Sensor Alignment |  |  |
| :---: | :---: | :---: | :---: |
|  |  |  |  |
|  | Green | Blue |  |
|  | Red | Green |  |
| 'grbg' |  |  |  |
|  | Green | Red |  |
|  | Blue | Green |  |
| ' bggr |  |  |  |
|  | Blue | Green |  |
|  | Green | Red |  |
| 'rggb ' |  |  |  |
|  | Red | Green |  |
|  | Green | Blue |  |

Class Support

Examples Convert a Bayer pattern encoded image that was photographed by a camera with a sensor alignment of 'bggr'.

```
I = imread('mandi.tif');
J = demosaic(I,'bggr');
imshow(I);
figure, imshow(J);
```



[^2]
## demosaic



Truecolor Image

Purpose Anonymize DICOM file
Syntax dicomanon(file_in, file_out)
dicomanon(..., 'keep', FIELDS)
dicomanon(..., 'update', ATTRS)

## Description

## Examples

Remove all confidential metadata from a file.
dicomanon('patient.dcm', 'anonymized.dcm')

Create a training file.
dicomanon('tumor.dcm', 'tumor_anon.dcm', 'keep',...

## dicomanon

```
{'PatientAge', 'PatientSex', 'StudyDescription'})
```

Anonymize a series of images, keeping the hierarchy.
values.StudyInstanceUID = dicomuid;
values.SeriesInstanceUID = dicomuid;

```
d = dir('*.dcm');
for p = 1:numel(d)
    dicomanon(d(p).name, sprintf('anon%d.dcm', p), ...
        'update', values)
end
```

See Also
dicominfo | dicomwrite

## Purpose

Get or set active DICOM data dictionary
Syntax
dicomdict('set', dictionary)
dictionary = dicomdict('get') dicomdict('factory')

## Description

dicomdict('set', dictionary) sets the Digital Imaging and Communications in Medicine (DICOM) data dictionary to the value stored in dictionary, a string containing the filename of the dictionary. DICOM-related functions use this dictionary by default, unless a different dictionary is provided at the command line.
dictionary = dicomdict('get') returns a string containing the filename of the stored DICOM data dictionary.
dicomdict('factory') resets the DICOM data dictionary to its default startup value.

Note The default data dictionary is a MAT-file, dicom-dict.mat. The toolbox also includes a text version of this default data dictionary, dicom-dict.txt. If you want to create your own DICOM data dictionary, open the dicom-dict.txt file in a text editor, modify it, and save it under another name.

```
Examples dictionary = dicomdict('get')
dictionary =
dicom-dict.mat
```

See Also dicominfo | dicomread | dicomwrite

## dicominfo

Purpose Read metadata from DICOM message
Syntax

info = dicominfo(filename)

info = dicominfo(filename, 'dictionary', D)
Description
Examples
info = dicominfo('CT-MONO2-16-ankle.dcm')
info =
Filename: [1x62 char]
FileModDate: '18-Dec-2000 11:06:43'
FileSize: 525436
Format: 'DICOM'
FormatVersion:
Width: 512
Height: 512
BitDepth: ..... 16
ColorType: 'grayscale'
SelectedFrames: ..... []
FileStruct: [1x1 struct]
StartOfPixelData: ..... 1140
FileMetaInformationGroupLength: ..... 192
FileMetaInformationVersion: [2x1 uint8]MediaStorageSOPClassUID: '1.2.840.10008.5.1.4.1.1.7'

See Also dicomdict | dicomread | dicomwrite | dicomuid

## dicomlookup

| Purpose | Find attribute in DICOM data dictionary |
| :---: | :---: |
| Syntax | $\begin{aligned} & \text { name = dicomlookup(group, element) } \\ & \text { [group, element] = dicomlookup(name) } \end{aligned}$ |
| Description | name = dicomlookup(group, element) looks into the current DICOM data dictionary for the attribute with the specified group and element tag and returns a string containing the name of the attribute. group and element can contain either a decimal value or hexadecimal string. <br> [group, element] = dicomlookup(name) looks into the current DICOM data dictionary for the attribute specified byname and returns the group and element tags associated with the attribute. The values are returned as decimal values. |
| Examples | Find the names of DICOM attributes using their tags. <br> name1 = dicomlookup('7FEO', '0010') <br> name2 $=$ dicomlookup (40, 4) <br> Look up a DICOM attribute's tag (GROUP and ELEMENT) using its name. <br> [group, element] = dicomlookup('TransferSyntaxUID') <br> Examine the metadata of a DICOM file. This returns the same value even if the data dictionary changes. <br> metadata = dicominfo('CT-MONO2-16-ankle.dcm'); <br> metadata.(dicomlookup('0028', '0004')) |
| See Also | dicomdict \| dicominfo |

Purpose Read DICOM image
Syntax X = dicomread(filename)
X = dicomread(info)
[X,map] = dicomread(...)
[X,map,alpha] = dicomread(...)
[X,map,alpha,overlays] = dicomread(...)
[...] = dicomread(filename, 'frames', v)

## Description

X = dicomread(filename) reads the image data from the compliant Digital Imaging and Communications in Medicine (DICOM) file filename. For single-frame grayscale images, X is an M-by-N array. For single-frame true-color images, X is an M-by-N-by-3 array. Multiframe images are always 4-D arrays.
$X=$ dicomread(info) reads the image data from the message referenced in the DICOM metadata structure info. The info structure is produced by the dicominfo function.
[X,map] = dicomread(...) returns the image X and the colormap map. If $X$ is a grayscale or true-color image, map is empty.
[X,map,alpha] = dicomread(...) returns the image X, the colormap map, and an alpha channel matrix for $X$. The values of alpha are 0 if the pixel is opaque; otherwise they are row indices into map. The RGB value in map should be substituted for the value in $X$ to use alpha. alpha has the same height and width as X and is $4-\mathrm{D}$ for a multiframe image.
[X,map,alpha,overlays] = dicomread(...) returns the image $X$, the colormap map, an alpha channel matrix for $X$, and any overlays from the DICOM file. Each overlay is a 1-bit black and white image with the same height and width as $X$. If multiple overlays are present in the file, overlays is a 4-D multiframe image. If no overlays are in the file, overlays is empty.
[...] = dicomread(filename, 'frames', v) reads only the frames in the vector $v$ from the image. $v$ must be an integer scalar, a vector of integers, or the string 'all'. The default value is 'all'.

## dicomread

```
Tips The dicomread function supports both reversible (lossless) and irreversible (lossy) JPEG-2000 compression in DICOM files.
```


## Class

$X$ can be uint8, int8, uint16, or int16. map must be double. alpha has the same size and type as X . overlays is a logical array.
Examples Use dicomread to retrieve the data array, $X$, and colormap matrix, map, needed to create a montage.

```
```

[X, map] = dicomread('US-PAL-8-10x-echo.dcm');

```
[X, map] = dicomread('US-PAL-8-10x-echo.dcm');
montage(X, map, 'Size', [2 5]);
montage(X, map, 'Size', [2 5]);
Call dicomread with the information retrieved from the DICOM file using dicominfo and display the image using imshow. Adjust the contrast of the image using imcontrast.
```

```
info = dicominfo('CT-MONO2-16-ankle.dcm');
```

info = dicominfo('CT-MONO2-16-ankle.dcm');
Y = dicomread(info);
Y = dicomread(info);
figure, imshow(Y);
figure, imshow(Y);
imcontrast;
imcontrast;
See Also
dicomdict | dicominfo | dicomwrite

```

\section*{Purpose Generate DICOM unique identifier}

\section*{Syntax UID = dicomuid}

Description UID = dicomuid creates a string UID containing a new DICOM unique identifier.

Multiple calls to dicomuid produce globally unique values. Two calls to dicomuid always return different values.

See Also dicominfo | dicomwrite

\section*{dicomwrite}

Purpose Write images as DICOM files
```

Syntax dicomwrite(X, filename)
dicomwrite(X, map, filename)
dicomwrite(..., param1, value1, param2, value2, ...)
dicomwrite(..., 'ObjectType', IOD,...)
dicomwrite(..., 'SOPClassUID', UID,...)
dicomwrite(..., meta_struct,...)
dicomwrite(..., info,...)
status = dicomwrite(...)

```

\section*{Description}
dicomwrite(X, filename) writes the binary, grayscale, or truecolor image \(X\) to the file filename, where filename is a string specifying the name of the Digital Imaging and Communications in Medicine (DICOM) file to create.
dicomwrite(X, map, filename) writes the indexed image X with colormap map.
dicomwrite(..., param1, value1, param2, value2, ...) specifies optional metadata to write to the DICOM file or parameters that affect how the file is written. param1 is a string containing the metadata attribute name or a dicomwrite-specific option. value 1 is the corresponding value for the attribute or option.

To find a list of the DICOM attributes that you can specify, see the data dictionary file, dicom-dict.txt, included with the Image Processing Toolbox software. The following table lists the options that you can specify, in alphabetical order. Default values are enclosed in braces (\{\}).
\begin{tabular}{l|l}
\hline Option Name & Description \\
\hline 'CompressionMode' & \begin{tabular}{l} 
String specifying the type of compression \\
to use when storing the image. Possible \\
values: \\
\{'None ' \} \\
'JPEG lossless ' \\
'JPEG lossy' \\
'JPEG2000 lossy ' \\
'JPEG2000 lossless' \\
'RLE'
\end{tabular} \\
\hline 'CreateMode ' & \begin{tabular}{l} 
Specifies the method used for creating the \\
data to put in the new file. Possible values: \\
\{'Create ' \} - Verify input values and \\
generate missing data values. \\
'Copy ' - Copy all values from the input \\
and do not generate missing values.
\end{tabular} \\
\hline & \begin{tabular}{l} 
String specifying the name of a DICOM \\
data dictionary.
\end{tabular} \\
\hline 'Dictionary ' & \begin{tabular}{l} 
String specifying the byte ordering of the \\
file. \\
'Big' \\
\{'Little ' \}
\end{tabular} \\
\hline & \begin{tabular}{l} 
Note If VR is set to 'Explicit ', 'Endian ' \\
must be 'Big'. dicomwrite ignores \\
this value if 'CompressionMode ' or \\
'TransferSyntax' is set.
\end{tabular} \\
\hline
\end{tabular}
\begin{tabular}{|c|c|}
\hline Option Name & Description \\
\hline 'MultiframeSingleFil & Logical value indicating whether multiframe imagery should be written to one file. When true (default), one file is created regardless of how many frames \(X\) contains. When false, one file is written for each frame in the image. \\
\hline \multirow[t]{2}{*}{'TransferSyntax'} & A DICOM UID specifying the 'Endian', 'VR', and 'CompressionMode' options. \\
\hline & Note If specified, dicomwrite ignores any values specified for the 'Endian', 'VR', and 'CompressionMode' options. The TransferSyntax value encodes values for these options. \\
\hline \multirow[t]{2}{*}{'VR'} & \begin{tabular}{l}
String specifying whether the two-letter value representation (VR) code should be written to the file. \\
'explicit' — Write VR to file. \\
\{'implicit'\} — Infer from data dictionary.
\end{tabular} \\
\hline & Note If you specify the 'Endian' value 'Big', you must specify 'Explicit'. \\
\hline 'WritePrivate' & \begin{tabular}{l}
Logical value indicating whether private data should be written to the file. Possible values: true - Write private data to file. \\
\{false\} - Do not write private data.
\end{tabular} \\
\hline
\end{tabular}
dicomwrite(..., 'ObjectType', IOD,...) writes a file containing the necessary metadata for a particular type of DICOM Information Object (IOD). Supported IODs are
- 'Secondary Capture Image Storage' (default)
- 'CT Image Storage'
- 'MR Image Storage'
dicomwrite(..., 'SOPClassUID', UID,...) provides an alternate method for specifying the IOD to create. UID is the DICOM unique identifier corresponding to one of the IODs listed above.
dicomwrite(..., meta_struct,...) specifies optional metadata or file options in structure meta_struct. The names of fields in meta_struct must be the names of DICOM file attributes or options. The value of a field is the value you want to assign to the attribute or option.
dicomwrite(..., info,...) specifies metadata in the metadata structure info, which is produced by the dicominfo function. For more information about this structure, see dicominfo.
status \(=\) dicomwrite (...) returns information about the metadata and the descriptions used to generate the DICOM file. This syntax can be useful when you specify an info structure that was created by dicominfo to the dicomwrite function. An info structure can contain many fields. If no metadata was specified, dicomwrite returns an empty matrix ([]).

The structure returned by dicomwrite contains these fields:
\begin{tabular}{l|l}
\hline Field & Description \\
\hline 'BadAttribute' & \begin{tabular}{l} 
The attribute's internal description is bad. It \\
might be missing from the data dictionary or \\
have incorrect data in its description.
\end{tabular} \\
\hline 'MissingCondition' & \begin{tabular}{l} 
The attribute is conditional but no condition \\
has been provided for when to use it.
\end{tabular} \\
\hline
\end{tabular}

\section*{dicomwrite}
\begin{tabular}{l|l}
\hline Field & Description \\
\hline 'MissingData' & \begin{tabular}{l} 
No data was provided for an attribute that \\
must appear in the file.
\end{tabular} \\
\hline 'SuspectAttribute' & \begin{tabular}{l} 
Data in the attribute does not match a \\
list of enumerated values in the DICOM \\
specification.
\end{tabular} \\
\hline
\end{tabular}

Tips
The DICOM format specification lists several Information Object Definitions (IODs) that can be created. These IODs correspond to images and metadata produced by different real-world modalities (e.g., MR, X-ray, Ultrasound, etc.). For each type of IOD, the DICOM specification defines the set of metadata that must be present and possible values for other metadata.
dicomwrite fully implements a limited number of these IODs, listed above in the ObjectType syntax. For these IODs, dicomwrite verifies that all required metadata attributes are present, creates missing attributes if necessary, and specifies default values where possible. Using these supported IODs is the best way to ensure that the files you create conform to the DICOM specification. This is dicomwrite default behavior and corresponds to the CreateMode option value of 'Create'.

To write DICOM files for IODs that dicomwrite doesn't implement, use the 'Copy ' value for the CreateMode option. In this mode, dicomwrite writes the image data to a file including the metadata that you specify as a parameter, shown above in the info syntax. The purpose of this option is to take metadata from an existing file of the same modality or IOD and use it to create a new DICOM file with different image pixel data.

\section*{dicomwrite}

\begin{abstract}
Note Because dicomwrite copies metadata to the file without verification in 'copy ' mode, it is possible to create a DICOM file that does not conform to the DICOM standard. For example, the file may be missing required metadata, contain superfluous metadata, or the metadata may no longer correspond to the modality settings used to generate the original image. When using 'Copy ' mode, make sure that the metadata you use is from the same modality and IOD. If the copy you make is unrelated to the original image, use dicomuid to create new unique identifiers for series and study metadata. See the IOD descriptions in Part 3 of the DICOM specification for more information on appropriate IOD values.
\end{abstract}

\section*{Examples}

See Also

Read a CT image from the sample DICOM file included with the toolbox and then write the CT image to a file, creating a secondary capture image.
```

X = dicomread('CT-MONO2-16-ankle.dcm');
dicomwrite(X, 'sc_file.dcm');

```

Write the CT image, X , to a DICOM file along with its metadata. Use the dicominfo function to retrieve metadata from a DICOM file.
```

metadata = dicominfo('CT-MONO2-16-ankle.dcm');
dicomwrite(X, 'ct_file.dcm', metadata);

```

Copy all metadata from one file to another. In this mode, dicomwrite does not verify the metadata written to the file.
```

dicomwrite(X, 'ct_copy.dcm', metadata, 'CreateMode', 'copy');

```
dicomdict | dicominfo | dicomread | dicomuid

\section*{edge}

Purpose Find edges in grayscale image

\section*{Note}
- The syntax \(B W=\) edge (... ,K) has been removed. Use the \(B W=\) edge(... , direction) syntax instead.
- The syntax edge(I, 'marr-hildreth', ...) has been removed. Use the edge(I,'log',...) syntax instead.
```

Syntax BW = edge(I)
BW = edge(I,'sobel')
BW = edge(I,'sobel',thresh)
BW = edge(I,'sobel',thresh,direction)
[BW,thresh] = edge(I,'sobel',...)
BW = edge(I,'prewitt')
BW = edge(I,'prewitt',thresh)
BW = edge(I,'prewitt',thresh,direction)
[BW,thresh] = edge(I,'prewitt',...)
BW = edge(I,'roberts')
BW = edge(I,'roberts',thresh)
[BW,thresh] = edge(I,'roberts',...)
BW = edge(I,'log')
BW = edge(I,'log',thresh)
BW = edge(I,'log',thresh,sigma)
[BW,threshold] = edge(I,'log',...)
BW = edge(I,'zerocross',thresh,h)
[BW,thresh] = edge(I,'zerocross',...)
BW = edge(I,'canny')
BW = edge(I,'canny',thresh)

```
```

BW = edge(I,'canny',thresh,sigma)
[BW,threshold] = edge(I,'canny',...)

```

\section*{Description}

BW = edge(I) takes a grayscale or a binary image I as its input, and returns a binary image BW of the same size as I, with 1's where the function finds edges in I and 0's elsewhere.

By default, edge uses the Sobel method to detect edges but the following provides a complete list of all the edge-finding methods supported by this function:
- The Sobel method finds edges using the Sobel approximation to the derivative. It returns edges at those points where the gradient of \(I\) is maximum.
- The Prewitt method finds edges using the Prewitt approximation to the derivative. It returns edges at those points where the gradient of \(I\) is maximum.
- The Roberts method finds edges using the Roberts approximation to the derivative. It returns edges at those points where the gradient of \(I\) is maximum.
- The Laplacian of Gaussian method finds edges by looking for zero crossings after filtering I with a Laplacian of Gaussian filter.
- The zero-cross method finds edges by looking for zero crossings after filtering I with a filter you specify.
- The Canny method finds edges by looking for local maxima of the gradient of I. The gradient is calculated using the derivative of a Gaussian filter. The method uses two thresholds, to detect strong and weak edges, and includes the weak edges in the output only if they are connected to strong edges. This method is therefore less likely than the others to be fooled by noise, and more likely to detect true weak edges.

The parameters you can supply differ depending on the method you specify. If you do not specify a method, edge uses the Sobel method.

\section*{edge}

\section*{Sobel Method}

BW = edge(I,'sobel') specifies the Sobel method.
BW = edge(I,'sobel',thresh) specifies the sensitivity threshold for the Sobel method. edge ignores all edges that are not stronger than thresh. If you do not specify thresh, or if thresh is empty ([]), edge chooses the value automatically.

BW = edge(I,'sobel',thresh,direction) specifies the direction of detection for the Sobel method. direction is a string specifying whether to look for 'horizontal' or 'vertical' edges or 'both' (the default).

BW = edge(I,'sobel',...,options) provides an optional string input. String 'nothinning' speeds up the operation of the algorithm by skipping the additional edge thinning stage. By default, or when 'thinning' string is specified, the algorithm applies edge thinning.
[BW,thresh] = edge(I,'sobel',...) returns the threshold value.

\section*{Prewitt Method}

BW = edge(I,'prewitt') specifies the Prewitt method.
BW = edge(I, 'prewitt', thresh) specifies the sensitivity threshold for the Prewitt method. edge ignores all edges that are not stronger than thresh. If you do not specify thresh, or if thresh is empty ([ ]), edge chooses the value automatically.

BW = edge(I, 'prewitt',thresh,direction) specifies the direction of detection for the Prewitt method. direction is a string specifying whether to look for 'horizontal' or 'vertical' edges or 'both' (default).
[BW,thresh] = edge(I,'prewitt',...) returns the threshold value.

\section*{Roberts Method}

BW = edge(I,'roberts') specifies the Roberts method.
BW = edge(I,'roberts',thresh) specifies the sensitivity threshold for the Roberts method. edge ignores all edges that are not stronger
than thresh. If you do not specify thresh, or if thresh is empty ([ ]), edge chooses the value automatically.
BW = edge(I, 'roberts', ..., options) where options can be the text string 'thinning' or 'nothinning'. When you specify 'thinning', or don't specify a value, the algorithm applies edge thinning. Specifying the 'nothinning' option can speed up the operation of the algorithm by skipping the additional edge thinning stage.
[BW,thresh] = edge(I,'roberts',...) returns the threshold value.

\section*{Laplacian of Gaussian Method}

BW = edge(I, 'log') specifies the Laplacian of Gaussian method.
BW = edge(I,'log',thresh) specifies the sensitivity threshold for the Laplacian of Gaussian method. edge ignores all edges that are not stronger than thresh. If you do not specify thresh, or if thresh is empty ([]), edge chooses the value automatically. If you specify a threshold of 0 , the output image has closed contours, because it includes all the zero crossings in the input image.

BW \(=\operatorname{edge}\left(\mathrm{I}, \mathrm{C}^{\prime} \log { }^{\prime}\right.\), thresh, sigma) specifies the Laplacian of Gaussian method, using sigma as the standard deviation of the LoG filter. The default sigma is 2 ; the size of the filter is \(n\)-by- \(n\), where \(n=\) ceil(sigma* 3 ) *2+1.
[BW,thresh] = edge(I,'log',...) returns the threshold value.

\section*{Zero-Cross Method}

BW = edge(I, 'zerocross',thresh,h) specifies the zero-cross method, using the filter h . thresh is the sensitivity threshold; if the argument is empty ([ ]), edge chooses the sensitivity threshold automatically. If you specify a threshold of 0 , the output image has closed contours, because it includes all the zero crossings in the input image.
[BW,thresh] = edge(I,'zerocross',...) returns the threshold value.

\section*{Canny Method}

BW = edge(I, 'canny') specifies the Canny method.

BW = edge(I,'canny',thresh) specifies sensitivity thresholds for the Canny method. thresh is a two-element vector in which the first element is the low threshold, and the second element is the high threshold. If you specify a scalar for thresh, this scalar value is used for the high threshold and \(0.4 *\) thresh is used for the low threshold. If you do not specify thresh, or if thresh is empty ([ ]), edge chooses low and high values automatically. The value for thresh is relative to the highest value of the gradient magnitude of the image.

BW = edge(I,'canny',thresh, sigma) specifies the Canny method, using sigma as the standard deviation of the Gaussian filter. The default sigma is sqrt(2); the size of the filter is chosen automatically, based on sigma.
[BW, thresh] = edge(I,'canny',...) returns the threshold values as a two-element vector.

\section*{Class Support}

I is a nonsparse numeric array. BW is of class logical.

Tips For the gradient-magnitude methods (Sobel, Prewitt, Roberts), thresh is used to threshold the calculated gradient magnitude. For the zero-crossing methods, including Lap, thresh is used as a threshold for the zero-crossings; in other words, a large jump across zero is an edge, while a small jump isn't.

The Canny method applies two thresholds to the gradient: a high threshold for low edge sensitivity and a low threshold for high edge sensitivity. edge starts with the low sensitivity result and then grows it to include connected edge pixels from the high sensitivity result. This helps fill in gaps in the detected edges.

In all cases, the default threshold is chosen heuristically in a way that depends on the input data. The best way to vary the threshold is to run edge once, capturing the calculated threshold as the second output argument. Then, starting from the value calculated by edge, adjust the threshold higher (fewer edge pixels) or lower (more edge pixels).

The function edge changed in Version 7.2 (R2011a). Previous versions of the Image Processing Toolbox used a different algorithm for computing the Canny method. If you need the same results produced by the previous implementation, use the following syntax:

BW = edge(I,'canny_old',...)
Examples
Find the edges of an image using the Prewitt and Canny methods.
```

I = imread('circuit.tif');
BW1 = edge(I,'prewitt');
BW2 = edge(I,'canny');
imshow(BW1);

```


\section*{Prewitt Method}
figure, imshow(BW2)


\section*{Canny Method}

\section*{References}
[1] Canny, John, "A Computational Approach to Edge Detection," IEEE Transactions on Pattern Analysis and Machine Intelligence,Vol. PAMI-8, No. 6, 1986, pp. 679-698.
[2] Lim, Jae S., Two-Dimensional Signal and Image Processing, Englewood Cliffs, NJ, Prentice Hall, 1990, pp. 478-488.
[3] Parker, James R., Algorithms for Image Processing and Computer Vision, New York, John Wiley \& Sons, Inc., 1997, pp. 23-29.

\footnotetext{
See Also
}
Purpose Taper discontinuities along image edges
Syntax J = edgetaper(I,PSF)
Description \(J=\) edgetaper (I, PSF) blurs the edges of the input image I using thepoint spread function PSF. The size of the PSF cannot exceed half ofthe image size in any dimension.The output image \(J\) is the weighted sum of the original image Iand its blurred version. The weighting array, determined by theautocorrelation function of PSF, makes \(J\) equal to \(I\) in its central region,and equal to the blurred version of I near the edges.
The edgetaper function reduces the ringing effect in image deblurring methods that use the discrete Fourier transform, such as deconvwnr, deconvreg, and deconvlucy.
Class
Support
I and PSF can be of class uint8, uint16, int16, single, or double. J is of the same class as I.
Examples
```

original = imread('cameraman.tif');
PSF = fspecial('gaussian',60,10);
edgesTapered = edgetaper(original,PSF);
figure, imshow(original,[]);
figure, imshow(edgesTapered,[]);

```
See Also deconvlucy | deconvreg | deconvwnr | otf2psf | padarray | psf2otf

\section*{Purpose Entropy of grayscale image}

\section*{Syntax E = entropy (I)}

Description

Class
Support
Notes

Examples

References

See Also
\(E=\) entropy (I) returns \(E\), a scalar value representing the entropy of grayscale image I. Entropy is a statistical measure of randomness that can be used to characterize the texture of the input image. Entropy is defined as
\[
-\operatorname{sum}(p . * \log 2(p))
\]
where p contains the histogram counts returned from imhist. By default, entropy uses two bins for logical arrays and 256 bins for uint8, uint16, or double arrays.
I can be a multidimensional image. If I has more than two dimensions, the entropy function treats it as a multidimensional grayscale image and not as an RGB image.

I can be logical, uint8, uint16, or double and must be real, nonempty, and nonsparse. E is double.
entropy converts any class other than logical to uint 8 for the histogram count calculation so that the pixel values are discrete and directly correspond to a bin value.
```

I = imread('circuit.tif');
J = entropy(I)

```
[1] Gonzalez, R.C., R.E. Woods, S.L. Eddins, Digital Image Processing Using MATLAB, New Jersey, Prentice Hall, 2003, Chapter 11.
imhist | entropyfilt
\begin{tabular}{|c|c|}
\hline Purpose & Local entropy of grayscale image \\
\hline Syntax & \[
\begin{aligned}
& J=\text { entropyfilt(I) } \\
& J=\text { entropyfilt(I,NHOOD) }
\end{aligned}
\] \\
\hline Description & \begin{tabular}{l}
\(J=\) entropyfilt(I) returns the array \(J\), where each output pixel contains the entropy value of the 9-by-9 neighborhood around the corresponding pixel in the input image I. I can have any dimension. If I has more than two dimensions, entropyfilt treats it as a multidimensional grayscale image and not as a truecolor (RGB) image. The output image \(J\) is the same size as the input image I. \\
For pixels on the borders of I, entropyfilt uses symmetric padding. In symmetric padding, the values of padding pixels are a mirror reflection of the border pixels in I. \\
\(J=\) entropyfilt(I,NHOOD) performs entropy filtering of the input image I where you specify the neighborhood in NHOOD. NHOOD is a multidimensional array of zeros and ones where the nonzero elements specify the neighbors. NHOOD's size must be odd in each dimension. \\
By default, entropyfilt uses the neighborhood true(9). entropyfilt determines the center element of the neighborhood by floor ((size (NHOOD) + 1)/2). To specify neighborhoods of various shapes, such as a disk, use the strel function to create a structuring element object and then use the getnhood function to extract the neighborhood from the structuring element object.
\end{tabular} \\
\hline \begin{tabular}{l}
Class \\
Support
\end{tabular} & \begin{tabular}{l}
I can be logical, uint8, uint16, or double, and must be real and nonsparse. NHOOD can be logical or numeric and must contain zeros or ones. The output array \(J\) is of class double. \\
entropyfilt converts any class other than logical to uint8 for the histogram count calculation so that the pixel values are discrete and directly correspond to a bin value.
\end{tabular} \\
\hline Examples & \[
\begin{aligned}
& \text { I }=\text { imread('circuit.tif'); } \\
& \text { J }=\text { entropyfilt(I); }
\end{aligned}
\] \\
\hline
\end{tabular}
imshow(I), figure, imshow(J,[]);

\author{
References [1] Gonzalez, R.C., R.E. Woods, S.L. Eddins, Digital Image Processing Using MATLAB, New Jersey, Prentice Hall, 2003, Chapter 11.
}

See Also entropy | imhist | rangefilt | stdfilt

Purpose
Convert fan-beam projections to parallel-beam
Syntax
```

P = fan2para(F,D)
P = fan2para(..., param1, val1, param2, val2,...)
[P ,parallel_locations,
parallel_rotation_angles] = fan2para(...)

```

Description
\(P=\) fan2para( \(F, D\) ) converts the fan-beam data \(F\) to the parallel-beam data \(P\). \(D\) is the distance in pixels from the fan-beam vertex to the center of rotation that was used to obtain the projections.
\(P=\) fan2para(..., param1, val1, param2, val2,...) specifies parameters that control various aspects of the fan2para conversion, listed in the following table. Parameter names can be abbreviated, and case does not matter.
\begin{tabular}{|c|c|}
\hline Parameter & Description \\
\hline 'FanCoverage' & \begin{tabular}{l}
String specifying the range through which the beams are rotated. \\
'cycle' - Rotate through the full range \([0,360)\). This is the default. \\
'minimal' - Rotate the minimum range necessary to represent the object.
\end{tabular} \\
\hline 'FanRotationIncrement' & Positive real scalar specifying the increment of the rotation angle of the fan-beam projections, measured in degrees. Default value is 1 . \\
\hline
\end{tabular}

\section*{fan2para}
\begin{tabular}{l|l}
\hline Parameter & Description \\
\hline 'FanSensorGeometry' & \begin{tabular}{l} 
String specifying how sensors are positioned. \\
'arc' — Sensors are spaced equally along a \\
circular arc at distance D from the center of \\
rotation. Default value is 'arc' \\
'line' — Sensors are spaced equally along a \\
line, the closest point of which is distance D from \\
the center of rotation. \\
See fanbeam for details.
\end{tabular} \\
\hline 'FanSensorSpacing' & \begin{tabular}{l} 
Positive real scalar specifying the spacing of the \\
fan-beam sensors. Interpretation of the value \\
depends on the setting of 'FanSensorGeometry '
\end{tabular} \\
& \begin{tabular}{l} 
If 'FanSensorGeometry ' is set to ' arc ' (the \\
default), the value defines the angular spacing in \\
degrees. Default value is 1. \\
If 'FanSensorGeometry' is 'line ', the value
\end{tabular} \\
specifies the linear spacing. Default value is 1. \\
See fanbeam for details.
\end{tabular}
\begin{tabular}{|c|c|}
\hline Parameter & Description \\
\hline 'Interpolation' & Text string specifying the type of interpolation used between the parallel-beam and fan-beam data.
```

'nearest' - Nearest-neighbor
\{'linear'\} - Linear
'spline' - Piecewise cubic spline
'pchip' — Piecewise cubic Hermite (PCHIP)
cubic' - Same as 'pchip'

``` \\
\hline 'ParallelCoverage' & Text string specifying the range of rotation. 'cycle' - Parallel data covers 360 degrees \{'halfcycle' \} — Parallel data covers 180 degrees \\
\hline 'ParallelRotationIncrement' & \begin{tabular}{l}
Positive real scalar specifying the parallel-beam rotation angle increment, measured in degrees. Parallel beam angles are calculated to cover \([0,180)\) degrees with increment PAR_ROT_INC, where PAR_ROT_INC is the value of 'ParallelRotationIncrement'. 180/PAR_ROT_INC must be an integer. \\
If 'ParallelRotationIncrement' is not specified, the increment is assumed to be the same as the increment of the fan-beam rotation angles.
\end{tabular} \\
\hline 'ParallelSensorSpacing' & Positive real scalar specifying the spacing of the parallel-beam sensors in pixels. The range of sensor locations is implied by the range of fan angles and is given by
\[
\begin{aligned}
& {\left[D^{*} \tan (\min (\text { FAN_ANGLES })), \ldots\right.} \\
& \text { D*tan }(\max (\text { FAN_ANGLES }))]
\end{aligned}
\] \\
\hline
\end{tabular}

\section*{fan2para}
\begin{tabular}{l|l}
\hline Parameter & Description \\
\hline
\end{tabular}

If 'ParallelSensorSpacing' is not specified, the spacing is assumed to be uniform and is set to the minimum spacing implied by the fan angles and sampled over the range implied by the fan angles.
```

[P ,parallel_locations, parallel_rotation_angles] =

```
fan2para(...) returns the parallel-beam sensor locations in
parallel_locations and rotation angles in parallel_rotation_angles.

\section*{Class \\ Support}

\section*{Examples}

The input arguments, F and D, can be double or single, and they must be nonsparse. All other numeric inputs are double. The output \(P\) is double.

Create synthetic parallel-beam data, derive fan-beam data, and then use the fan-beam data to recover the parallel-beam data.
```

ph = phantom(128);
theta = 0:179;
[Psynthetic,xp] = radon(ph,theta);
imshow(Psynthetic,[],...
'XData',theta,'YData',xp,'InitialMagnification','fit')
axis normal
title('Synthetic Parallel-Beam Data')
xlabel('0 (degrees)')
ylabel('x''')
colormap(hot), colorbar
Fsynthetic = para2fan(Psynthetic,100,'FanSensorSpacing',1);

```

Recover original parallel-beam data.
```

[Precovered,Ploc,Pangles] = fan2para(Fsynthetic,100,...
'FanSensorSpacing',1,...
'ParallelSensorSpacing',1);
figure
imshow(Precovered,[],'XData', Pangles,...

```
```

    'YData',Ploc,'InitialMagnification','fit')
    axis normal
title('Recovered Parallel-Beam Data')
xlabel('Rotation Angles (degrees)')
ylabel('Parallel Sensor Locations (pixels)')
colormap(hot), colorbar

```

\author{
See Also \\ fanbeam | ifanbeam | iradon | para2fan | phantom | radon
}

Purpose Fan-beam transform
```

Syntax
F = fanbeam(I, D)
F = fanbeam(..., param1, val1, param1, val2,...)
[F, fan_sensor_positions, fan_rotation_angles] = fanbeam(...)

```

\section*{Description}
\(F=\) fanbeam ( \(I, D\) ) computes the fan-beam data (sinogram) \(F\) from the image I. A sinogram is a special x-ray procedure that is done with contrast media (x-ray dye) to visualize any abnormal opening (sinus) in the body.
\(D\) is the distance in pixels from the fan-beam vertex to the center of rotation. The center of rotation is the center pixel of the image, defined as floor ( (size (I) +1)/2). D must be large enough to ensure that the fan-beam vertex is outside of the image at all rotation angles. See "Tips" on page 3-183 for guidelines on specifying D. The following figure illustrates \(D\) in relation to the fan-beam vertex for one fan-beam geometry. See the FanSensorGeometry parameter for more information.


Each column of \(F\) contains the fan-beam sensor samples at one rotation angle. The number of columns in \(F\) is determined by the fan rotation increment. By default, the fan rotation increment is 1 degree so \(F\) has 360 columns.

The number of rows in \(F\) is determined by the number of sensors. fanbeam determines the number of sensors by calculating how many beams are required to cover the entire image for any rotation angle.

For information about how to specify the rotation increment and sensor spacing, see the documentation for the FanRotationIncrement and FanSensorSpacing parameters, below.

F = fanbeam(..., param1, val1, param1, val2,...) specifies parameters, listed below, that control various aspects of the fan-beam projections. Parameter names can be abbreviated, and case does not matter.
'FanRotationIncrement' -- Positive real scalar specifying the increment of the rotation angle of the fan-beam projections. Measured in degrees. Default value is 1 .
'FanSensorGeometry' -- Text string specifying how sensors are positioned. Valid values are 'arc' or 'line'. In the 'arc' geometry, sensors are spaced equally along a circular arc, as shown below. This is the default value.


In 'line' geometry, sensors are spaced equally along a line, as shown below.

\section*{fanbeam}

'FanSensorSpacing' -- Positive real scalar specifying the spacing of the fan-beam sensors. Interpretation of the value depends on the setting of 'FanSensorGeometry'. If 'FanSensorGeometry' is set to 'arc' (the default), the value defines the angular spacing in degrees. Default value is 1 . If 'FanSensorGeometry' is 'line', the value specifies the linear spacing. Default value is 1 .

Note This linear spacing is measured on the \(x\) ' axis. The \(x\) ' axis for each column, col, of \(F\) is oriented at fan_rotation_angles (col) degrees counterclockwise from the x -axis. The origin of both axes is the center pixel of the image.
[F, fan_sensor_positions, fan_rotation_angles] = fanbeam(...) returns the location of fan-beam sensors in fan_sensor_positions and the rotation angles where the fan-beam projections are calculated in fan_rotation_angles.

If 'FanSensorGeometry' is 'arc' (the default), fan_sensor_positions contains the fan-beam spread angles. If 'FanSensorGeometry' is 'line', fan_sensor_positions contains the fan-beam sensor positions along the \(x\) 'axis. See 'FanSensorSpacing' for more information.

\section*{Class \\ Support}

Tips
I can be logical or numeric. All other numeric inputs and outputs can be double. None of the inputs can be sparse.

As a guideline, try making D a few pixels larger than half the image diagonal dimension, calculated as follows
```

sqrt(size(I,1)^2 + size(I,2)^2)

```

The values returned in F are a numerical approximation of the fan-beam projections. The algorithm depends on the Radon transform, interpolated to the fan-beam geometry. The results vary depending on the parameters used. You can expect more accurate results when the image is larger, \(D\) is larger, and for points closer to the middle of the image, away from the edges.

\section*{Examples}

The following example computes the fan-beam projections for rotation angles that cover the entire image.
```

iptsetpref('ImshowAxesVisible','on')
ph = phantom(128);
imshow(ph)
[F,Fpos,Fangles] = fanbeam(ph,250);
figure
imshow(F,[],'XData',Fangles,'YData',Fpos,...
'InitialMagnification','fit')
axis normal
xlabel('Rotation Angles (degrees)')
ylabel('Sensor Positions (degrees)')
colormap(hot), colorbar

```

The following example computes the Radon and fan-beam projections and compares the results at a particular rotation angle.
```

I = ones(100);
D = 200;
dtheta = 45;

```

\section*{fanbeam}
```

% Compute fan-beam projections for 'arc' geometry
[Farc,FposArcDeg,Fangles] = fanbeam(I,D,...
'FanSensorGeometry','arc',...
'FanRotationIncrement',dtheta);
% Convert angular positions to linear distance
% along x-prime axis
FposArc = D*tan(FposArcDeg*pi/180);
% Compute fan-beam projections for 'line' geometry
[Fline,FposLine] = fanbeam(I,D,...
'FanSensorGeometry','line',...
'FanRotationIncrement',dtheta);
% Compute the corresponding Radon transform
[R,Rpos]=radon(I,Fangles);
% Display the three projections at one particular rotation
% angle. Note the three are very similar. Differences are
% due to the geometry of the sampling, and the numerical
% approximations used in the calculations.
figure
idx = find(Fangles==45);
plot(Rpos,R(:,idx),...
FposArc,Farc(:,idx),...
FposLine,Fline(:,idx))
legend('Radon','Arc','Line')

```

\section*{References \\ [1] Kak, A.C., \& Slaney, M., Principles of Computerized Tomographic}
``` Imaging, IEEE Press, NY, 1988, pp. 92-93.
```

[^3]| Purpose | Find output bounds for spatial transformation |
| :---: | :---: |
| Syntax | outbounds = findbounds(TFORM, inbounds) |
| Description | outbounds $=$ findbounds(TFORM, inbounds) estimates the output bounds corresponding to a given spatial transformation and a set of input bounds. TFORM, as returned by maketform, is a spatial transformation structure. inbounds is a 2 -by-num_dims matrix. The first row of inbounds specifies the lower bounds for each dimension, and the second row specifies the upper bounds. num_dims has to be consistent with the ndims_in field of TFORM. <br> outbounds has the same form as inbounds. It is an estimate of the smallest rectangular region completely containing the transformed rectangle represented by the input bounds. Since outbounds is only an estimate, it might not completely contain the transformed input rectangle. |
| Tips | findbounds gets called by imtransform if 'XData' and 'YData', the parameters that control the output-space bounding box in imtransform, are not specified. findbounds computes the output-space bounding box. |
| Algorithms | 1 findbounds first creates a grid of input-space points. These points are located at the center, corners, and middle of each edge in the image. |
|  | ```I = imread('rice.png'); h = imshow(I); set(h,'AlphaData',0.3); axis on, grid on``` |
|  | $\begin{gathered} \text { in_points }=\left[\begin{array}{l} \ldots .5000 \\ 0.5000 \end{array}, ~\right. \end{gathered}$ |
|  | 0.5000256 .5000 |
|  | $256.5000 \quad 0.5000$ |
|  | 256.5000256 .5000 |
|  | 0.5000128 .5000 |
|  | 128.50000 .5000 |

## findbounds

```
    128.5000 128.5000
    128.5000 256.5000
    256.5000 128.5000];
hold on
plot(in_points(:,1),in_points(:,2),'.','MarkerSize',18)
hold off
```



## Grid of Input-Space Points

2 Next, findbounds transforms the grid of input-space points to output space. If tform contains a forward transformation (a nonempty forward_fon field), then findbounds transforms the input-space points using tformfwd. For example:

```
tform = maketform('affine', ...
    [1.1067 -0.2341 0; 0.5872 1.1769 0; 1000 -300 1]);
out_points = tformfwd(tform, in_points)
```

The output appears below:

```
out_points =
    1.0e+003 *
```

| 1.0008 | -0.2995 |
| ---: | ---: |
| 1.1512 | 0.0018 |
| 1.2842 | -0.3595 |
| 1.4345 | -0.0582 |
| 1.0760 | -0.1489 |
| 1.1425 | -0.3295 |
| 1.2177 | -0.1789 |
| 1.2928 | -0.0282 |
| 1.3593 | -0.2088 |

If TFORM does not contain a forward transformation, then findbounds estimates the output bounds using the Nelder-Mead optimization function fminsearch.

3 Finally, findbounds computes the bounding box of the transformed grid of points.

See Also

cp2tform | imtransform | maketform | tformarray | tformfwd tforminv

## fliptform

Purpose Flip input and output roles of TFORM structure

## Syntax TFLIP = fliptform( $T$ )

Description TFLIP $=$ fliptform $(T)$ creates a new spatial transformation structure, a TFORM struct, by flipping the roles of the inputs and outputs in an existing TFORM struct.

## Examples <br> T = maketform('affine', [. $500 ; .520 ; 001]) ;$ T2 = fliptform(T)

The following are equivalent:
x = tformfwd ([-3 7],T)
x = tforminv([-3 7],T2)

See Also<br>maketform | tformfwd | tforminv

## Purpose

2-D frequency response
Syntax

```
[H, f1, f2] = freqz2(h, n1, n2)
[H, f1, f2] = freqz2(h, [n2 n1])
[H, f1, f2] = freqz2(h)
[H, f1, f2] = freqz2(h, f1, f2)
[...] = freqz2(h,...,[dx dy])
[...] = freqz2(h,...,dx)
freqz2(...)
```


## Description

[H, f1, f2] = freqz2(h, n1, n2) returns H, the n2-by-n1 frequency response of $h$, and the frequency vectors $f 1$ (of length $n 1$ ) and f2 (of length n 2 ). h is a two-dimensional FIR filter, in the form of a computational molecule. f 1 and f 2 are returned as normalized frequencies in the range -1.0 to 1.0 , where 1.0 corresponds to half the sampling frequency, or $п$ radians.
[ $H, f 1, f 2]=$ freqz2(h, [n2 n1]) returns the same result returned by $[H, f 1, f 2]=\operatorname{freqz2(h,n1,n2)}$.
[H, f1, f2] = freqz2(h) uses [n2 n1] = [64 64].
[ $\mathrm{H}, \mathrm{f} 1, \mathrm{f} 2$ ] $=\mathrm{freqz2}(\mathrm{~h}, \mathrm{f} 1, \mathrm{f} 2)$ returns the frequency response for the FIR filter $h$ at frequency values in $f 1$ and $f 2$. These frequency values must be in the range -1.0 to 1.0 , where 1.0 corresponds to half the sampling frequency, or $п$ radians.
$[. .]=.\operatorname{freqz2}(h, \ldots,[d x d y])$ uses [dx $d y]$ to override the intersample spacing in h . dx determines the spacing for the $x$ dimension and dy determines the spacing for the $y$ dimension. The default spacing is 0.5 , which corresponds to a sampling frequency of 2.0 .
$[. .]=$. freqz2( $h, \ldots, d x$ ) uses $d x$ to determine the intersample spacing in both dimensions.
freqz2 (...) produces a mesh plot of the two-dimensional magnitude frequency response when no output arguments are specified.

## freqz2

## Class

Support

## Examples

The input matrix h can be of class double or of any integer class. All other inputs to freqz2 must be of class double. All outputs are of class double.

Use the window method to create a 16 -by- 16 filter, then view its frequency response using freqz2.

```
Hd = zeros(16,16);
Hd(5:12,5:12) = 1;
Hd(7:10,7:10) = 0;
h = fwind1(Hd,bartlett(16));
colormap(jet(64))
freqz2(h,[32 32]); axis ([-1 1 -1 1 0 1])
```



See Also freqz

## Purpose

Syntax

Description

Class
Support

## Examples

2-D FIR filter using frequency sampling
h = fsamp2(Hd)
h = fsamp2(f1, f2, Hd,[m n])
$h=$ fsamp2(Hd) designs a two-dimensional FIR filter with frequency response Hd, and returns the filter coefficients in matrix h . (fsamp2 returns $h$ as a computational molecule, which is the appropriate form to use with filter2.) The filter $h$ has a frequency response that passes through points in Hd. If Hd is m-by-n, then $h$ is also m-by-n.
fsamp2 designs two-dimensional FIR filters based on a desired two-dimensional frequency response sampled at points on the Cartesian plane. Hd is a matrix containing the desired frequency response sampled at equally spaced points between -1.0 and 1.0 along the $x$ and $y$ frequency axes, where 1.0 corresponds to half the sampling frequency, or $п$ radians.

$$
H_{d}\left(f_{1}, f_{2}\right)=\left.H_{d}\left(\omega_{1}, \omega_{2}\right)\right|_{\omega_{1}=\pi f_{1}, \omega_{2}=\pi f_{1}}
$$

For accurate results, use frequency points returned by freqspace to create Hd .
h = fsamp2(f1, f2, Hd,[m n]) produces an m-by-n FIR filter by matching the filter response at the points in the vectors f1 and f2. The frequency vectors $f 1$ and $f 2$ are in normalized frequency, where 1.0 corresponds to half the sampling frequency, or $п$ radians. The resulting filter fits the desired response as closely as possible in the least squares sense. For best results, there must be at least $m * n$ desired frequency points. fsamp2 issues a warning if you specify fewer than $m * n$ points.

The input matrix Hd can be of class double or of any integer class. All other inputs to fsamp2 must be of class double. All outputs are of class double.

Use fsamp2 to design an approximately symmetric two-dimensional bandpass filter with passband between 0.1 and 0.5 (normalized

## fsamp2

frequency, where 1.0 corresponds to half the sampling frequency, or п radians):

1 Create a matrix Hd that contains the desired bandpass response. Use freqspace to create the frequency range vectors $f 1$ and $f 2$.

```
[f1,f2] = freqspace(21,'meshgrid');
Hd = ones(21);
r = sqrt(f1.^2 + f2.^2);
Hd((r<0.1)|(r>0.5)) = 0;
colormap(jet(64))
mesh(f1,f2,Hd)
```



2 Design the filter that passes through this response.

```
h = fsamp2(Hd);
freqz2(h)
```



## Algorithms

## References

See Also
fsamp2 computes the filter h by taking the inverse discrete Fourier transform of the desired frequency response. If the desired frequency response is real and symmetric (zero phase), the resulting filter is also zero phase.
[1] Lim, Jae S., Two-Dimensional Signal and Image Processing, Englewood Cliffs, NJ, Prentice Hall, 1990, pp. 213-217.

Purpose Create predefined 2-D filter
Syntax $\quad h=$ fspecial (type)
h = fspecial(type, parameters)
Description
$h=$ fspecial(type) creates a two-dimensional filter $h$ of the specified type. fspecial returns $h$ as a correlation kernel, which is the appropriate form to use with imfilter. type is a string having one of these values.

| Value | Description |
| :--- | :--- |
| average | Averaging filter |
| disk | Circular averaging filter (pillbox) |
| gaussian | Gaussian lowpass filter |
| laplacian | Approximates the two-dimensional Laplacian <br> operator |
| log | Laplacian of Gaussian filter |
| motion | Approximates the linear motion of a camera |
| prewitt | Prewitt horizontal edge-emphasizing filter |
| sobel | Sobel horizontal edge-emphasizing filter |
| unsharp | Unsharp contrast enhancement filter |

h = fspecial(type, parameters) accepts the filter specified by type plus additional modifying parameters particular to the type of filter chosen. If you omit these arguments, fspecial uses default values for the parameters.

The following list shows the syntax for each filter type. Where applicable, additional parameters are also shown.

- $h=$ fspecial('average', hsize) returns an averaging filter $h$ of size hsize. The argument hsize can be a vector specifying the
number of rows and columns in h , or it can be a scalar, in which case $h$ is a square matrix. The default value for hsize is [ $\left.\begin{array}{ll}3 & 3\end{array}\right]$.
- $\mathrm{h}=$ fspecial('disk', radius) returns a circular averaging filter (pillbox) within the square matrix of side $2 *$ radius +1 . The default radius is 5 .
- h = fspecial('gaussian', hsize, sigma) returns a rotationally symmetric Gaussian lowpass filter of size hsize with standard deviation sigma (positive). hsize can be a vector specifying the number of rows and columns in $h$, or it can be a scalar, in which case $h$ is a square matrix. The default value for hsize is [3 3]; the default value for sigma is 0.5 .
- $\mathrm{h}=\mathrm{fspecial}($ 'laplacian', alpha) returns a 3-by-3 filter approximating the shape of the two-dimensional Laplacian operator. The parameter alpha controls the shape of the Laplacian and must be in the range 0.0 to 1.0. The default value for alpha is 0.2 .
- h = fspecial('log', hsize, sigma) returns a rotationally symmetric Laplacian of Gaussian filter of size hsize with standard deviation sigma (positive). hsize can be a vector specifying the number of rows and columns in $h$, or it can be a scalar, in which case $h$ is a square matrix. The default value for hsize is [5 5] and 0.5 for sigma.
- $\mathrm{h}=\mathrm{fspec} i a l($ (motion', len, theta) returns a filter to approximate, once convolved with an image, the linear motion of a camera by len pixels, with an angle of theta degrees in a counterclockwise direction. The filter becomes a vector for horizontal and vertical motions. The default len is 9 and the default theta is 0 , which corresponds to a horizontal motion of nine pixels.
To compute the filter coefficients, h , for 'motion':
1 Construct an ideal line segment with the desired length and angle, centered at the center coefficient of $h$.

2 For each coefficient location (i,j), compute the nearest distance between that location and the ideal line segment.

3 h = max(1-nearest_distance, 0);
4 Normalize h:h = h/(sum(h(:))

- $\mathrm{h}=\mathrm{fspecial}($ 'prewitt') returns the 3 -by-3 filter h (shown below) that emphasizes horizontal edges by approximating a vertical gradient. If you need to emphasize vertical edges, transpose the filter $\mathrm{h}^{\prime}$.

```
[ 1 1 1
    0 0 0
    -1 -1 -1 ]
```

To find vertical edges, or for $x$-derivatives, use $h^{\prime}$.

- $\mathrm{h}=\mathrm{fspecial}\left(\mathrm{'sobel}^{\prime}\right)$ returns a 3-by-3 filter h (shown below) that emphasizes horizontal edges using the smoothing effect by approximating a vertical gradient. If you need to emphasize vertical edges, transpose the filter $\mathrm{h}^{\prime}$.

```
[ 1 2 1
    0 0}
    -1 -2 -1 ]
```

- h = fspecial('unsharp', alpha) returns a 3-by-3 unsharp contrast enhancement filter. fspecial creates the unsharp filter from the negative of the Laplacian filter with parameter alpha. alpha controls the shape of the Laplacian and must be in the range 0.0 to 1.0. The default value for alpha is 0.2 .

Note Do not be confused by the name of this filter: an unsharp filter is an operator used to sharpen images. The name comes from a publishing industry process in which an image is sharpened by subtracting a blurred (unsharp) version of the image from itself.


#### Abstract

fspecial supports the generation of efficient, production-quality C/C++ code from MATLAB. For best results, all inputs must be constants at compilation time. Expressions or variables are allowed if their values do not change. To see a complete list of toolbox functions that support code generation, see "Supported Functions".


Class $\quad \mathrm{h}$ is of class double.

Examples $\quad$ I = imread('cameraman.tif');
subplot(2,2,1);
imshow(I); title('Original Image');
H = fspecial('motion', 20,45);
MotionBlur = imfilter(I,H,'replicate');
subplot(2,2,2);
imshow(MotionBlur);title('Motion Blurred Image');
H = fspecial('disk',10);
blurred = imfilter(I,H,'replicate');
subplot (2,2,3);
imshow(blurred); title('Blurred Image');
H = fspecial('unsharp');
sharpened = imfilter(I,H,'replicate');
subplot(2,2,4);
imshow(sharpened); title('Sharpened Image');


Algorithms fspecial creates Gaussian filters using

$$
\begin{aligned}
& h_{g}\left(n_{1}, n_{2}\right)=e^{\frac{-\left(n_{1}^{2}+n_{2}^{2}\right)}{2 \sigma^{2}}} \\
& h\left(n_{1}, n_{2}\right)=\frac{h_{g}\left(n_{1}, n_{2}\right)}{\sum_{n_{1}} \sum_{n_{2}} h_{g}}
\end{aligned}
$$

fspecial creates Laplacian filters using

$$
\begin{aligned}
& \nabla^{2}=\frac{\partial^{2}}{\partial x^{2}}+\frac{\partial^{2}}{\partial y^{2}} \\
& \nabla^{2}=\frac{4}{(\alpha+1)}\left[\begin{array}{ccc}
\frac{\alpha}{4} & \frac{1-\alpha}{4} & \frac{\alpha}{4} \\
\frac{1-\alpha}{4} & -1 & \frac{1-\alpha}{4} \\
\frac{\alpha}{4} & \frac{1-\alpha}{4} & \frac{\alpha}{4}
\end{array}\right]
\end{aligned}
$$

fspecial creates Laplacian of Gaussian (LoG) filters using

$$
\begin{aligned}
& h_{g}\left(n_{1}, n_{2}\right)=e^{\frac{-\left(n_{1}^{2}+n_{2}^{2}\right)}{2 \sigma^{2}}} \\
& h\left(n_{1}, n_{2}\right)=\frac{\left(n_{1}^{2}+n_{2}^{2}-2 \sigma^{2}\right) h_{g}\left(n_{1}, n_{2}\right)}{2 \pi \sigma^{6} \sum_{n_{1}} \sum_{n_{2}} h_{g}}
\end{aligned}
$$

fspecial creates averaging filters using ones( $\mathrm{n}(1), \mathrm{n}(2)) /(\mathrm{n}(1)$ *n(2))
fspecial creates unsharp filters using

$$
\frac{1}{(\alpha+1)}\left[\begin{array}{ccc}
-\alpha & \alpha-1 & -\alpha \\
\alpha-1 & \alpha+5 & \alpha-1 \\
-\alpha & \alpha-1 & -\alpha
\end{array}\right]
$$

See Also
conv2 | edge | filter2 | fsamp2 | fwind1 | fwind2 | imfilter | del2

## ftrans2

Purpose
2-D FIR filter using frequency transformation

## Syntax

h = ftrans2(b, t)
h = ftrans2(b)
$h=f t r a n s 2(b, t)$ produces the two-dimensional FIR filter $h$ that corresponds to the one-dimensional FIR filter b using the transform t. (ftrans2 returns h as a computational molecule, which is the appropriate form to use with filter2.) b must be a one-dimensional, Type I (even symmetric, odd-length) filter such as can be returned by fir1, fir2, or remez in the Signal Processing Toolbox software. The transform matrix $t$ contains coefficients that define the frequency transformation to use. If $t$ is $m$-by- $n$ and $b$ has length $Q$, then $h$ is size $((m-1) *(Q-1) / 2+1)$-by- $((n-1) *(Q-1) / 2+1)$.
$h=f t r a n s 2(b)$ uses the McClellan transform matrix $t$.
$\mathrm{t}=[121 ; 2$-4 2; 121$] / 8 ;$

All inputs and outputs should be of class double.
Tips
The transformation below defines the frequency response of the two-dimensional filter returned by ftrans2.

$$
H_{\left(\omega_{1}, \omega_{2}\right)}=\left.B(\omega)\right|_{\cos \omega=T\left(\omega_{1}, \omega_{2}\right)},
$$

where $B(\omega)$ is the Fourier transform of the one-dimensional filter b :

$$
B(\omega)=\sum_{n=-N}^{N} b(n) e^{-j \omega n}
$$

and $T\left(\omega_{1}, \omega_{2}\right)$ is the Fourier transform of the transformation matrix t :

$$
T\left(\omega_{1}, \omega_{2}\right)=\sum_{n_{2}} \sum_{n_{1}} t\left(n_{1}, n_{2}\right) e^{-j \omega_{1} n_{1}} e^{-j \omega_{2} n_{2}} .
$$

The returned filter h is the inverse Fourier transform of $H\left(\omega_{1}, \omega_{2}\right)$ :

$$
h\left(n_{1}, n_{2}\right)=\frac{1}{(2 \pi)^{2}} \int_{-\pi}^{\pi} \int_{-\pi}^{\pi} H\left(\omega_{1}, \omega_{2}\right) e^{j \omega_{1} n_{1}} e^{j \omega_{2} n_{2}} d \omega_{1} d \omega_{2} .
$$

## Examples

Use ftrans2 to design an approximately circularly symmetric two-dimensional bandpass filter with passband between 0.1 and 0.6 (normalized frequency, where 1.0 corresponds to half the sampling frequency, or п radians):

1 Since ftrans2 transforms a one-dimensional FIR filter to create a two-dimensional filter, first design a one-dimensional FIR bandpass filter using the Signal Processing Toolbox function remez.

```
colormap(jet(64))
b = remez(10,[0 0.05 0.15 0.55 0.65 1],[0 0 1 1 0 0]);
[H,w] = freqz(b,1,128,'whole');
plot(w/pi-1,fftshift(abs(H)))
```



## ftrans2

2 Use ftrans2 with the default McClellan transformation to create the desired approximately circularly symmetric filter.

```
h = ftrans2(b);
freqz2(h)
```



References [1] Lim, Jae S., Two-Dimensional Signal and Image Processing, Englewood Cliffs, NJ, Prentice Hall, 1990, pp. 218-237.

See Also conv2 | filter2 | fsamp2 | fwind1 | fwind2

## Purpose

2-D FIR filter using 1-D window method
Syntax
h = fwind1(Hd, win)
$h=$ fwind1(Hd, win1, win2)
h = fwind1(f1, f2, Hd,...)

## Description

fwind1 designs two-dimensional FIR filters using the window method. fwind1 uses a one-dimensional window specification to design a two-dimensional FIR filter based on the desired frequency response Hd. fwind1 works with one-dimensional windows only; use fwind2 to work with two-dimensional windows.
$\mathrm{h}=\mathrm{fwind1}(\mathrm{Hd}$, win) designs a two-dimensional FIR filter h with frequency response Hd. (fwind 1 returns $h$ as a computational molecule, which is the appropriate form to use with filter2.) fwind1 uses the one-dimensional window win to form an approximately circularly symmetric two-dimensional window using Huang's method. You can specify win using windows from the Signal Processing Toolbox software, such as boxcar, hamming, hanning, bartlett, blackman, kaiser, or chebwin. If length (win) is $n$, then $h$ is $n$-by- $n$.

Hd is a matrix containing the desired frequency response sampled at equally spaced points between -1.0 and 1.0 (in normalized frequency, where 1.0 corresponds to half the sampling frequency, or $п$ radians) along the $x$ and $y$ frequency axes. For accurate results, use frequency points returned by freqspace to create Hd. (See the entry for freqspace for more information.)
h = fwind1(Hd, win1, win2) uses the two one-dimensional windows win1 and win2 to create a separable two-dimensional window. If length (win1) is $n$ and length (win2) is $m$, then $h$ is m-by- $n$.
$h=f w i n d 1(f 1, f 2, H d, \ldots)$ lets you specify the desired frequency response Hd at arbitrary frequencies ( f 1 and f 2 ) along the $x$ - and $y$-axes. The frequency vectors $f 1$ and $f 2$ should be in the range -1.0 to 1.0 , where 1.0 corresponds to half the sampling frequency, or $n$ radians. The length of the windows controls the size of the resulting filter, as above.

## Class <br> Support

## Examples

The input matrix Hd can be of class double or of any integer class. All other inputs to fwind1 must be of class double. All outputs are of class double.

Use fwind1 to design an approximately circularly symmetric two-dimensional bandpass filter with passband between 0.1 and 0.5 (normalized frequency, where 1.0 corresponds to half the sampling frequency, or п radians):

1 Create a matrix Hd that contains the desired bandpass response. Use freqspace to create the frequency range vectors f1 and f2.

```
[f1,f2] = freqspace(21,'meshgrid');
Hd = ones(21);
r = sqrt(f1.^2 + f2.^2);
Hd((r<0.1)|(r>0.5)) = 0;
colormap(jet(64))
mesh(f1,f2,Hd)
```



2 Design the filter using a one-dimensional Hamming window.

```
h = fwind1(Hd,hamming(21));
freqz2(h)
```



## Algorithms

fwind1 takes a one-dimensional window specification and forms an approximately circularly symmetric two-dimensional window using Huang's method,

$$
w\left(n_{1}, n_{2}\right)=\left.w(t)\right|_{t=\sqrt{n_{1}^{2}+n_{2}^{2}}},
$$

where $w(t)$ is the one-dimensional window and $w\left(n_{1}, n_{2}\right)$ is the resulting two-dimensional window.

Given two windows, fwind1 forms a separable two-dimensional window:

$$
w\left(n_{1}, n_{2}\right)=w_{1}\left(n_{1}\right) w_{2}\left(n_{2}\right) .
$$

fwind1 calls fwind2 with Hd and the two-dimensional window. fwind2 computes h using an inverse Fourier transform and multiplication by the two-dimensional window:

$$
\begin{aligned}
& h_{d}\left(n_{1}, n_{2}\right)=\frac{1}{(2 \pi)^{2}} \int_{-\pi}^{\pi} \int_{-\pi}^{\pi} H_{d}\left(\omega_{1}, \omega_{2}\right) e^{j \omega_{1} n_{1}} e^{j \omega_{2} n_{2}} d \omega_{1} d \omega_{2} \\
& h\left(n_{1}, n_{2}\right)=h_{d}\left(n_{1}, n_{2}\right) w\left(n_{2}, n_{2}\right)
\end{aligned}
$$

References [1] Lim, Jae S., Two-Dimensional Signal and Image Processing, Englewood Cliffs, NJ, Prentice Hall, 1990.

See Also conv2 | filter2 | fsamp2 | freqspace | ftrans2 | fwind2

## Purpose

Syntax

Description

## Class <br> Support

Examples

2-D FIR filter using 2-D window method
h = fwind2(Hd, win)
h = fwind2(f1, f2, Hd, win)
Use fwind2 to design two-dimensional FIR filters using the window method. fwind2 uses a two-dimensional window specification to design a two-dimensional FIR filter based on the desired frequency response Hd. fwind2 works with two-dimensional windows; use fwind1 to work with one-dimensional windows.
$\mathrm{h}=\mathrm{fwind}$ (Hd, win) produces the two-dimensional FIR filter h using an inverse Fourier transform of the desired frequency response Hd and multiplication by the window win. Hd is a matrix containing the desired frequency response at equally spaced points in the Cartesian plane. fwind 2 returns $h$ as a computational molecule, which is the appropriate form to use with filter2. $h$ is the same size as win.
For accurate results, use frequency points returned by freqspace to create Hd. (See the entry for freqspace for more information.)
h = fwind2(f1, f2, Hd, win) lets you specify the desired frequency response Hd at arbitrary frequencies ( f 1 and f 2 ) along the $x$ - and $y$-axes. The frequency vectors $f 1$ and $f 2$ should be in the range -1.0 to 1.0 , where 1.0 corresponds to half the sampling frequency, or $п$ radians. $h$ is the same size as win.

The input matrix Hd can be of class double or of any integer class. All other inputs to fwind2 must be of class double. All outputs are of class double.

Use fwind2 to design an approximately circularly symmetric two-dimensional bandpass filter with passband between 0.1 and 0.5 (normalized frequency, where 1.0 corresponds to half the sampling frequency, or п radians):

1 Create a matrix Hd that contains the desired bandpass response. Use freqspace to create the frequency range vectors f1 and f2.

## fwind2

[f1,f2] = freqspace(21,'meshgrid');
$\mathrm{Hd}=$ ones(21);
$r=\operatorname{sqrt}\left(f 1 .{ }^{\wedge} 2+f 2 . \wedge 2\right) ;$
$H d((r<0.1) \mid(r>0.5))=0 ;$
colormap (jet(64))
mesh(f1,f2,Hd)


2 Create a two-dimensional Gaussian window using fspecial.

```
win = fspecial('gaussian',21,2);
win = win ./ max(win(:)); % Make the maximum window value be 1.
mesh(win)
```



3 Design the filter using the window from step 2.
h = fwind2(Hd,win);
freqz2(h)

## fwind2



## Algorithms

fwind2 computes h using an inverse Fourier transform and multiplication by the two-dimensional window win.

$$
\begin{aligned}
& h_{d}\left(n_{1}, n_{2}\right)=\frac{1}{(2 \pi)^{2}} \int_{-\pi}^{\pi} \int_{-\pi}^{\pi} H_{d}\left(\omega_{1}, \omega_{2}\right) e^{j \omega_{1} n_{1}} e^{j \omega_{2} n_{2}} d \omega_{1} d \omega_{2} \\
& h\left(n_{1}, n_{2}\right)=h_{d}\left(n_{1}, n_{2}\right) w\left(n_{1}, n_{2}\right)
\end{aligned}
$$

References

See Also
[1] Lim, Jae S., Two-Dimensional Signal and Image Processing, Englewood Cliffs, NJ, Prentice Hall, 1990, pp. 202-213.
Purpose Height of structuring element
Syntax H = getheight(SE)
Description $H$ = getheight(SE) returns an array the same size as getnhood(SE)containing the height associated with each of the structuring elementneighbors. H is all zeros for a flat structuring element.
Class SE is a STREL object. H is of class double.
Support
Examples se $=$ strel(ones(3,3),magic(3)); getheight(se)
See Also strel | getnhood

Purpose Image data from axes
Syntax $\quad A=$ getimage $(h)$
[ $\mathrm{x}, \mathrm{y}, \mathrm{A}]=$ getimage $(\mathrm{h})$
[..., A, flag] = getimage(h)
[...] = getimage

## Description

$A=$ getimage ( $h$ ) returns the first image data contained in the Handle Graphics object h . h can be a figure, axes, or image. A is identical to the image CData; it contains the same values and is of the same class (uint8, uint16, double, or logical) as the image CData. If $h$ is not an image or does not contain an image, $A$ is empty.
$[x, y, A]=$ getimage $(h)$ returns the image XData in $x$ and the YData in $y$. XData and YData are two-element vectors that indicate the range of the $x$-axis and $y$-axis.
[..., A, flag] = getimage $(\mathrm{h})$ returns an integer flag that indicates the type of image $h$ contains. This table summarizes the possible values for flag.

| Flag | Type of Image |
| :--- | :--- |
| 0 | Not an image; A is returned as an empty matrix |
| 1 | Indexed image |
| 2 | Intensity image with values in standard range ([0,1] for <br> single and double arrays, [0,255] for uint8 arrays, <br> $[0,65535]$ for uint16 arrays) |
| 3 | Intensity data, but not in standard range |
| 4 | RGB image |
| 5 | Binary image |

[...] = getimage returns information for the current axes object. It is equivalent to [...] = getimage(gca).

## Class Support

## Note

The output array A is of the same class as the image CData. All other inputs and outputs are of class double.

For int16 and single images, the image data returned by getimage is of class double, not int16 or single. This is because the getimage function gets the data from the image object's CData property and image objects store int16 and single image data as class double.
For example, create an image object of class int16. If you retrieve the CData from the object and check its class, it returns double.

```
h = imshow(ones(10,'int16'));
class(get(h,'CData'))
```

Therefore, if you get the image data using the getimage function, the data it returns is also of class double. The flag return value is set to 3 .

```
[img,flag] = getimage(h);
class(img)
```

The same is true for an image of class single. Getting the CData directly from the image object or by using getimage, the class of the returned data is double.

```
h = imshow(ones(10,'single'));
class(get(h,'CData'))
[img,flag] = getimage(h);
class(img)
```

For images of class single, the flag return value is set to 2 because single and double share the same dynamic range.

## Examples

After using imshow or imtool to display an image directly from a file, use getimage to get the image data into the workspace.

```
imshow rice.png
```

I = getimage;

## getimage

imtool cameraman.tif I = getimage(imgca);

See Also imshow | imtool

| Purpose | Image model object from image object |
| :--- | :--- |
| Syntax | imgmodel = getimagemodel(himage) |
| Description | imgmodel = getimagemodel(himage) returns the image model object <br> associated with himage. himage must be a handle to an image object or <br> an array of handles to image objects. |
|  | The return value imgmodel is an image model object. If himage is an <br> array of handles to image objects, imgmodel is an array of image models. <br> If himage does not have an associated image model object, <br> getimagemodel creates one. |
| Examples | h = imshow('bag. png'); <br> imgmodel $=$ getimagemodel $(\mathrm{h}) ;$ |
| See Also | imagemodel |

Purpose $\quad$ Select polyline with mouse

Syntax $\quad$| $[x, y]$ | $=\operatorname{getline}(f i g)$ |
| ---: | :--- |
| $[x, y]$ | $=\operatorname{getline}(a x)$ |
| $[x, y]$ | $=\operatorname{getline}$ |
| $[x, y]$ | $=\operatorname{getline}\left(\ldots\right.$, ' closed $\left.^{\prime}\right)$ |

Description
$[x, y]=$ getline(fig) lets you select a polyline in the current axes of figure fig using the mouse. Coordinates of the polyline are returned in $X$ and $Y$. Use normal button clicks to add points to the polyline. A shift-, right-, or double-click adds a final point and ends the polyline selection. Pressing Return or Enter ends the polyline selection without adding a final point. Pressing Backspace or Delete removes the previously selected point from the polyline.
$[x, y]=$ getline(ax) lets you select a polyline in the axes specified by the handle ax.
$[x, y]=$ getline is the same as $[x, y]=$ getline (gcf).
[x, y] = getline(...,'closed') animates and returns a closed polygon.

## See Also <br> getpts | getrect

Purpose Structuring element neighbor locations and heights
Syntax [offsets, heights] = getneighbors(SE)
Description
[offsets, heights] = getneighbors(SE) returns the relativelocations and corresponding heights for each of the neighbors in thestructuring element object SE.offsets is a P-by- N array where P is the number of neighbors in thestructuring element and N is the dimensionality of the structuringelement. Each row of offsets contains the location of the correspondingneighbor, relative to the center of the structuring element.
heights is a P-element column vector containing the height of each structuring element neighbor.
Class
Support
SE is a STREL object. The return values offsets and heights are arrays of double-precision values.
Examples
se = strel([1 0 1],[5 0 -5])
[offsets, heights] = getneighbors(se)
se =
Nonflat STREL object containing 2 neighbors.
Neighborhood:
101
Height:
$5 \quad 0 \quad-5$
offsets =
$0-1$
$0 \quad 1$
heights =
$5-5$
See Also strel | getnhood | getheight
Purpose Structuring element neighborhood
Syntax NHOOD = getnhood(SE)
Description NHOOD = getnhood(SE) returns the neighborhood associated with the structuring element SE .
Class SE is a STREL object. NHOOD is a logical array. Support
Examples se = strel(eye(5));
NHOOD = getnhood(se)
See Also strel | getneighbors

## Purpose Specify points with mouse

Syntax
[x, y] = getpts(fig)
$[x, y]=$ getpts(ax)
[x, y] = getpts
Description
$[x, y]=$ getpts(fig) lets you choose a set of points in the current axes of figure fig using the mouse. Coordinates of the selected points are returned in X and Y .

Use normal button clicks to add points. A shift-, right-, or double-click adds a final point and ends the selection. Pressing Return or Enter ends the selection without adding a final point. Pressing Backspace or Delete removes the previously selected point.
$[\mathrm{x}, \mathrm{y}]=$ getpts(ax) lets you choose points in the axes specified by the handle ax.
$[x, y]=$ getpts is the same as $[x, y]=$ getpts(gcf).
See Also getline | getrect

## Purpose Default display range of image based on its class

```
Syntax range = getrangefromclass(I)
```

Description range $=$ getrangefromclass(I) returns the default display range of the image I, based on its class type. The function returns range, a two-element vector specifying the display range in the form [min max].
$\begin{array}{ll}\text { Class } & \text { I can be uint8, uint16, int16, logical, single, or double. range is } \\ \text { Support } & \text { of class double. }\end{array}$
Note

Examples Read in the 16 -bit DICOM image and get the default display range.

```
CT = dicomread('CT-MONO2-16-ankle.dcm');
r = getrangefromclass(CT)
r =
```

$$
-32768 \quad 32767
$$

See Also intmin | intmax

## Purpose Specify rectangle with mouse

Syntax<br>Description

rect = getrect
rect = getrect(fig)
rect = getrect(ax)
rect $=$ getrect lets you select a rectangle in the current axes using the mouse. Use the mouse to click and drag the desired rectangle. rect is a four-element vector with the form [xmin ymin width height]. To constrain the rectangle to be a square, use a shift- or right-click to begin the drag.
rect $=$ getrect(fig) lets you select a rectangle in the current axes of figure fig using the mouse.
rect $=$ getrect (ax) lets you select a rectangle in the axes specified by the handle ax.

## Examples Select a rectangle in an image of the moon: <br> ```imshow('moon.tif')``` <br> rect = getrect

See Also getline | getpts

## Purpose Sequence of decomposed structuring elements

## Syntax $\quad$ SEQ $=$ getsequence $(S E)$

Description

## Class <br> Support

Examples The strel function uses decomposition for square structuring elements larger than 3-by-3. Use getsequence to extract the decomposed structuring elements.

```
se = strel('square',5)
se =
Flat STREL object containing 25 neighbors.
Decomposition: 2 STREL objects containing a total of 10 neighbors
Neighborhood:
\begin{tabular}{lllll}
1 & 1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 & 1
\end{tabular}
seq = getsequence(se)
seq =
2x1 array of STREL objects
```

Use imdilate with the 'full' option to see that dilating sequentially with the decomposed structuring elements really does form a 5 -by- 5 square:
imdilate(1,seq,'full')

See Also imdilate | imerode | strel

## Purpose Convert grayscale or binary image to indexed image

```
Syntax
[X, map] = gray2ind(I,n)
[X, map] = gray2ind(BW,n)
```

Class Support

Examples
Convert a grayscale image into an indexed image and then view the result.

I = imread('cameraman.tif');
[X, map] = gray2ind(I, 16);
imshow(X, map);
See Also grayslice | ind2gray | mat2gray

## Purpose

Create gray-level co-occurrence matrix from image

## Syntax

glcm = graycomatrix(I)
glcms = graycomatrix(I, param1, val1, param2, val2,...) [glcm, SI] = graycomatrix(...)

## Description

glcm = graycomatrix(I) creates a gray-level co-occurrence matrix (GLCM) from image I. graycomatrix creates the GLCM by calculating how often a pixel with gray-level (grayscale intensity) value $i$ occurs horizontally adjacent to a pixel with the value $j$. (You can specify other pixel spatial relationships using the 'Offsets' parameter -- see Parameters.) Each element ( $i, j$ ) in glcm specifies the number of times that the pixel with value $i$ occurred horizontally adjacent to a pixel with value $j$.
graycomatrix calculates the GLCM from a scaled version of the image. By default, if I is a binary image, graycomatrix scales the image to two gray-levels. If I is an intensity image, graycomatrix scales the image to eight gray-levels. You can specify the number of gray-levels graycomatrix uses to scale the image by using the 'NumLevels' parameter, and the way that graycomatrix scales the values using the 'GrayLimits ' parameter - see Parameters.

The following figure shows how graycomatrix calculates several values in the GLCM of the 4 -by- 5 image I. Element $(1,1)$ in the GLCM contains the value 1 because there is only one instance in the image where two, horizontally adjacent pixels have the values 1 and 1 . Element $(1,2)$ in the GLCM contains the value 2 because there are two instances in the image where two, horizontally adjacent pixels have the values 1 and 2. graycomatrix continues this processing to fill in all the values in the GLCM.

glcms = graycomatrix(I, param1, val1, param2, val2,...) returns one or more gray-level co-occurrence matrices, depending on the values of the optional parameter/value pairs. Parameter names can be abbreviated, and case does not matter.

Parameters
The following table lists these parameters in alphabetical order.

| Parameter | Description | Default |
| :---: | :---: | :---: |
| 'GrayLimits' | Two-element vector, [low high], that specifies how the grayscale values in I are linearly scaled into gray levels. Grayscale values less than or equal to low are scaled to 1 . Grayscale values greater than or equal to high are scaled to NumLevels. If graylimits is set to [], graycomatrix uses the minimum and maximum grayscale values in the image as limits, $[\min (I(:)) \quad \max (I(:))]$. | Minimum and maximum specified by class, e.g. double [0 1] int16 [-32768 32767] |
| 'NumLevels' | Integer specifying the number of gray-levels to use when scaling the grayscale values in I. For example, if NumLevels is 8, graycomatrix scales | 8 (numeric) <br> 2 (binary) |


| Parameter | Description | Default |
| :---: | :---: | :---: |
|  | the values in I so they are integers between 1 and 8 . The number of gray-levels determines the size of the gray-level co-occurrence matrix ( glcm ). |  |
| 'Offset' | p-by- 2 array of integers specifying the distance between the pixel of interest and its neighbor. Each row in the array is a two-element vector, [row_offset, col_offset], that specifies the relationship, or offset, of a pair of pixels. row_offset is the number of rows between the pixel-of-interest and its neighbor. col_offset is the number of columns between the pixel-of-interest and its neighbor. Because the offset is often expressed as an angle, the following table lists the offset values that specify common angles, given the pixel distance D . <br> The figure illustrates the array: offset $=$ [0 $1 ;-11 ;-10 ;-1 \begin{gathered}-1] \\ 90^{-}[-10]\end{gathered}$ | $\left[\begin{array}{ll}0 & 1\end{array}\right]$ |
| 'Symmetric' | Boolean that creates a GLCM where the ordering of values in the pixel pairs is not considered. For example, when 'Symmetric' is set to true, | false |

## graycomatrix

| Parameter | Description | Default |
| :--- | :--- | :--- |
|  | graycomatrix counts both 1,2 and 2,1 pairings <br> when calculating the number of times the value <br> 1 is adjacent to the value 2. When 'Symmetric' <br> is set to false, graycomatrix only counts 1,2 <br> or 2,1, depending on the value of 'offset '. See <br> "Notes" on page 3-228. |  |

[glcm, SI] = graycomatrix(...) returns the scaled image, SI, used to calculate the gray-level co-occurrence matrix. The values in SI are between 1 and NumLevels.

## Class Support

Notes

I can be numeric or logical but must be two-dimensional, real, and nonsparse. SI is a double matrix having the same size as I. glcms is a 'NumLevels'-by- 'NumLevels'-by-P double array where $P$ is the number of offsets in 'Offset'.

Another name for a gray-level co-occurrence matrix is a gray-level spatial dependence matrix. Also, the word co-occurrence is frequently used in the literature without a hyphen, cooccurrence.
graycomatrix ignores pixel pairs if either of the pixels contains a NaN.
graycomatrix replaces positive Infs with the value NumLevels and replaces negative Infs with the value 1.
graycomatrix ignores border pixels, if the corresponding neighbor pixel falls outside the image boundaries.

The GLCM created when 'Symmetric' is set to true is symmetric across its diagonal, and is equivalent to the GLCM described by Haralick (1973). The GLCM produced by the following syntax, with 'Symmetric' set to true

```
graycomatrix(I, 'offset', [0 1], 'Symmetric', true)
```

is equivalent to the sum of the two GLCMs produced by the following statements where 'Symmetric' is set to false.

```
graycomatrix(I, 'offset', [0 1], 'Symmetric', false)
graycomatrix(I, 'offset', [0 -1], 'Symmetric', false)
```


## Examples

Calculate the gray-level co-occurrence matrix for a grayscale image.

```
I = imread('circuit.tif');
glcm = graycomatrix(I,'Offset',[2 0]);
```

Calculate the gray-level co-occurrence matrix and return the scaled version of the image, SI, used by graycomatrix to generate the GLCM.

```
I = [ 1 1 5 6 8 8; 2 3 5 7 0 2; 0 2 3 5 6 7];
[glcm,SI] = graycomatrix(I,'NumLevels',9,'G',[])
```

References Haralick, R.M., K. Shanmugan, and I. Dinstein, "Textural Features for Image Classification", IEEE Transactions on Systems, Man, and Cybernetics, Vol. SMC-3, 1973, pp. 610-621.<br>Haralick, R.M., and L.G. Shapiro. Computer and Robot Vision: Vol. 1, Addison-Wesley, 1992, p. 459.

## See Also

| Purpose | Properties of gray-level co-occurrence matrix |
| :--- | :--- |
| Syntax | stats = graycoprops (glcm, properties) |
| Description | stats $=$ graycoprops (glcm, properties) calculates the statistics <br> specified in properties from the gray-level co-occurence matrix glcm. <br> glcm is an $m$-by $n$ - by-p array of valid gray-level co-occurrence matrices. |
| If glcm is an array of GLCMs, stats is an array of statistics for each |  |
| glcm. |  |
| graycoprops normalizes the gray-level co-occurrence matrix (GLCM) |  |
| so that the sum of its elements is equal to 1 . Each element (r,c) in the |  |
| normalized GLCM is the joint probability occurrence of pixel pairs |  |
| with a defined spatial relationship having gray level values r and c |  |
| in the image. graycoprops uses the normalized GLCM to calculate |  |
| properties. |  |


| Property | Description | Formula |
| :---: | :---: | :---: |
| 'Contrast' | Returns a measure of the intensity contrast between a pixel and its neighbor over the whole image. $\text { Range }=[0 \text { (size(GLCM, 1)-1)^2] }$ <br> Contrast is 0 for a constant image. | $\sum_{i, j}\|i-j\|^{2} p(i, j)$ |
| Correlation' | Returns a measure of how correlated a pixel is to its neighbor over the whole image. $\text { Range }=\left[\begin{array}{ll} -1 & 1 \end{array}\right]$ <br> Correlation is 1 or -1 for a perfectly positively or negatively correlated image. Correlation is NaN for a constant image. | $\sum_{i, j} \frac{(i-\mu i)(j-\mu j) p(i, j)}{\sigma_{i} \sigma_{j}}$ |


| Property | Description | Formula |
| :--- | :--- | :--- |
| 'Energy ' | Returns the sum of squared elements in <br> the GLCM. <br> Range $=\left[\begin{array}{ll}0 & 1\end{array}\right]$ <br> Energy is 1 for a constant image. | $\sum_{i, j} p(i, j)^{2}$ |
| 'Homogeneity' | Returns a value that measures the <br> closeness of the distribution of elements <br> in the GLCM to the GLCM diagonal. <br> Range $=\left[\begin{array}{ll}0 & 1\end{array}\right]$ <br> Homogeneity is 1 for a diagonal GLCM. | $\sum_{i, j} \frac{p(i, j)}{1+\|i-j\|}$ |

stats is a structure with fields that are specified by properties. Each field contains a $1 \times \mathrm{p}$ array, where p is the number of gray-level co-occurrence matrices in GLCM. For example, if GLCM is an $8 \times 8 \times 3$ array and properties is 'Energy', then stats is a structure containing the field Energy, which contains a $1 \times 3$ array.

## Notes

Energy is also known as uniformity, uniformity of energy, and angular second moment.

Contrast is also known as variance and inertia.

## Class <br> Support

Examples $\quad$ GLCM $=\left[\begin{array}{lllllllllllll}0 & 1 & 2 & 3 ; 1 & 1 & 2 & 3 ; 1 & 0 & 2 & 0 ; 0 & 0 & 0 & 3\end{array}\right]$;
stats = graycoprops(GLCM)
I = imread('circuit.tif');
GLCM2 = graycomatrix(I,'Offset',[2 0;0 2]);
stats $=$ graycoprops(GLCM2, \{'contrast', 'homogeneity' $\}$ )

## graycoprops

See Also graycomatrix

## Purpose

Gray-weighted distance transform of grayscale image
Syntax
T = graydist (A,mask)
T = graydist(A,C,R)
T = graydist(A,ind)
T = graydist(..., method)

## Input <br> A

Grayscale image.

## mask

Logical image the same size as A that specifies seed locations.

## C,R

Numeric vectors that contain the positive integer row and column coordinates of the seed locations. Coordinate values are valid C,R subscripts in A.

## ind

Numeric vector of positive integer, linear indices of seed locations.

## method

Type of distance metric. method can have any of these values.

| Method | Description |
| :--- | :--- |
| 'cityblock' | In 2-D, the cityblock distance between $\left(x_{1}, y_{1}\right)$ and <br> $\left(x_{2}, y_{2}\right)$ is $\left\|x_{1}-x_{2}\right\|+\left\|y_{1}-y_{2}\right\|$. |
| 'chessboard' | The chessboard distance is <br> max $\left(\left\|x_{1}-x_{2}\right\|,\left\|y_{1}-y_{2}\right\|\right)$. |
| 'quasi- <br> euclidean' | The quasi-Euclidean distance is <br> $\left\|x_{1}-x_{2}\right\|+(\sqrt{2}-1)\left\|y_{1}-y_{2}\right\|,\left\|x_{1}-x_{2}\right\|>\left\|y_{1}-y_{2}\right\|$ <br> $(\sqrt{2}-1)\left\|x_{1}-x_{2}\right\|+\left\|y_{1}-y_{2}\right\|$, otherwise. |

Default: 'chessboard'


## Examples

## T

Array the same size as A that specifies the gray-weighted distance transform. If the input numeric type of $A$ is double, the output numeric type of T is double. If the input is any other numeric type, the output $T$ is single.

A can be numeric or logical, and it must be nonsparse. mask is a logical array of the same size as A. C, R, and ind are numeric vectors that contain positive integer values.

The output $T$ is an array of the same size as $A$. If the input numeric type of $A$ is double, the output $T$ is double. If the input is any other numeric type, the output $T$ is single.

Matrices generated by the magic function have equal row, column and diagonal sums. The minimum path between the upper left and lower
right corner is along the diagonal. The following example demonstrates how the graydist function computes this path:

```
A = magic(3)
T1 = graydist(A,1,1);
T2 = graydist(A,3,3);
T = T1 + T2
A =
\begin{tabular}{lll}
8 & 1 & 6 \\
3 & 5 & 7 \\
4 & 9 & 2
\end{tabular}
T =
\begin{tabular}{lll}
10 & 11 & 17 \\
13 & 10 & 13 \\
17 & 17 & 10
\end{tabular}
```

As expected, there is a constant-value minimum path along the diagonal.

## Algorithms

graydist uses the geodesic time algorithm described in Soille, P., Generalized geodesy via geodesic time,, Pattern Recognition Letters, vol.15, December 1994; pp. 1235-1240
The basic equation for geodesic time along a path is:

$$
\tau_{f}(P)=\frac{f\left(p_{o}\right)}{2}+\frac{f\left(p_{l}\right)}{2}+\sum_{i=1}^{l-1} f\left(p_{i}\right)
$$

See Also bwdist | bwdistgeodesic | watershed

## Purpose

Convert grayscale image to indexed image using multilevel thresholding

## Syntax

X = grayslice(I, n)
$X$ = grayslice $(\mathrm{I}, \mathrm{n})$ thresholds the intensity image I returning an indexed image in $X$. grayslice uses the threshold values:
$\frac{1}{n}, \frac{2}{n}, \ldots, \frac{n-1}{n}$
$\mathrm{X}=$ grayslice $(\mathrm{I}, \mathrm{v})$ thresholds the intensity image I using the values of $v$, where $v$ is a vector of values between 0 and 1 , returning an indexed image in $X$.

You can view the thresholded image using imshow ( X, map) with a colormap of appropriate length.

## Class Support

## Examples

The input image I can be of class uint8, uint16, int16, single, or double, and must be nonsparse. Note that the threshold values are always between 0 and 1 , even if $I$ is of class uint 8 or uint16. In this case, each threshold value is multiplied by 255 or 65535 to determine the actual threshold to use.

The class of the output image $X$ depends on the number of threshold values, as specified by $n$ or length ( $v$ ). If the number of threshold values is less than 256 , then $X$ is of class uint 8 , and the values in $X$ range from 0 to $n$ or length ( $v$ ). If the number of threshold values is 256 or greater, $X$ is of class double, and the values in $X$ range from 1 to $n+1$ or length ( v ) +1 .

```
I = imread('snowflakes.png');
X = grayslice(I,16);
imshow(I)
figure, imshow(X,jet(16))
```


## grayslice



See Also gray2ind

| Purpose | Global image threshold using Otsu's method |
| :---: | :---: |
| Syntax | level = graythresh(I) <br> [level EM] = graythresh(I) |
| Description | level $=$ graythresh(I) computes a global threshold (level) that can be used to convert an intensity image to a binary image with im2bw. level is a normalized intensity value that lies in the range [ 0,1$]$. |
|  | The graythresh function uses Otsu's method, which chooses the threshold to minimize the intraclass variance of the black and white pixels. |
|  | Multidimensional arrays are converted automatically to 2-D arrays using reshape. The graythresh function ignores any nonzero imaginary part of I. |
|  | [level EM] = graythresh(I) returns the effectiveness metric, EM, as the second output argument. The effectiveness metric is a value in the range [01] that indicates the effectiveness of the thresholding of the input image. The lower bound is attainable only by images having a single gray level, and the upper bound is attainable only by two-valued images. |
| Class Support | The input image I can be of class uint8, uint16, int16, single,or double and it must be nonsparse. The return value level is a double scalar. The effectiveness metric EM is a double scalar. |
| Examples | $\begin{aligned} & I=\text { imread('coins.png'); } \\ & \text { level = graythresh(I) ; } \\ & \text { BW }=\text { im2bw(I,level); } \\ & \text { imshow(BW) } \end{aligned}$ |
| References | [1] Otsu, N., "A Threshold Selection Method from Gray-Level Histograms," IEEE Transactions on Systems, Man, and Cybernetics, Vol. 9, No. 1, 1979, pp. 62-66. |
| See Also | im2bw |

## hdrread

Purpose Read high dynamic range (HDR) image
Syntax $\quad$ hdr $=$ hdrread (filename)
Description hdr = hdrread(filename) reads the high dynamic range (HDR) image from the file specified by filename. hdr is an m-by-n-by-3 RGB array in the range [ 0, inf) of type single. For scene-referred data sets, these values usually are scene illumination in radiance units. To display these images, use an appropriate tone-mapping operator.

## Class Support

The output image hdr is an m-by-n-by-3 image of type single.

```
Examples hdr = hdrread('office.hdr');
rgb = tonemap(hdr);
imshow(rgb);
```

References [1] Larson, Greg W. "Radiance File<br>Formats"http://radsite.lbl.gov/radiance/refer/filefmts.pdf

See Also hdrwrite | makehdr | tonemap

# Purpose Write Radiance high dynamic range (HDR) image file 

## Syntax hdrwrite(hdr, filename)

Description hdrwrite(hdr, filename) creates a Radiance high dynamic range (HDR) image file from HDR, a single- or double-precision high dynamic range RGB image. The HDR file with the name filename uses run-length encoding to minimize file size.

See Also hdrread I makehdr I tonemap

Purpose Enhance contrast using histogram equalization
Syntax $\quad J=$ histeq(I, hgram)
$J=$ histeq(I, n)
[J, T] = histeq(I,...)
newmap $=$ histeq(X, map, hgram)
newmap $=$ histeq( $X$, map)
[newmap, T] = histeq(X,...)

## Description

histeq enhances the contrast of images by transforming the values in an intensity image, or the values in the colormap of an indexed image, so that the histogram of the output image approximately matches a specified histogram.
$J=$ histeq(I, hgram) transforms the intensity image I so that the histogram of the output intensity image $J$ with length (hgram) bins approximately matches hgram. The vector hgram should contain integer counts for equally spaced bins with intensity values in the appropriate range: $[0,1]$ for images of class double, $[0,255]$ for images of class uint8, and [0,65535] for images of class uint16. histeq automatically scales hgram so that sum (hgram) $=\operatorname{prod}(\operatorname{size}(\mathrm{I}))$. The histogram of $J$ will better match hgram when length (hgram) is much smaller than the number of discrete levels in I.
$J=$ histeq (I, n) transforms the intensity image I, returning in $J$ an intensity image with $n$ discrete gray levels. A roughly equal number of pixels is mapped to each of the $n$ levels in $J$, so that the histogram of $J$ is approximately flat. (The histogram of $J$ is flatter when $n$ is much smaller than the number of discrete levels in I.) The default value for n is 64 .
[J, T] = histeq(I,...) returns the grayscale transformation that maps gray levels in the image I to gray levels in $J$.
newmap $=$ histeq( $X$, map, hgram) transforms the colormap associated with the indexed image $X$ so that the histogram of the gray component of the indexed image ( $X$, newmap) approximately matches hgram. The histeq function returns the transformed colormap in newmap. length (hgram) must be the same as size (map,1).

Class Support

## Examples

newmap $=$ histeq(X, map) transforms the values in the colormap so that the histogram of the gray component of the indexed image $X$ is approximately flat. It returns the transformed colormap in newmap.
[newmap, $T$ ] $=$ histeq $(X, \ldots)$ returns the grayscale transformation $T$ that maps the gray component of map to the gray component of newmap.

For syntax that include an intensity image I as input, I can be of class uint8, uint16, int16, single, or double. The output image $J$ has the same class as I.

For syntax that include an indexed image $X$ as input, $X$ can be of class uint8, single, or double; the output colormap is always of class double. The optional output T (the gray-level transform) is always of class double.

Enhance the contrast of an intensity image using histogram equalization.

```
I = imread('tire.tif');
J = histeq(I);
imshow(I)
figure, imshow(J)
```



Display a histogram of the original image.
figure; imhist(I,64)


Compare it to a histogram of the processed image.
figure; imhist(J,64)


## Algorithms

When you supply a desired histogram hgram, histeq chooses the grayscale transformation $T$ to minimize

$$
\left|c_{1}(T(k))-c_{0}(k)\right|,
$$

where $c_{0}$ is the cumulative histogram of $\mathrm{A}, c_{1}$ is the cumulative sum of hgram for all intensities $k$. This minimization is subject to the constraints that $T$ must be monotonic and $c_{1}(T(a))$ cannot overshoot $c_{0}(a)$ by more than half the distance between the histogram counts at $a$. histeq uses the transformation $b=T(a)$ to map the gray levels in X (or the colormap) to their new values.

If you do not specify hgram, histeq creates a flat hgram,

```
hgram = ones(1,n)*prod(size(A))/n;
```

and then applies the previous algorithm.

See Also brighten | imadjust | imhist

## Purpose Hough transform

Syntax [H, theta, rho] = hough (BW)
[H, theta, rho] = hough(BW, ParameterName, ParameterValue)
Description
[ H , theta, rho] = hough(BW) computes the Standard Hough Transform (SHT) of the binary image BW. Use the hough function to detect lines in an image. The function returns H, the Hough transform matrix. theta (in degrees) and rho are the arrays of rho and theta values over which hough generates the Hough transform matrix. BW can be logical or numeric, and it must be real, 2-D, and nonsparse.
[H, theta, rho] = hough(BW, ParameterName, ParameterValue) computes the SHT using parameter name/value pairs. When ParameterName is 'RhoResolution', specify a real scalar value between 0 and norm(size(BW)), exclusive, to determine the spacing of the Hough transform bins along the rho axis. The default value is 1 .

When ParameterName is 'Theta', specify a vector of Hough transform theta values. Each element of the vector determines the theta value for the corresponding column of the output matrix H. The acceptable range of theta values is $-90^{\circ} \leq \theta<90^{\circ}$, and the default is -90:89.

## Examples

Compute and display the Hough transform of a gantrycrane image.

```
RGB = imread('gantrycrane.png');
% Convert to intensity.
I = rgb2gray(RGB);
% Extract edges.
BW = edge(I,'canny');
[H,T,R] = hough(BW,'RhoResolution',0.5,'Theta',-90:0.5:89.5);
% Display the original image.
subplot(2,1,1);
imshow(RGB);
```

```
title('Gantrycrane Image');
% Display the Hough matrix.
subplot(2,1,2);
imshow(imadjust(mat2gray(H)),'XData',T,'YData',R,...
    'InitialMagnification','fit');
title('Hough Transform of Gantrycrane Image');
xlabel('0'), ylabel('\rho');
axis on, axis normal, hold on;
colormap(hot);
```

Gantrycrane Image


Compute the Hough transform over a limited theta range for the gantrycrane image.

```
RGB = imread('gantrycrane.png');
I = rgb2gray(RGB);
BW = edge(I,'canny');
[H,T,R] = hough(BW, 'Theta', 44:0.5:46);
figure
```

```
imshow(imadjust(mat2gray(H)),'XData',T,'YData',R,...
    'InitialMagnification','fit');
title('Limited Theta Range Hough Transform of Gantrycrane Image');
xlabel('0'), ylabel('\rho');
axis on, axis normal;
colormap(hot)
```



## Algorithms

The hough function implements the Standard Hough Transform (SHT). The SHT uses the parametric representation of a line:

```
rho = x* cos(theta) + y*sin(theta)
```

The variable rho is the distance from the origin to the line along a vector perpendicular to the line. theta is the angle of the perpendicular projection from the origin to the line measured in degrees clockwise from the positive $x$-axis. The range of theta is $-90^{\circ} \leq \theta<90^{\circ}$. The angle of the line itself is $\theta+90^{\circ}$, also measured clockwise with respect to the positive $x$-axis.

## hough



The SHT is a parameter space matrix whose rows and columns correspond to rho and theta values respectively. The elements in the SHT represent accumulator cells. Initially, the value in each cell is zero. Then, for every non-background point in the image, rho is calculated for every theta. rho is rounded off to the nearest allowed row in SHT. That accumulator cell is incremented. At the end of this procedure, a value of $Q$ in $S H T(r, c)$ means that $Q$ points in the $x y$-plane lie on the line specified by theta(c) and rho(r). Peak values in the SHT represent potential lines in the input image.

The Hough transform matrix, H , is nrho-by-ntheta.

## Values of nrho and ntheta

```
nrho = 2*(ceil(D/RhoResolution)) + 1, where
D = sqrt((numRowsInBW - 1)^2 + (numColsInBW - 1)^2).
rho values range from -diagonal to diagonal, where
diagonal = RhoResolution*ceil(D/RhoResolution).
ntheta = length(theta)
```

See Also houghlines | houghpeaks

## hough

How To

- "Detecting Lines Using the Hough Transform"


## houghlines

Purpose Extract line segments based on Hough transform

```
Syntax lines = houghlines(BW, theta, rho, peaks)
lines = houghlines(..., param1, val1, param2, val2)
```

Description
lines $=$ houghlines(BW, theta, rho, peaks) extracts line segments in the image BW associated with particular bins in a Hough transform. theta and rho are vectors returned by function hough. peaks is a matrix returned by the houghpeaks function that contains the row and column coordinates of the Hough transform bins to use in searching for line segments.

The houghlines function returns lines, a structure array whose length equals the number of merged line segments found. Each element of the structure array has these fields:

| Field | Description |
| :--- | :--- |
| point1 | Two element vector [X Y] specifying the coordinates <br> of the end-point of the line segment |
| point2 | Two element vector [X Y] specifying the coordinates <br> of the end-point of the line segment |
| theta | Angle in degrees of the Hough transform bin |
| rho | rho axis position of the Hough transform bin |

lines = houghlines(..., param1, val1, param2, val2) specifies parameter/value pairs, listed in the following table. Parameter names can be abbreviated, and case does not matter.

| Parameter | Description |
| :--- | :--- |
| 'FillGap' | Positive real scalar value that specifies the distance <br> between two line segments associated with the same <br> Hough transform bin. When the distance between <br> the line segments is less the value specified, the <br> houghlines function merges the line segments into <br> a single line segment. Default: 20 |
| 'MinLength' | Positive real scalar value that specifies whether <br> merged lines should be kept or discarded. Lines <br> shorter than the value specified are discarded. <br> Default: 40 |

## Class

BW can be logical or numeric and it must be real, 2-D, and nonsparse.

Examples Search for line segments in an image and highlight the longest segment.

```
I = imread('circuit.tif');
rotI = imrotate(I,33,'crop');
BW = edge(rotI,'canny');
[H,T,R] = hough(BW);
imshow(H,[],'XData',T,'YData',R,...
    'InitialMagnification','fit');
xlabel('0'), ylabel('\rho');
axis on, axis normal, hold on;
P = houghpeaks(H,5,'threshold',ceil(0.3*max(H(:))));
x = T(P(:,2)); y = R(P(:,1));
plot(x,y,'s','color','white');
% Find lines and plot them
lines = houghlines(BW,T,R,P,'FillGap',5,'MinLength',7);
figure, imshow(rotI), hold on
max_len = 0;
for k = 1:length(lines)
    xy = [lines(k).point1; lines(k).point2];
    plot(xy(:,1),xy(:,2),'LineWidth',2,'Color','green');
```


## houghlines

```
    % Plot beginnings and ends of lines
    plot(xy(1,1),xy(1,2),'x','LineWidth',2,'Color','yellow');
    plot(xy(2,1),xy(2,2),'x','LineWidth',2,'Color','red');
    % Determine the endpoints of the longest line segment
    len = norm(lines(k).point1 - lines(k).point2);
    if ( len > max_len)
        max_len = len;
        xy_long = xy;
    end
end
% highlight the longest line segment
plot(xy_long(:,1),xy_long(:,2),'LineWidth',2,'Color','blue');
```

See Also hough | houghpeaks

Purpose Identify peaks in Hough transform
Syntax

```
peaks = houghpeaks(H, numpeaks)
peaks = houghpeaks(..., param1, val1, param2, val2)
```

Description
peaks $=$ houghpeaks ( H , numpeaks) locates peaks in the Hough transform matrix, H, generated by the hough function. numpeaks is a scalar value that specifies the maximum number of peaks to identify. If you omit numpeaks, it defaults to 1 .

The function returns peaks, a Q-by-2 matrix, where $Q$ can range from 0 to numpeaks. Q holds the row and column coordinates of the peaks.
peaks = houghpeaks(..., param1, val1, param2, val2) specifies parameter/value pairs, listed in the following table. Parameter names can be abbreviated, and case does not matter.

| Parameter | Description |
| :--- | :--- |
| 'Threshold' | Nonnegative scalar value that specifies the <br> threshold at which values of H are considered to be <br> peaks. Threshold can vary from 0 to Inf. Default <br> is 0.5*max $(\mathrm{H}(:))$. |
| 'NHoodSize' | Two-element vector of positive odd integers: <br> [M N]. 'NHoodSize' specifies the size of <br> the suppression neighborhood. This is the <br> neighborhood around each peak that is set to zero <br> after the peak is identified. Default: smallest odd <br> values greater than or equal to size $(\mathrm{H}) / 50$. |

## Class

Support
Examples Locate and display two peaks in the Hough transform of a rotated image.

```
```

I = imread('circuit.tif');

```
```

I = imread('circuit.tif');
BW = edge(imrotate(I,50,'crop'),'canny');

```
```

BW = edge(imrotate(I,50,'crop'),'canny');

```
```


## houghpeaks

```
[H,T,R] = hough(BW);
P = houghpeaks(H,2);
imshow(H,[],'XData',T,'YData',R,'InitialMagnification','fit');
xlabel('0'), ylabel('\rho');
axis on, axis normal, hold on;
plot(T(P(:,2)),R(P(:,1)),'s','color','white');
```

See Also hough | houghlines

## Purpose Search for ICC profiles

```
Syntax P = iccfind(directory)
[P, descriptions] = iccfind(directory)
[...] = iccfind(directory, pattern)
```


## Description

$P=$ iccfind(directory) searches for all of the ICC profiles in the directory specified by directory. The function returns P, a cell array of structures containing profile information.
[P, descriptions] = iccfind(directory) searches for all of the ICC profiles in the specified directory and returns $P$, a cell array of structures containing profile information, and descriptions, a cell array of text strings, where each string describes the corresponding profile in P. Each text string is the value of the Description. String field in the profile information structure.
[...] = iccfind(directory, pattern) returns all of the ICC profiles in the specified directory with the given pattern in their Description.String fields. iccfind performs case-insensitive pattern matching.

> Note To improve performance, iccfind caches copies of the ICC profiles in memory. Adding or modifying profiles might not change the results of iccfind. To clear the cache, use the clear functions command.

## Examples

Get all the ICC profiles in the default system directory where profiles are stored

```
profiles = iccfind(iccroot);
```

Get a listing of all the ICC profiles with text strings that describe each profile

```
[profiles, descriptions ] = iccfind(iccroot);
```


## iccfind

Find the profiles whose descriptions contain the text string RGB.

```
[profiles, descriptions] = iccfind(iccroot, 'rgb');
```

See Also iccread | iccroot | iccwrite

## Purpose <br> Read ICC profile

Syntax $\quad P=$ iccread(filename)
Description
$P=$ iccread(filename) reads the International Color Consortium (ICC) color profile information from the file specified by filename. The file can be either an ICC profile file or a TIFF file containing an embedded ICC profile. To determine if a TIFF file contains an embedded ICC profile, use the imfinfo function to get information about the file and look for the ICCProfileOffset field. iccread looks for the file in the current directory, a directory on the MATLAB path, or in the directory returned by iccroot, in that order.
iccread returns the profile information in the structure P , a 1-by-1 structure array whose fields contain the data structures (called tags) defined in the ICC specification. iccread can read profiles that conform with either Version 2 (ICC.1:2001-04) or Version 4 (ICC.1:2001-12) of the ICC specification. For more information about ICC profiles, visit the ICC web site, www.color.org.

ICC profiles provide color management systems with the information necessary to convert color data between native device color spaces and device independent color spaces, called the Profile Connection Space (PCS). You can use the profile as the source or destination profile with the makecform function to compute color space transformations.

The number of fields in $P$ depends on the profile class and the choices made by the profile creator. iccread returns all the tags for a given profile, both public and private. Private tags and certain public tags are left as encoded uint8 data. The following table lists fields that are found in any profile structure generated by iccread, in the order they appear in the structure.

| Field | Data Type | Description |
| :--- | :--- | :--- |
| Header | 1 -by-1 <br> struct <br> array | Profile header fields |
| TagTable | n-by-3 cell <br> array | Profile tag table |
| Copyright | Text string | Profile copyright notice |
| Description | 1 -by-1 <br> struct <br> array | The String field in this structure <br> contains a text string describing <br> the profile. |
| MediaWhitepoint | double <br> array | XYZ tristimulus values of the <br> device's media white point |
| PrivateTags | m-by-2 cell <br> array | Contents of all the private <br> tags or tags not defined in <br> the ICC specifications. The <br> tag signatures are in the first <br> column, and the contents of the <br> tags are in the second column. <br> Note that iccread leaves the <br> contents of these tags in unsigned <br> 8-bit encoding. |
| Filename | Text string | Name of the file containing the <br> profile |

Additionally, P might contain one or more of the following transforms:

- Three-component, matrix-based transform: A simple transform that is often used to transform between the RGB and $X Y Z$ color spaces. If this transform is present, P contains a field called MatTRC.
- N-component LUT-based transform: A transform that is used for transforming between color spaces that have a more complex relationship. This type of transform is found in any of the following fields in $P$ :

| AToB0 | BToA0 | Preview0 |
| :--- | :--- | :--- |
| AToB1 | BToA1 | Preview1 |
| AToB2 | BToA2 | Preview2 |
| AToB3 | BToA3 | Gamut |

## Examples

The example reads the ICC profile that describes a typical PC computer monitor.

```
P = iccread('sRGB.icm')
P =
                    Header: [1x1 struct]
                    TagTable: {17x3 cell}
                    Copyright: 'Copyright (c) 1999 Hewlett-Packard Company'
            Description: [1x1 struct]
        MediaWhitePoint: [0.9505 1 1.0891]
        MediaBlackPoint: [0 O O]
            DeviceMfgDesc: [1x1 struct]
        DeviceModelDesc: [1x1 struct]
        ViewingCondDesc: [1x1 struct]
ViewingConditions: [1x1 struct]
            Luminance: [76.0365 80 87.1246]
            Measurement: [1x36 uint8]
            Technology: [115 105 103 32 0 0 0 0 67 82 84 32]
            MatTRC: [1x1 struct]
            PrivateTags: {}
            Filename: 'sRGB.icm'
```

The profile header provides general information about the profile, such as its class, color space, and PCS. For example, to determine the source color space, view the ColorSpace field in the Header structure.
P.Header.ColorSpace
ans $=$

## iccread

See Also
applycform | iccfind | iccroot | iccwrite | isicc | makecform

| Purpose | Find system default ICC profile repository |
| :--- | :--- |
| Syntax | rootdir $=$ iccroot |
| Description | rootdir $=$ iccroot returns the system directory containing ICC <br> profiles. Additional profiles can be stored in other directories, but this <br> is the default location used by the color management system. |

Note Only Windows and Mac OS X platforms are supported.

Examples Return information on all the profiles in the root directory.
iccfind(iccroot)
See Also iccfind | iccread | iccwrite

## Purpose Write ICC color profile to disk file

```
Syntax P_new = iccwrite(P, filename)
```

Description P_new = iccwrite(P, filename) writes the International Color
Consortium (ICC) color profile data in structure $P$ to the file specified by filename.
$P$ is a structure representing an ICC profile in the data format returned by iccread and used by makecform and applycform to compute color-space transformations. P must contain all the tags and fields required by the ICC profile specification. Some fields may be inconsistent, however, because of interactive changes to the structure. For instance, the tag table may not be correct because tags may have been added, deleted, or modified since the tag table was constructed. iccwrite makes any necessary corrections to the profile structure before writing it to the file and returns this corrected structure in $P_{-}$new.

Note Because some applications use the profile description string in the ICC profile to present choices to users, the ICC recommends modifying the profile description string in the ICC profile data before writing the data to a file. Each profile should have a unique description string. For more information, see the example.
iccwrite can write the color profile data using either Version 2 (ICC.1:2001-04) or Version 4 (ICC.1:2001-12) of the ICC specification, depending on the value of the Version field in the file profile header. If any required fields are missing, iccwrite errors. For more information about ICC profiles, visit the ICC web site, www. color.org.

> Note iccwrite does not perform automatic conversions from one version of the ICC specification to another. Such conversions have to be done manually, by adding fields or modifying fields. Use isicc to validate a profile.

Examples

See Also

Read a profile into the MATLAB workspace and export the profile data to a new file. The example changes the profile description string in the profile data before writing the data to a file.

```
P = iccread('monitor.icm');
P.Description.String
ans =
sgC4_050102_d50.pf
P.Description.String = 'my new description';
pmon = iccwrite(P, 'monitor2.icm');
```

applycform | iccread | isicc | makecform

Purpose
2-D inverse discrete cosine transform
Syntax
$B=\operatorname{idct2}(A)$
$B=\operatorname{idct2}(A, m, n)$
$B=\operatorname{idct2}(A,[m n])$
Description

Class
Support

## Algorithms

 transform (DCT) of A. [ m n ] < size(A), idct2 crops A before transforming.$B=\operatorname{idct2}(A,[m n])$ same as above. output matrix $B$ is of class double.
idct2 computes the two-dimensional inverse DCT using:
$B=$ idct2 $(A)$ returns the two-dimensional inverse discrete cosine
$B=\operatorname{idct2}(A, m, n)$ pads $A$ with 0 's to size $m$-by- $n$ before transforming. If

For any A, idct2(dct2(A)) equals A to within roundoff error.
The input matrix A can be of class double or of any numeric class. The

$$
A_{m n}=\sum_{p=0}^{M-1} \sum_{q=0}^{N-1} \alpha_{p} \alpha_{q} B_{p q} \cos \frac{\pi(2 m+1) p}{2 M} \cos \frac{\pi(2 n+1) q}{2 N}, \begin{aligned}
& 0 \leq m \leq M-1 \\
& 0 \leq n \leq N-1
\end{aligned},
$$

where

$$
\alpha_{p}=\left\{\begin{array}{l}
\frac{1}{\sqrt{M}}, p=0 \\
\sqrt{\frac{2}{M}}, 1 \leq p \leq M-1
\end{array}\right.
$$

and

$$
\alpha_{q}=\left\{\begin{array}{l}
\frac{1}{\sqrt{N}}, q=0 \\
\sqrt{\frac{2}{N}}, 1 \leq q \leq N-1
\end{array} .\right.
$$

```
Examples Create a DCT matrix.
RGB = imread('autumn.tif');
I = rgb2gray (RGB);
\(J=\operatorname{dct2}(\mathrm{I})\);
imshow(log(abs(J)),[]), colormap(jet), colorbar
```

Set values less than magnitude 10 in the DCT matrix to zero, then reconstruct the image using the inverse DCT function idct2.
$J(\operatorname{abs}(J)<10)=0 ;$
K = idct2(J);
figure, imshow(I)
figure, imshow(K,[0 255])

References [1] Jain, A. K., Fundamentals of Digital Image Processing, Englewood Cliffs, NJ, Prentice Hall, 1989, pp. 150-153.

[2] Pennebaker, W. B., and J. L. Mitchell, JPEG: Still Image Data Compression Standard, New York, Van Nostrand Reinhold, 1993.

See Also dct2|dctmtx|fft2|ifft2

Purpose Inverse fan-beam transform

```
Syntax
I = ifanbeam(F,D)
I = ifanbeam(..., param1,val1,param2,val2,...)
[I,H] = ifanbeam(...)
```


## Description

I = ifanbeam(F,D) reconstructs the image I from projection data in the two-dimensional array F. Each column of F contains fan-beam projection data at one rotation angle. ifanbeam assumes that the center of rotation is the center point of the projections, which is defined as ceil(size(F,1)/2).

The fan-beam spread angles are assumed to be the same increments as the input rotation angles split equally on either side of zero. The input rotation angles are assumed to be stepped in equal increments to cover [0:359] degrees.
$D$ is the distance from the fan-beam vertex to the center of rotation.
I = ifanbeam(..., param1,val1,param2,val2,...) specifies parameters that control various aspects of the ifanbeam reconstruction, described in the following table. Parameter names can be abbreviated, and case does not matter. Default values are in braces (\{\}).

| Parameter | Description |
| :--- | :--- |
| 'FanCoverage' | String specifying the range through <br> which the beams are rotated. <br> \{'cycle' $\}$ - Rotate through the full <br> range [0,360). <br> 'minimal' - Rotate the minimum range <br> necessary to represent the object. |
| 'FanRotationIncrement' | Positive real scalar specifying the <br> increment of the rotation angle of the <br> fan-beam projections, measured in <br> degrees. See fanbeam for details. |


| Parameter | Description |
| :--- | :--- |
| 'FanSensorGeometry' | String specifying how sensors are <br> positioned. <br> 'arc' — Sensors are spaced equally <br> along a circular arc at distance D from <br> the center of rotation. Default value is <br> 'arc' <br> ' line' — Sensors are spaced equally <br> along a line, the closest point of which is <br> distance D from the center of rotation. <br> See fanbeam for details. |
| 'FanSensorSpacing' | Positive real scalar specifying the spacing <br> of the fan-beam sensors. Interpretation <br> of the value depends on the setting of <br> 'FanSensorGeometry ' . |
|  | If 'FanSensorGeometry ' is set to ' arc ' <br> (the default), the value defines the <br> angular spacing in degrees. Default <br> value is 1. |
|  | If 'FanSensorGeometry ' is ' line ', <br> the value specifies the linear spacing. <br> Default value is 1. See fanbeam for <br> details. |
| 'Filter' | String specifying the name of a filter. <br> See iradon for details. |
| 'FrequencyScaling' | Scalar in the range (0,1] that modifies <br> the filter by rescaling its frequency axis. <br> See iradon for details. |


| Parameter | Description |
| :---: | :---: |
| 'Interpolation' | Text string specifying the type of interpolation used between the parallel-beam and fan-beam data. <br> 'nearest' - Nearest-neighbor <br> \{'linear'\} - Linear <br> 'spline' - Piecewise cubic spline <br> 'pchip' —. Piecewise cubic Hermite <br> (PCHIP) <br> 'cubic' - Same as 'pchip' |
| 'OutputSize' | Positive scalar specifying the number of rows and columns in the reconstructed image. <br> If 'OutputSize' is not specified, ifanbeam determines the size automatically. <br> If you specify 'OutputSize', ifanbeam reconstructs a smaller or larger portion of the image, but does not change the scaling of the data. |
|  | Note If the projections were calculated with the fanbeam function, the reconstructed image might not be the same size as the original image. |

$[\mathrm{I}, \mathrm{H}]=$ ifanbeam (...) returns the frequency response of the filter in the vector H .

## Notes <br> Class Support

## Examples

ifanbeam converts the fan-beam data to parallel beam projections and then uses the filtered back projection algorithm to perform the inverse Radon transform. The filter is designed directly in the frequency domain and then multiplied by the FFT of the projections. The projections are zero-padded to a power of 2 before filtering to prevent spatial domain aliasing and to speed up the FFT.

The input arguments, F and D, can be double or single. All other numeric input arguments must be double. The output arguments are double.

## Example 1

This example creates a fan-beam transformation of the phantom head image and then calls the ifanbeam function to recreate the phantom image from the fan-beam transformation.

```
ph = phantom(128);
d = 100;
F = fanbeam(ph,d);
I = ifanbeam(F,d);
imshow(ph), figure, imshow(I);
```


## Example 2

This example illustrates use of the ifanbeam function with the 'fancoverage' option set to 'minimal'.
ph = phantom(128);
P = radon(ph);
[F,obeta,otheta] = para2fan(P, 100,...
'FanSensorSpacing',0.5,...
'FanCoverage','minimal',...
'FanRotationIncrement', 1);
phReconstructed $=$ ifanbeam(F,100,...
'FanSensorSpacing', 0.5,...
'Filter', 'Shepp-Logan', ...
'OutputSize',128,...
'FanCoverage','minimal',...
'FanRotationIncrement',1);
imshow(ph), figure, imshow(phReconstructed)
References [1] Kak, A. C., and M. Slaney, Principles of Computerized Tomographic Imaging, New York, NY, IEEE Press, 1988.
See Also fan2para | fanbeam | iradon | para2fan | phantom | radon

## Purpose <br> Convert image to binary image, based on threshold

```
Syntax
BW = im2bw(I, level)
BW = im2bw(X, map, level)
BW = im2bw(RGB, level)
```


## Description

## Class <br> Support

Examples
$B W=i m 2 b w(I, ~ l e v e l)$ converts the grayscale image I to a binary image. The output image BW replaces all pixels in the input image with luminance greater than level with the value 1 (white) and replaces all other pixels with the value 0 (black). Specify level in the range $[0,1]$. This range is relative to the signal levels possible for the image's class. Therefore, a level value of 0.5 is midway between black and white, regardless of class. To compute the level argument, you can use the function graythresh. If you do not specify level, im2bw uses the value 0.5 .

BW = im2bw(X, map, level) converts the indexed image $X$ with colormap map to a binary image.

BW = im2bw(RGB, level) converts the truecolor image RGB to a binary image.

If the input image is not a grayscale image, im2bw converts the input image to grayscale, and then converts this grayscale image to binary by thresholding.

The input image can be of class uint8, uint16, single, int16, or double, and must be nonsparse. The output image BW is of class logical. I and X must be 2-D. RGB images are M-by-N-by-3.
load trees

BW = im2bw(X,map,0.4);
imshow(X,map), figure, imshow(BW)

## im2bw


graythresh | ind2gray | rgb2gray

## Purpose Rearrange image blocks into columns

Syntax $\quad B=\operatorname{im2col}(A,[m n]$, block_type $)$
B = im2col(A,'indexed',...)
Description
$B=i m 2 \operatorname{col}\left(A,[m n], b l o c k \_t y p e\right)$ rearranges image blocks into columns. block_type is a string that can have one of these values. The default value is enclosed in braces (\{\}).

| Value | Description |
| :---: | :---: |
| 'distinct' | Rearranges each distinct $m$-by- $n$ block in the image $A$ into a column of B. im2col pads A with 0's, if necessary, so its size is an integer multiple of m-by-n. If $A=[A 11$ A12; A21 A22], where each $A_{i j}$ is m-by-n, then $B=$ [A11(:) A12(:) A21(:) A22(:)]. |
| \{'sliding'\} | Converts each sliding $m$-by- $n$ block of $A$ into a column of $B$, with no zero padding. $B$ has $m * n$ rows and contains as many columns as there are m-by-n neighborhoods of $A$. If the size of $A$ is [ $\mathrm{mm} n \mathrm{n}$ ], then the size of $B$ is $(m * n)$-by- $((m m-m+1) *(n n-n+1))$. |

For the sliding block case, each column of B contains the neighborhoods of A reshaped as $\operatorname{NHOOD}(:)$ where NHOOD is a matrix containing an m -by- n neighborhood of A . im2col orders the columns of $B$ so that they can be reshaped to form a matrix in the normal way. For Examples, suppose you use a function, such as sum (B), that returns a scalar for each column of B. You can directly store the result in a matrix of size ( $m m-m+1$ )-by-(nn-n+1), using these calls.
$B=i m 2 c o l(A,[m n], ' s l i d i n g ') ;$
$C=\operatorname{reshape}(\operatorname{sum}(B), m m-m+1, n n-n+1) ;$
B = im2col(A,'indexed',...) processes A as an indexed image, padding with 0 's if the class of $A$ is uint8, or 1's if the class of $A$ is double.

## im2col

```
Class
Support
Examples Calculate the local mean using a [2 2] neighborhood with zero padding:
```

```
A = reshape(linspace(0,1,16),[4 4])'
```

A = reshape(linspace(0,1,16),[4 4])'
B = im2col(A,[2 2])
B = im2col(A,[2 2])
M = mean(B)
M = mean(B)
newA = col2im(M,[1 1],[3 3])
newA = col2im(M,[1 1],[3 3])
The output appears like this:
newA $=$

| 0.1667 | 0.2333 | 0.3000 |
| :--- | :--- | :--- |
| 0.4333 | 0.5000 | 0.5667 |
| 0.7000 | 0.7667 | 0.8333 |

See Also
blockproc | col2im | colfilt | nlfilter

```
\begin{tabular}{|c|c|}
\hline Purpose & Convert image to double precision \\
\hline Syntax & ```
I2 = im2double(I)
RGB2 = im2double(RGB)
I = im2double(BW)
X2 = im2double(X,'indexed')
``` \\
\hline Description & \begin{tabular}{l}
I2 = im2double(I) converts the intensity image I to double precision, rescaling the data if necessary. \\
If the input image is of class double, the output image is identical. \\
RGB2 = im2double (RGB) converts the truecolor image RGB to double precision, rescaling the data if necessary. \\
I = im2double(BW) converts the binary image BW to a double-precision intensity image. \\
X2 = im2double(X,'indexed') converts the indexed image X to double precision, offsetting the data if necessary.
\end{tabular} \\
\hline \begin{tabular}{l}
Class \\
Support
\end{tabular} & Intensity and truecolor images can be uint8, uint16, double, logical, single, or int16. Indexed images can be uint8, uint16, double or logical. Binary input images must be logical. The output image is double. \\
\hline Examples & \[
\begin{aligned}
& \left.\mathrm{I} 1=\text { reshape }(\text { uint8(linspace }(1,255,25)),\left[\begin{array}{l}
5 \\
\mathrm{I}
\end{array}\right]\right) \\
& \mathrm{I} 2=\text { im2double(I1) }
\end{aligned}
\] \\
\hline See Also & double | im2single | im2int16 | im2uint8 | im2uint16 \\
\hline
\end{tabular}

\section*{im2int 16}

\section*{Purpose Convert image to 16-bit signed integers}
```

Syntax I2 $=$ im2int16(I)
RGB2 $=$ im2int16(RGB)
I = im2int16(BW)

```

\section*{Description}

\section*{Class \\ Support}

Examples

See Also

I2 = im2int16(I) converts the intensity image I to int16, rescaling the data if necessary. If the input image is of class int16, the output image is identical to it.

RGB2 \(=\) im2int16(RGB) converts the truecolor image RGB to int16, rescaling the data if necessary.

I = im2int16(BW) converts the binary image BW to an int16 intensity image, changing false-valued elements to -32768 and true-valued elements to 32767 .

Intensity and truecolor images can be uint8, uint16, int16, single, double, or logical. Binary input images must be logical. The output image is int16.

I = reshape(linspace (0,1,20),[54])
I2 = im2int16(I)

\section*{Purpose Convert image to Java buffered image}

Syntax
jimage = im2java2d(I)
jimage = im2java2d(X,MAP)
Description
jimage \(=\) im2java2d(I) converts the image I to an instance of the Java image class java.awt.image. BufferedImage. The image I can be an intensity (grayscale), RGB, or binary image.
jimage = im2java2d(X,MAP) converts the indexed image \(X\) with colormap MAP to an instance of the Java class java.awt.image.BufferedImage.

> Note The im2java2d function works with the Java 2D API. The im2java function works with the Java Abstract Windowing Toolkit (AWT).

Class Intensity, indexed, and RGB input images can be of class uint8, uint16, Support or double. Binary input images must be of class logical.

Examples Read an image into the MATLAB workspace and then use im2java2d to convert it into an instance of the Java class java.awt.image.BufferedImage.
```

I = imread('moon.tif');
javaImage = im2java2d(I);
frame = javax.swing.JFrame;
icon = javax.swing.ImageIcon(javaImage);
label = javax.swing.JLabel(icon);
frame.getContentPane.add(label);
frame.pack
frame.show

```

\section*{im2single}

\section*{Purpose Convert image to single precision}
```

Syntax I2 = im2single(I)
RGB2 = im2single(RGB)
I = im2single(BW)
X2 = im2single(X,'indexed')

```

Description

\section*{Class \\ Support}

Examples

See Also

I2 = im2single(I) converts the intensity image I to single, rescaling the data if necessary. If the input image is of class single, the output image is identical to it.

RGB2 = im2single(RGB) converts the truecolor image RGB to single, rescaling the data if necessary.
\(\mathrm{I}=\) im2single(BW) converts the binary image BW to a single-precision intensity image.
X2 = im2single( X , 'indexed') converts the indexed image X to single precision, offsetting the data if necessary.

Intensity and truecolor images can be uint8, uint16, int16, single, double, or logical. Indexed images can be uint8, uint16, double or logical. Binary input images must be logical. The output image is single.

I = reshape(uint8(linspace (1,255,25)),[5 5])
I2 = im2single(I)
im2double | im2int16 | im2uint8 | im2uint16 | single
\begin{tabular}{|c|c|}
\hline Purpose & Convert image to 16-bit unsigned integers \\
\hline Syntax & ```
I2 = im2uint16(I)
RGB2 = im2uint16(RGB)
I = im2uint16(BW)
X2 = im2uint16(X,'indexed')
``` \\
\hline Description & \begin{tabular}{l}
I2 = im2uint16(I) converts the intensity image I to uint16, rescaling the data if necessary. If the input image is of class uint16, the output image is identical to it. \\
RGB2 = im2uint16(RGB) converts the truecolor image RGB to uint16, rescaling the data if necessary. \\
I = im2uint16(BW) converts the binary image BW to a uint16 intensity image, changing 1 -valued elements to 65535. \\
X2 = im2uint16(X,'indexed') converts the indexed image \(X\) to uint16, offsetting the data if necessary. If \(X\) is of class double, \(\max (\mathrm{X}(:))\) must be 65536 or less.
\end{tabular} \\
\hline \begin{tabular}{l}
Class \\
Support
\end{tabular} & Intensity and truecolor images can be uint8, uint16, double, logical, single, or int16. Indexed images can be uint8, uint16, double, or logical. Binary input images must be logical. The output image is uint16. \\
\hline Examples & \[
\begin{aligned}
& I=\text { reshape(linspace }(0,1,20),\left[\begin{array}{ll}
5 & 4
\end{array}\right) \\
& \text { I2 }=\text { im2uint16(I) }
\end{aligned}
\] \\
\hline See Also & im2uint8 | double | im2double | uint8 | uint16 | imapprox \\
\hline
\end{tabular}

\section*{im2uint8}
```

Purpose Convert image to 8-bit unsigned integers
Syntax $\quad$ I2 $=$ im2uint8(I1)
RGB2 = im2uint8(RGB1)
I = im2uint8(BW)
X2 = im2uint8(X1,'indexed')

```

Description

Class

\section*{Examples}

See Also
im2uint8 takes an image as input and returns an image of class uint8. If the input image is of class uint8, the output image is identical to the input image. If the input image is not uint8, im2uint8 returns the equivalent image of class uint8, rescaling or offsetting the data as necessary.

I2 \(=\) im2uint8(I1) converts the grayscale image I1 to uint8, rescaling the data if necessary.

RGB2 = im2uint8(RGB1) converts the truecolor image RGB1 to uint8, rescaling the data if necessary.

I = im2uint8(BW) converts the binary image BW to a uint8 grayscale image, changing 1 -valued elements to 255.

X2 = im2uint8(X1,'indexed') converts the indexed image X1 to uint8, offsetting the data if necessary. Note that it is not always possible to convert an indexed image to uint8. If X 1 is of class double, the maximum value of \(X 1\) must be 256 or less; if \(X 1\) is of class uint16, the maximum value of X 1 must be 255 or less.

Grayscale and truecolor images can be uint8, uint16, int16, single, double, or logical. Indexed images can be uint8, uint16, double, or logical. Binary input images must be logical. The output image is uint8.

I1 = reshape(uint16(linspace \((0,65535,25)),[5\) 5])
I2 = im2uint8(I1)
im2double | im2int16 | im2single | im2uint16 | uint8

\section*{Purpose Absolute difference of two images}
\[
\text { Syntax } \quad Z=\operatorname{imabsdiff}(X, Y)
\]
\(Z=\) imabsdiff( \(X, Y\) ) subtracts each element in array \(Y\) from the corresponding element in array \(X\) and returns the absolute difference in the corresponding element of the output array \(Z . X\) and \(Y\) are real, nonsparse numeric arrays with the same class and size. \(Z\) has the same class and size as \(X\) and \(Y\). If \(X\) and \(Y\) are integer arrays, elements in the output that exceed the range of the integer type are truncated.

If \(X\) and \(Y\) are double arrays, you can use the expression abs ( \(X-Y\) ) instead of this function.

Note This function may take advantage of hardware optimization for data types uint8, int16, and single to run faster. Hardware optimization requires that arrays \(X\) and \(Y\) are of the same size and class.

\section*{Examples}

Calculate the absolute difference between two uint8 arrays. Note that the absolute value prevents negative values from being rounded to zero in the result, as they are with imsubtract.
```

X = uint8([ 255 10 75; 44 225 100]);
Y = uint8([ 50 50 50; 50 50 50 ]);
Z = imabsdiff(X,Y)
Z =
205 40 25
6 175 50

```

Display the absolute difference between a filtered image and the original.
```

I = imread('cameraman.tif');
J = uint8(filter2(fspecial('gaussian'), I));
K = imabsdiff(I,J);

```

\section*{imabsdiff}

\author{
imshow(K,[]) \% [] = scale data automatically \\ See Also imadd | imcomplement | imdivide | imlincomb | immultiply | imsubtract | ippl
}

\section*{Purpose \\ Add two images or add constant to image}

\section*{Syntax}
\(Z=\) imadd(X,Y)
\(Z=i \operatorname{madd}(X, Y)\) adds each element in array \(X\) with the corresponding element in array \(Y\) and returns the sum in the corresponding element of the output array \(Z\). \(X\) and \(Y\) are real, nonsparse numeric arrays with the same size and class, or \(Y\) is a scalar double. \(Z\) has the same size and class as X , unless X is logical, in which case Z is double.

If \(X\) and \(Y\) are integer arrays, elements in the output that exceed the range of the integer type are truncated, and fractional values are rounded.

Note On Intel architecture processors, imadd can take advantage of the Intel Integrated Performance Primitives (Intel IPP) library, thus accelerating its execution time. The Intel IPP library is activated if arrays \(X, Y\), and \(Z\) are of class logical, uint8, or single and are of the same class. The Intel IPP library is also activated if \(Y\) is a double scalar and arrays \(X\) and \(Z\) are uint8, int16, or single and are of the same class.

\section*{Examples}

Add two uint8 arrays. Note the truncation that occurs when the values exceed 255.
```

X = uint8([ 255 0 75; 44 225 100]);
Y = uint8([ 50 50 50; 50 50 50 ]);
Z = imadd(X,Y)
Z =
255 50 125
94 255 150

```

Add two images together and specify an output class.
```

I = imread('rice.png');

```
```

J = imread('cameraman.tif');
K = imadd(I,J,'uint16');
imshow(K,[])

```

Add a constant to an image.
```

I = imread('rice.png');
J = imadd(I,50);
subplot(1,2,1), imshow(I)
subplot(1,2,2), imshow(J)

```

See Also imabsdiff | imcomplement | imdivide | imlincomb | immultiply | imsubtract | ippl

Purpose
Syntax
Description
Adjust image intensity values or colormap
```

J = imadjust(I)
J = imadjust(I,[low_in; high_in],[low_out; high_out])
J = imadjust(I,[low_in; high_in],[low_out; high_out],gamma)
newmap = imadjust(map,[low_in; high_in],[low_out; high_out],
gamma)
RGB2 = imadjust(RGB1,...)

```
\(J=\) imadjust(I) maps the intensity values in grayscale image I to new values in \(J\) such that \(1 \%\) of data is saturated at low and high intensities of I. This increases the contrast of the output image J. This syntax is equivalent to imadjust(I, stretchlim(I)).

J = imadjust(I,[low_in; high_in],[low_out; high_out]) maps the values in I to new values in \(J\) such that values between low_in and high_in map to values between low_out and high_out. Values for low_in, high_in, low_out, and high_out must be between 0 and 1. Values below low_in and above high_in are clipped; that is, values below low_in map to low_out, and those above high_in map to high_out. You can use an empty matrix ([ ]) for [low_in high_in] or for [low_out high_out] to specify the default of [0 1].

J = imadjust(I,[low_in; high_in],[low_out; high_out],gamma) maps the values in I to new values in \(J\), where gamma specifies the shape of the curve describing the relationship between the values in I and \(J\). If gamma is less than 1 , the mapping is weighted toward higher (brighter) output values. If gamma is greater than 1 , the mapping is weighted toward lower (darker) output values. If you omit the argument, gamma defaults to 1 (linear mapping).
newmap = imadjust(map,[low_in; high_in],[low_out; high_out ], gamma) transforms the colormap associated with an indexed image. If low_in, high_in, low_out, high_out, and gamma are scalars, then the same mapping applies to red, green, and blue components. Unique mappings for each color component are possible when
low_in and high_in are both 1-by-3 vectors.

\section*{imadjust}
low_out and high_out are both 1-by-3 vectors, or gamma is a 1 -by- 3 vector.

The rescaled colormap newmap is the same size as map.
RGB2 = imadjust(RGB1, ...) performs the adjustment on each image plane (red, green, and blue) of the RGB image RGB1. As with the colormap adjustment, you can apply unique mappings to each plane.

Note If high_out < low_out, the output image is reversed, as in a photographic negative.

Class Support

\section*{Examples}

For syntax variations that include an input image (rather than a colormap), the input image can be of class uint8, uint16, int16, single, or double. The output image has the same class as the input image. For syntax variations that include a colormap, the input and output colormaps are of class double.

Adjust a low-contrast grayscale image.


Adjust the grayscale image, specifying the contrast limits.
```

K = imadjust(I,[0.3 0.7],[]);
figure, imshow(K)

```

Adjust an RGB image.
RGB1 = imread('football.jpg');
RGB2 = imadjust(RGB1,[.2 . 3 0; . 6 . 7 1],[]);
imshow(RGB1), figure, imshow(RGB2)


See Also brighten | histeq | stretchlim

\section*{ImageAdapter}

\section*{Purpose Interface for image I/O}

Description

Construction

ImageAdapter, an abstract class, specifies the Image Processing Toolbox interface for region-based reading and writing of image files. You can use classes that inherit from the ImageAdapter interface with the blockproc function for file-based processing of arbitrary image file formats.
adapter \(=\) ClassName(...) handles object initialization, manages file opening or creation, and sets the initial values of class properties. The class constructor can take any number of arguments.

\section*{Properties \\ Colormap}

Specifies a colormap. Use the Colormap property when working with indexed images.

Data Type: 2-D, real, M-by-3 matrix
Default: Empty ([]), indicating either a grayscale, logical, or truecolor image

\section*{ImageSize}

Holds the size of the entire image. When you construct a new class that inherits from ImageAdapter, set the ImageSize property in your class constructor.

Data Type: 2- or 3 -element vector specified as [rows cols] or [rows cols bands], where rows indicates height and cols indicates width

Methods Classes that inherit from ImageAdapter must implement the readRegion and close methods to support basic region-based reading of images. The writeRegion method allows for incremental, region-based writing of images and is optional. Image Adapter classes that do not implement the writeRegion method are read-only.
\begin{tabular}{ll} 
close & Close ImageAdapter object \\
readRegion & Read region of image \\
writeRegion & Write block of data to region of \\
& image
\end{tabular}

See Also blockproc
Tutorials \(\quad\) Computing Statistics for Large Images
How To . "Defining Abstract Classes"
- "Working with Data in Unsupported Formats"

\section*{ImageAdapter.close}

Purpose Close ImageAdapter object
Syntax adapter.close
Description adapter.close closes the ImageAdapter object and performs any necessary clean-up, such as closing file handles. When you construct a class that inherits from the ImageAdapter class, implement this method.

\section*{ImageAdapter.readRegion}
\begin{tabular}{ll} 
Purpose & Read region of image \\
Syntax & data = adapter.readRegion(region_start, region_size)
\end{tabular}

\section*{ImageAdapter.writeRegion}

Purpose Write block of data to region of image
Syntax adapter.writeRegion(region_start, region_data)
Description
adapter.writeRegion(region_start, region_data) writes a contiguous block of data to a region of the image. The method writes the block of data specified by the region_data argument. The two-element vector, region_start, specifies the [row col] location of the first pixel (minimum-row, minimum-column) of the target region in the image. When you construct a class that inherits from the ImageAdapter class, implement this method if you need to write data.
\begin{tabular}{ll} 
Purpose & Image Information tool \\
Syntax & \begin{tabular}{l} 
imageinfo \\
imageinfo(h) \\
imageinfo(filename) \\
imageinfo(info) \\
imageinfo(himage, filename) \\
imageinfo(himage,info) \\
hfig = imageinfo(...)
\end{tabular}
\end{tabular}

\section*{Description}
imageinfo creates an Image Information tool associated with the image in the current figure. The tool displays information about the basic attributes of the target image in a separate figure. imageinfo gets information about image attributes by querying the image object's CData.

The following table lists the basic image information included in the Image Information tool display. Note that the tool contains either four or six fields, depending on the type of image.
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Atribute \\
Name
\end{tabular} & Value \\
\hline \begin{tabular}{l} 
Width \\
(columns)
\end{tabular} & Number of columns in the image \\
\hline Height (rows) & Number of rows in the image \\
\hline Class & Data type used by the image, such as uint8. \\
\cline { 2 - 3 } & \begin{tabular}{l} 
Note For single or int16 images, imageinfo \\
returns a class value of double, because image objects \\
convert the cData of these images to double.
\end{tabular} \\
\hline Image type & \begin{tabular}{l} 
One of the image types identified by the Image \\
Processing Toolbox software: ' intensity ' \\
'truecolor', 'binary', or ' 'indexed'
\end{tabular} \\
\hline
\end{tabular}

\section*{imageinfo}
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Attribute \\
Name
\end{tabular} & Value \\
\hline \begin{tabular}{l} 
Minimum \\
intensity or \\
index
\end{tabular} & \begin{tabular}{l} 
For grayscale images, this value represents the lowest \\
intensity value of any pixel.
\end{tabular} \\
\begin{tabular}{l} 
For indexed images, this value represents the lowest \\
index value into a color map. \\
Not included for 'binary ' or 'truecolor' images.
\end{tabular} \\
\hline \begin{tabular}{l} 
Maximum \\
intensity or \\
index
\end{tabular} & \begin{tabular}{l} 
For grayscale images, this value represents the \\
highest intensity value of any pixel. \\
For indexed images, this value represents the highest \\
index value into a color map. \\
Not included for 'binary ' or 'truecolor' images.
\end{tabular} \\
\hline
\end{tabular}
imageinfo( h ) creates an Image Information tool associated with h , where h is a handle to a figure, axes, or image object.
imageinfo(filename) creates an Image Information tool containing image metadata from the graphics file filename. The image does not have to be displayed in a figure window. filename can be any file type that has been registered with an information function in the file formats registry, imformats, so its information can be read by imfinfo. filename can also be a DICOM, NITF, Interfile, or Analyze file.
imageinfo(info) creates an Image Information tool containing the image metadata in the structure info. info is a structure returned by the functions imfinfo, dicominfo, nitfinfo interfileinfo, or analyze75info. info can also be a user-created structure.
imageinfo(himage, filename) creates an Image Information tool containing information about the basic attributes of the image specified by the handle himage and the image metadata from the graphics file filename.
imageinfo(himage, info) creates an Image Information tool containing information about the basic attributes of the image specified by the handle himage and the image metadata in the structure info.
hfig = imageinfo(...) returns a handle to the Image Information tool figure.
```

Examples imageinfo('peppers.png')
h = imshow('bag.png');
info = imfinfo('bag.png');
imageinfo(h,info);
imshow('canoe.tif');
imageinfo;
See Also analyze75info | dicominfo | imattributes | imfinfo | imformats | imtool | interfileinfo | nitfinfo

```
Purpose Image Model object
Syntax imgmodel = imagemodel(himage)

API An image model object stores information about an image such as class, Functions type, display range, width, height, minimum intensity value, and maximum intensity value.

The image model object supports methods that you can use to access this information, get information about the pixels in an image, and perform special text formatting. Brief descriptions of these methods follow.

\section*{Methods}
imagemodel supports the following methods. Type methods imagemodel to see a list of methods, or type help imagemodel/methodname for more information about a specific method.

\section*{getClassType - Return class of image}
str = getClassType(imgmodel) returns a string indicating the class of the image, where imgmodel is a valid image model and str is a text string, such as 'uint8'.
getDisplayRange - Return display range of intensity image
disp_range = getDisplayRange(imgmodel), where imgmodel is a valid image model and disp_range is an array of doubles such as [ 0 255], returns a double array containing the minimum and maximum
values of the display range for an intensity image. For image types other than intensity, the value returned is an empty array.

\section*{getImageHeight - Return number of rows}
height = getImageHeight(imgmodel), where imgmodel is a valid image model and height is a double scalar, returns a double scalar containing the number of rows.

\section*{getImageType - Return image type}
str = getImageType(imgmodel), where imgmodel is a valid image model and str is one of the text strings ('intensity', 'truecolor', 'binary', or 'indexed'), returns a text string indicating the image type.

\section*{getImageWidth - Return number of columns}
width = getImageWidth(imgmodel), where imgmodel is a valid image model and width is a double scalar, returns a double scalar containing the number of columns.

\section*{getMinIntensity - Return minimum value in image}
minval = getMinIntensity (imgmodel), where imgmodel is a valid image model and minval is a numeric value, returns the minimum value in the image calculated as min(Image(:)). For an intensity image, the value returned is the minimum intensity. For an indexed image, the value returned is the minimum index. For any other image type, the value returned is an empty array. The class of minval depends on the class of the target image.

\section*{getMaxIntensity - Return maximum value in image}
maxval = getMaxIntensity(imgmodel), where imgmodel is a valid image model and maxval is a numeric value, returns the maximum value in the image calculated as max (Image(:)). For an intensity image, the value returned is the maximum intensity. For an indexed image, the value returned is the maximum index. For any other image type, the value returned is an empty array. The class of maxval depends on the class of the target image.

\section*{getNumberFormatFcn - Return handle to function that converts numeric value into string}
fun = getNumberFormatFcn(imgmodel), where imgmodel is a valid image model, returns the handle to a function that converts a numeric value into a string.
For example, str \(=\) fun(getPixelValue(imgmodel, 100, 100)) converts the numeric return value of the getPixelValue method into a text string.
getPixelInfoString - Return value of specific pixel as text string str = getPixelInfoString(imgmodel, row, column), where str is a character array, imgmodel is a valid image model, and row and column are numeric scalar values, returns a text string containing the value of the pixel at the location specified by row and column. For example, for an RGB image, the method returns a text string such as '[ \(\left.\begin{array}{lll}66 & 35 & 60\end{array}\right]\) '.

\section*{getPixelRegionFormatFen - Return handle to function that formats value of pixel into text string}
fun = getPixelRegionFormatFcn(imgmodel), takes a valid image model, imgmodel, and returns fun, a handle to a function that accepts the location (row, column) of a pixel in the target image and returns the value of the pixel as a specially formatted text string. For example, when used with an RGB image, this function returns a text string of the form 'R:000 G:000 B:000' where 000 is the actual pixel value.
str \(=\) fun \((100,100)\)
getPixelValue - Return value of specific pixel as numeric array val = getPixelValue(imgmodel, row, column), where imgmodel is a valid image model and row and column are numeric scalar values, returns the value of the pixel at the location specified by row and column as a numeric array. The class of val depends on the class of the target image.

\section*{getDefaultPixelInfoString - Return pixel information type as text string}
str = getDefaultPixelInfoString(imgmodel), where imgmodel is a valid image model, returns a text string indicating the pixel information type. This string can be used in place of actual pixel information
values. Depending on the image type, str can be the text string 'Intensity','[R G B]','BW', or '<Index> [R G B]'.

\section*{getDefaultPixelRegionString - Return type of information displayed in Pixel Region tool}
str = getDefaultPixelRegionString(imgmodel), where imgmodel is a valid image model, returns a text string indicating the type of information displayed in the Pixel Region tool for each image type. This string can be used in place of actual pixel values. Depending on the image type, str can be the text string '000','R:000 G:000 B:000]', 'O', or '<000> R:0.00 G:0.00 B:0.00'.
getScreenPixelRGBValue - Return screen display value of specific pixel
val = getScreenPixelRGBValue(imgmodel, row, col) returns the screen display value of the pixel at the location specified by row and col as a double array. imgmodel is a valid image model, row and col are numeric scalar values, and val is an array of doubles, such as [0.2 0.50 .3 .

\section*{Examples Create an image model.}
```

h = imshow('peppers.png');
im = imagemodel(h);
figure,subplot(1,2,1)
h1 = imshow('hestain.png');
subplot(1,2,2)
h2 = imshow('coins.png');
im = imagemodel([h1 h2]);

```

\section*{See Also getimagemodel}

\section*{imapplymatrix}

Purpose Linear combination of color channels
```

Syntax $\quad Y=$ imapplymatrix $(M, X)$
$Y$ = imapplymatrix (M, X, C)
Y = imapplymatrix(..., output_type)

```

\section*{Description}

\section*{Input}

Arguments
\(Y=\) imapplymatrix \((M, X)\) computes the linear combination of the rows of \(M\) with the color channels of \(X\). The output data type is the same as the type of \(X\).
\(Y=\) imapplymatrix ( \(M, X, C\) ) computes the linear combination of the rows of \(M\) with the color channels of \(X\), adding the corresponding constant value from \(C\) to each combination. The output data type is the same as the type of \(X\).
\(Y=\) imapplymatrix(..., output_type) returns the result of the linear combination in an array of type output_type.

\section*{M}

Matrix that contains the coefficients of the weighting matrix. If x is \(m\)-by- \(n\)-by- \(p\), M must be \(q\)-by- \(p\), where \(q\) is in the range \([1, p\) ].

\section*{X}

An image.

\section*{C}

A vector with the same number of elements as the number of rows in \(M\), or a scalar applied to every channel.

\section*{output_type}

A string that describes the output type. Possible values include uint8, int8, uint16, int16, uint32, int32, single, or double.

\section*{Output \\ Arguments}

Examples

\section*{Y}

Array that contains the linear combination of the rows of \(M\) with the color channels of \(X\).

Convert RGB values to grayscale:
RGB = imread('peppers.png');
M = [0.30, 0.59, 0.11];
gray = imapplymatrix(M, RGB);
figure
subplot(1,2,1), imshow(RGB), title('Original RGB')
subplot(1,2,2), imshow(gray), title('Grayscale Conversion')

Original RGB

imlincomb | immultiply

\section*{See Also}

\section*{imattributes}

Purpose Information about image attributes
\begin{tabular}{rl} 
Syntax \(\quad\) & attrs \(=\) imattributes \\
attrs \(=\) imattributes \((\) himage \()\) \\
attrs \(=\) imattributes \((\) imgmodel \()\)
\end{tabular}

\section*{Description}
attrs = imattributes returns information about an image in the current figure. If the current figure does not contain an image, imattributes returns an empty array.
attrs = imattributes(himage) returns information about the image specified by himage, a handle to an image object. imattributes gets the image attributes by querying the image object's CData.
imattributes returns image attribute information in attrs, a 4-by-2 or 6 -by- 2 cell array, depending on the image type. The first column of the cell array contains the name of the attribute as a text string. The second column contains the value of the attribute, also represented as a text string. The following table lists these attributes in the order they appear in the cell array.
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Attribute \\
Name
\end{tabular} & Value \\
\hline \begin{tabular}{l} 
Width \\
(columns)
\end{tabular} & Number of columns in the image \\
\hline Height (rows) & Number of rows in the image \\
\hline Class & Data type used by the image, such as uint8. \\
& \begin{tabular}{l} 
Note For single or int16 images, imageinfo \\
returns a class value of double, because image \\
objects convert CData of these classes to double.
\end{tabular} \\
\hline
\end{tabular}
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Atrribute \\
Name
\end{tabular} & Value \\
\hline Image type & \begin{tabular}{l} 
One of the image types identified by the Image \\
Processing Toolbox software: 'intensity, \\
'truecolor' ' 'binary ', or 'indexed'.
\end{tabular} \\
\hline \begin{tabular}{l} 
Minimum \\
intensity
\end{tabular} & \begin{tabular}{l} 
For intensity images, this value represents the lowest \\
intensity value of any pixel.
\end{tabular} \\
\hline \begin{tabular}{l} 
For indexed images, this value represents the lowest \\
index value into a color map. \\
Not included for 'binary ' or 'truecolor' images.
\end{tabular} \\
\hline Maximum & \begin{tabular}{l} 
For intensity images, this value represents the \\
highest intensity value of any pixel. \\
For indexed images, this value represents the highest \\
index value into a color map. \\
Not included for 'binary ' or 'truecolor' images.
\end{tabular} \\
\hline
\end{tabular}
attrs \(=\) imattributes(imgmodel) returns information about the image represented by the image model object, imgmodel.

\section*{Examples Retrieve the attributes of a grayscale image.}
```

h = imshow('liftingbody.png');
attrs = imattributes(h)
attrs =

```
```

    'Width (columns)' '512'
    'Height (rows)' '512'
    'Class' 'uint8'
    'Image type' 'intensity'
    'Minimum intensity' '0'
    'Maximum intensity' '255'
    ```

Retrieve the attributes of a truecolor image.

\section*{imattributes}
```

h = imshow('gantrycrane.png');
im = imagemodel(h);
attrs = imattributes(im)
attrs =
'Width (columns)' '400'
'Height (rows)' '264'
'Class' 'uint8'
'Image type' 'truecolor'

```
See Also imagemodel
\begin{tabular}{ll} 
Purpose & Bottom-hat filtering \\
Syntax & \begin{tabular}{l} 
IM2 = imbothat (IM, SE) \\
IM2 = imbothat (IM, NHOOD)
\end{tabular} \\
Description & \begin{tabular}{l} 
IM2 = imbothat (IM, SE) performs morphological bottom-hat filtering \\
on the grayscale or binary input image, IM, returning the filtered image, \\
IM2. The argument SE is a structuring element returned by the strel \\
function. SE must be a single structuring element object, not an array \\
containing multiple structuring element objects.
\end{tabular} \\
Class & \begin{tabular}{l} 
IM2 = imbothat (IM, NHOOD) performs morphological bottom-hat \\
filtering where NHOOD is an array of 0's and 1's that specifies the \\
size and shape of the structuring element. This is equivalent to \\
imbothat (IM, strel (NHOOD) ).
\end{tabular} \\
Support & \begin{tabular}{l} 
IM can be numeric or logical and must be nonsparse. The output image \\
has the same class as the input image. If the input is binary (logical), \\
then the structuring element must be flat.
\end{tabular} \\
Examples & \begin{tabular}{l} 
Top-hat filtering and bottom-hat filtering can be used together to \\
enhance contrast in an image.
\end{tabular} \\
I Read the image into the MATLAB workspace.
\end{tabular}

\section*{imbothat}


2 Create disk-shaped structuring element, needed for morphological processing.
se = strel('disk',3);

3 Add the original image I to the top-hat filtered image, and then subtract the bottom-hat filtered image.
```

J = imsubtract(imadd(I,imtophat(I,se)), imbothat(I,se));

```
figure, imshow(J)


See Also imtophat | strel

\section*{imclearborder}
\begin{tabular}{ll} 
Purpose & Suppress light structures connected to image border \\
Syntax & \begin{tabular}{l} 
IM2 = imclearborder (IM) \\
IM2 = imclearborder(IM, conn)
\end{tabular} \\
Description \(\quad\)\begin{tabular}{l} 
IM2 = imclearborder (IM) suppresses structures that are lighter than \\
their surroundings and that are connected to the image border. (In \\
other words, use this function to clear the image border.) IM can be \\
a grayscale or binary image. The output image, IM2, is grayscale or \\
binary, respectively. The default connectivity is 8 for two dimensions, \\
26 for three dimensions, and conndef(ndims (BW), 'maximal' ) for \\
higher dimensions.
\end{tabular}
\end{tabular}

Note For grayscale images, imclearborder tends to reduce the overall intensity level in addition to suppressing border structures.

IM2 = imclearborder(IM, conn) specifies the desired connectivity. conn can have any of the following scalar values.
\begin{tabular}{l|l}
\hline Value & Meaning \\
\hline Two-dimensional connectivities \\
\hline 4 & 4-connected neighborhood \\
\hline 8 & 8 -connected neighborhood \\
\hline Three-dimensional connectivities \\
\hline 6 & 6 -connected neighborhood \\
\hline 18 & 18 -connected neighborhood \\
\hline 26 & 26 -connected neighborhood \\
\hline
\end{tabular}

Connectivity can also be defined in a more general way for any dimension by using for conn a 3-by-3-by- ... -by-3 matrix of 0's and 1's. The 1 -valued elements define neighborhood locations relative to the
center element of conn. Note that conn must be symmetric about its center element.

Note A pixel on the edge of the input image might not be considered to be a border pixel if a nondefault connectivity is specified. For example, if conn = [000; \(1111 ; 000]\), elements on the first and last row are not considered to be border pixels because, according to that connectivity definition, they are not connected to the region outside the image.

\section*{Class Support}

IM can be a numeric or logical array of any dimension, and it must be nonsparse and real. IM2 has the same class as IM.

\section*{Examples}

The following examples use this simple binary image to illustrate the effect of imclearborder when you specify different connectivities.
\(\mathrm{BW}=\)\begin{tabular}{lllllllll} 
& & & & & & & 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 \\
1 & 0 & 0 & 1 & 1 & 1 & 0 & 0 & 0 \\
0 & 1 & 0 & 1 & 1 & 1 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 1 & 1 & 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
\end{tabular}

Using a 4-connected neighborhood, the pixel at \((5,2)\) is not considered connected to the border pixel \((4,1)\), so it is not cleared.

BWc1 = imclearborder(BW,4)
BWC1 =
\begin{tabular}{lllllllll}
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
\end{tabular}

\section*{imclearborder}
\begin{tabular}{lllllllll}
0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 & 0 \\
0 & 1 & 0 & 1 & 1 & 1 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 1 & 1 & 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
\end{tabular}

Using an 8-connected neighborhood, pixel \((5,2)\) is considered connected to pixel \((4,1)\) so both are cleared.

BWc2 = imclearborder(BW,8)
BWc2 =
\begin{tabular}{lllllllll}
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 & 1 & 1 & 1 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 1 & 1 & 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
\end{tabular}
Algorithms
References [1] Soille, P., Morphological Image Analysis: Principles and Applications, Springer, 1999, pp. 164-165.
See Also ..... conndef

\section*{Purpose \\ Morphologically close image}

Syntax
IM2 = imclose(IM, SE)
IM2 = imclose(IM,NHOOD)

Description

\section*{Class \\ Support}

\section*{Examples}

IM2 = imclose(IM, SE) performs morphological closing on the grayscale or binary image IM, returning the closed image, IM2. The structuring element, SE, must be a single structuring element object, as opposed to an array of objects. The morphological close operation is a dilation followed by an erosion, using the same structuring element for both operations.

IM2 = imclose(IM,NHOOD) performs closing with the structuring element strel(NHOOD), where NHOOD is an array of 0's and 1's that specifies the structuring element neighborhood.

IM can be any numeric or logical class and any dimension, and must be nonsparse. If IM is logical, then SE must be flat. IM2 has the same class as IM.

Use imclose to join the circles in the image together by filling in the gaps between them and by smoothing their outer edges.

1 Read the image into the MATLAB workspace and view it.
```

originalBW = imread('circles.png');
imshow(originalBW);

```

\section*{imclose}


2 Create a disk-shaped structuring element. Use a disk structuring element to preserve the circular nature of the object. Specify a radius of 10 pixels so that the largest gap gets filled.
```

se = strel('disk',10);

```

3 Perform a morphological close operation on the image.
```

closeBW = imclose(originalBW,se);

```
figure, imshow(closeBW)


\section*{See Also}
```

imdilate | imerode | imopen | strel

```
\begin{tabular}{ll} 
Purpose & Choose Colormap tool \\
Syntax & \begin{tabular}{l} 
imcolormaptool \\
imcolormaptool(hclientfig) \\
hfig \(=\) imcolormaptool (...)
\end{tabular} \\
&
\end{tabular}

Description The Choose Colormap tool is an interactive colormap selection tool that allows you to change the colormap of the target (current) figure by selecting a colormap from a list of MATLAB colormap functions or workspace variables, or by entering a custom MATLAB expression.
imcolormaptool launches the Choose Colormap tool in a separate figure, which is associated with the target figure.
imcolormaptool(hclientfig) launches the Choose Colormap tool using hclientfig as the target figure. hclientfig must contain either a grayscale or an indexed image.
hfig = imcolormaptool(...) returns a handle to the Choose Colormap tool, hfig.
```

Examples h = figure;
imshow('cameraman.tif');
imcolormaptool(h);

```

\section*{imcolormaptool}


\section*{Choose Colormap Tool}

See Also
colormap | imshow | imtool

\section*{Purpose}

Complement image
Syntax IM2 = imcomplement(IM)
Description

Examples Create the complement of a uint8 array.
```

X = uint8([ 255 10 75; 44 225 100]);
X2 = imcomplement(X)
x2 =
0 245 180
211 30 155

```

Reverse black and white in a binary image.
```

bw = imread('text.png');
bw2 = imcomplement(bw);
subplot(1,2,1),imshow(bw)
subplot(1,2,2),imshow(bw2)

```

Create the complement of an intensity image.
```

I = imread('glass.png');

```
J = imcomplement(I);

\section*{imcomplement}
imshow(I), figure, imshow(J)


Original Image


Complement Image

See Also
imabsdiff | imadd | imdivide | imlincomb | immultiply | imsubtract
Purpose Create contour plot of image data
Syntax

imcontour(I)

imcontour(I, n)

imcontour(I,v)

imcontour(x,y,...)

imcontour(..., LineSpec)

[C,handle] = imcontour(...)

\section*{Description}

Class Support

Examples \(\quad I=\) imread('circuit.tif');
imcontour(I,3)

\section*{imcontour}


See Also clabel | contour | LineSpec

\section*{Purpose}

Adjust Contrast tool

\section*{Syntax}
imcontrast
imcontrast(h)
hfigure = imcontrast(...)

\section*{Description}
imcontrast creates an Adjust Contrast tool in a separate figure that is associated with the grayscale image in the current figure, called the target image. The Adjust Contrast tool is an interactive contrast and brightness adjustment tool, shown in the following figure, that you can use to adjust the black-to-white mapping used to display the image. When you use the tool, imcontrast adjusts the contrast of the displayed image by modifying the axes CLim property. To modify the actual pixel values in the target image, click the Adjust Data button. (This button is unavailable until you make a change to the contrast of the image.) For more information about using the tool, see "Tips" on page 3-322.


\section*{imcontrast}

Note The Adjust Contrast tool can handle grayscale images of class double and single with data ranges beyond the default display range, which is [ 0 1]. For these images, imcontrast sets the histogram limits to fit the image data range, with padding at the upper and lower bounds.
imcontrast (h) creates the Adjust Contrast tool associated with the image specified by the handle h . h can be a handle to a figure, axes, uipanel, or image object. If \(h\) is an axes or figure handle, imcontrast uses the first image returned by findobj( H, 'Type ', 'image').
hfigure \(=\) imcontrast(...) returns a handle to the Adjust Contrast tool figure.

The Adjust Contrast tool presents a scaled histogram of pixel values (overly represented pixel values are truncated for clarity). Dragging on the left red bar in the histogram display changes the minimum value. The minimum value (and any value less than the minimum) displays as black. Dragging on the right red bar in the histogram changes the maximum value. The maximum value (and any value greater than the maximum) displays as white. Values in between the red bars display as intermediate shades of gray.

Together the minimum and maximum values create a "window". Stretching the window reduces contrast. Shrinking the window increases contrast. Changing the center of the window changes the brightness of the image. It is possible to manually enter the minimum, maximum, width, and center values for the window. Changing one value automatically updates the other values and the image.
For more information about using the Adjust Contrast tool, see "Adjusting Image Contrast Using the Adjust Contrast Tool".

\section*{Window/Level Interactivity}

Clicking and dragging the mouse within the target image interactively changes the image's window values. Dragging the mouse horizontally from left to right changes the window width (i.e., contrast). Dragging
the mouse vertically up and down changes the window center (i.e., brightness). Holding down the Ctrl key before clicking and dragging the mouse accelerates the rate of change; holding down the Shift key before clicking and dragging the mouse slows the rate of change. Keys must be pressed before clicking and dragging.

\section*{Examples imshow('pout.tif') \\ imcontrast(gca)}

See Also imadjust | imtool | stretchlim

Purpose Crop image
Syntax \(\quad \begin{array}{ll} & I=\operatorname{imcrop} \\ & I 2=\operatorname{imcrop}(I) \\ & X 2=\operatorname{imcrop}(X, \operatorname{map}) \\ & I=\operatorname{imcrop}(h) \\ & I 2=\operatorname{imcrop}(I, r e c t) \\ & X 2=\operatorname{imcrop}(X, \operatorname{map}, \operatorname{rect}) \\ & {[\ldots]=\operatorname{imcrop}(x, y, \ldots)} \\ & {[I 2 \operatorname{rect}]=\operatorname{imcrop}()} \\ & {[X, Y, I 2, r e c t]=\operatorname{imcrop}()}\end{array}\)
Description
I = imcrop creates an interactive Crop Image tool associated with the image displayed in the current figure, called the target image. The Crop Image tool is a moveable, resizable rectangle that you can position interactively using the mouse. When the Crop Image tool is active, the pointer changes to cross hairs \({ }{ }^{\text {when }}\) you move it over the target image. Using the mouse, you specify the crop rectangle by clicking and dragging the mouse. You can move or resize the crop rectangle using the mouse. When you are finished sizing and positioning the crop rectangle, create the cropped image by double-clicking the left mouse button or by choosing Crop Image from the context menu. imcrop returns the cropped image, I. The following figure illustrates the Crop Image tool with the context menu displayed. For more information about the interactive capabilities of the tool, see the table that follows.

\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} & Description \\
\hline \begin{tabular}{l} 
Deleting the Crop \\
Image tool.
\end{tabular} & \begin{tabular}{l} 
Press Backspace, Escape or Delete, or \\
right-click inside the crop rectangle and select \\
Cancel from the context menu. \\
Note: If you delete the ROI, the function \\
returns empty values.
\end{tabular} \\
\hline \begin{tabular}{l} 
Resizing the Crop \\
Image tool.
\end{tabular} & \begin{tabular}{l} 
Select any of the resize handles on the \\
crop rectangle. The pointer changes to a \\
double-headed arrow \(\leftrightarrows\). Click and drag the \\
mouse to resize the crop rectangle.
\end{tabular} \\
\hline
\end{tabular}
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} & Description \\
\hline \begin{tabular}{l} 
Moving the Crop \\
Image tool.
\end{tabular} & \begin{tabular}{l} 
Move the pointer inside the boundary of the \\
crop rectangle. The pointer changes to a fleur \\
shape \\
the rectangle over the image.
\end{tabular} \\
\hline \begin{tabular}{l} 
Changing the color \\
used to display the \\
crop rectangle.
\end{tabular} & \begin{tabular}{l} 
Right-click inside the boundary of the crop \\
rectangle and select Set Color from the \\
context menu.
\end{tabular} \\
\hline Cropping the image. & \begin{tabular}{l} 
Double-click the left mouse button or \\
right-click inside the boundary of the crop \\
rectangle and select Crop Image from the \\
context menu.
\end{tabular} \\
\hline \begin{tabular}{l} 
Retrieving the \\
coordinates of the \\
crop rectangle.
\end{tabular} & \begin{tabular}{l} 
Right-click inside the boundary of the crop \\
rectangle and select Copy Position from the \\
context menu. imcrop copies a four-element \\
position vector ([xmin ymin width height ]) \\
to the clipboard.
\end{tabular} \\
\hline
\end{tabular}

I2 \(=\) imcrop( I ) displays the image I in a figure window and creates a cropping tool associated with that image. I can be a grayscale image, a truecolor image, or a logical array. The cropped image returned, I2, is of the same type as I.

X2 \(=\) imcrop( \(X\), map) displays the indexed image \(X\) in a figure using the colormap map, and creates a cropping tool associated with that image.
I = imcrop(h) creates a cropping tool associated with the image specified by handle \(h\). h may be an image, axes, uipanel, or figure handle. If \(h\) is an axes, uipanel, or figure handle, the cropping tool acts on the first image found in the container object.

Note With these interactive syntaxes, the cropping tool blocks the MATLAB command line until you complete the operation.

I2 = imcrop(I, rect) crops the image I. rect is a four-element position vector[xmin ymin width height] that specifies the size and position of the crop rectangle.

X2 = imcrop(X, map, rect) crops the indexed image X. map specifies the colormap used with \(X\). rect is a four-element position vector [ \(x m i n\) ymin width height] that specifies the size and position of the cropping rectangle.
[...] = imcrop(x, y,...) specifies a non-default spatial coordinate system for the target image. \(x\) and \(y\) are two-element vectors specifying XData and YData.
[I2 rect] = imcrop( ) returns the cropping rectangle in rect, a four-element position vector.
\([\mathrm{X}, \mathrm{Y}, \mathrm{I} 2\), rect \(]=\) imcrop ( ) returns X and y , two-element vectors that specify the XData and YData of the target image.

\section*{Class \\ Support}

If you specify rect as an input argument, the input image can be logical or numeric, and must be real and nonsparse. rect is of class double.

If you do not specify rect as an input argument, imcrop calls imshow. imshow expects I to be logical, uint8, uint16, int16, single, or double. A truecolor image can be uint8, int16, uint16, single, or double. \(X\) can be logical, uint8, uint16, single, or double. The input image must be real and nonsparse.

If you specify an image as an input argument, the output image has the same class as the input image.

If you don't specify an image as an input argument, i.e., you call imcrop with no input arguments or a handle, the output image has the same class as the input image except for int 16 or single. If the input image is int16 or single, the output image is double.

Tips

\section*{Examples}

\section*{See Also}


Because rect is specified in terms of spatial coordinates, the width and height elements of rect do not always correspond exactly with the size of the output image. For example, suppose rect is [20 20 40 30], using the default spatial coordinate system. The upper-left corner of the specified rectangle is the center of the pixel \((20,20)\) and the lower-right corner is the center of the pixel \((50,60)\). The resulting output image is 31 -by- 41 , not 30 -by- 40 , because the output image includes all pixels in the input image that are completely or partially enclosed by the rectangle.
```

I = imread('circuit.tif');

```
I = imread('circuit.tif');
I2 = imcrop(I,[75 68 130 112]);
I2 = imcrop(I,[75 68 130 112]);
imshow(I), figure, imshow(I2)
```

imshow(I), figure, imshow(I2)

```


\footnotetext{
imrect | zoom
}

\section*{Purpose \\ Syntax \\ Description}

Dilate image

IM2 = imdilate(IM,SE)
IM2 = imdilate(IM,NHOOD)
IM2 = imdilate(IM,SE,PACKOPT)
IM2 = imdilate(...,SHAPE)
IM2 = imdilate(IM, SE) dilates the grayscale, binary, or packed binary image IM, returning the dilated image, IM2. The argument SE is a structuring element object, or array of structuring element objects, returned by the strel function.

If IM is logical and the structuring element is flat, imdilate performs binary dilation; otherwise, it performs grayscale dilation. If SE is an array of structuring element objects, imdilate performs multiple dilations of the input image, using each structuring element in SE in succession.

IM2 = imdilate(IM, NHOOD) dilates the image IM, where NHOOD is a matrix of 0's and 1's that specifies the structuring element neighborhood. This is equivalent to the syntax imdilate(IM, strel(NHOOD)). The imdilate function determines the center element of the neighborhood by floor ((size (NHOOD)+1)/2).

IM2 = imdilate(IM,SE,PACKOPT) or imdilate(IM, NHOOD, PACKOPT) specifies whether IM is a packed binary image. PACKOPT can have either of the following values. Default value is enclosed in braces ( \(\}\) ).
\begin{tabular}{l|l}
\hline Value & Description \\
\hline 'ispacked ' & \begin{tabular}{l} 
IM is treated as a packed binary image as produced \\
by bwpack. IM must be a 2-D uint32 array and \\
SE must be a flat 2-D structuring element. If the \\
value of PACKOPT is 'ispacked ', PADOPT must be \\
'same '.
\end{tabular} \\
\hline \{'notpacked ' \} & IM is treated as a normal array. \\
\hline
\end{tabular}

\section*{imdilate}

IM2 = imdilate(..., SHAPE) specifies the size of the output image. SHAPE can have either of the following values. Default value is enclosed in braces (\{\}).
\begin{tabular}{l|l}
\hline Value & Description \\
\hline \{'same' \} & \begin{tabular}{l} 
Make the output image the same size as the input \\
image. If the value of PACKOPT is 'ispacked ', PADOPT \\
must be 'same'.
\end{tabular} \\
\hline 'full' & Compute the full dilation. \\
\hline
\end{tabular}

\section*{Definitions}

The binary dilation of \(A\) by \(B\), denoted \(A \oplus B\), is defined as the set operation:
\[
A \oplus B=\left\{z \mid(\hat{B})_{z} \cap A \neq \varnothing\right\},
\]
where \(\hat{B}\) is the reflection of the structuring element \(B\). In other words, it is the set of pixel locations \(z\), where the reflected structuring element overlaps with foreground pixels in \(A\) when translated to \(z\). Note that some people use a definition of dilation in which the structuring element is not reflected.

In the general form of gray-scale dilation, the structuring element has a height. The gray-scale dilation of \(A(x, y)\) by \(B(x, y)\) is defined as:
\[
(A \oplus B)(x, y)=\max \left\{A\left(x-x^{\prime}, y-y^{\prime}\right)+B\left(x^{\prime}, y^{\prime}\right) \mid\left(x^{\prime}, y^{\prime}\right) \in D_{B}\right\}
\]
where \(D_{B}\) is the domain of the structuring element \(B\) and \(A(x, y)\) is assumed to be \(-\infty\) outside the domain of the image. To create a structuring element with nonzero height values, use the syntax strel(nhood, height), where height gives the height values and nhood corresponds to the structuring element domain, \(D_{B}\).
Most commonly, gray-scale dilation is performed with a flat structuring element \((B(x, y)=0)\). Gray-scale dilation using such a structuring element is equivalent to a local-maximum operator:
\[
(A \oplus B)(x, y)=\max \left\{A\left(x-x^{\prime}, y-y^{\prime}\right) \mid\left(x^{\prime}, y^{\prime}\right) \in D_{B}\right\}
\]

All of the strel syntaxes except for strel(nhood, height), strel('arbitrary', nhood, height), and strel('ball', ...) produce flat structuring elements.

For more information about binary dilation, see [1].

\section*{Class Support}

\section*{Examples}

IM can be logical or numeric and must be real and nonsparse. It can have any dimension. If IM is logical, SE must be flat. The output has the same class as the input. If the input is packed binary, then the output is also packed binary.

Dilate a binary image with a vertical line structuring element.
```

bw = imread('text.png');
se = strel('line',11,90);
bw2 = imdilate(bw,se);
imshow(bw), title('Original')
figure, imshow(bw2), title('Dilated')

```


Dilate a grayscale image with a rolling ball structuring element.
```

I = imread('cameraman.tif');
se = strel('ball',5,5);
I2 = imdilate(I,se);
imshow(I), title('Original')

```

\section*{imdilate}
```

figure, imshow(I2), title('Dilated')

```


To determine the domain of the composition of two flat structuring elements, dilate the scalar value 1 with both structuring elements in sequence, using the 'full' option.
```

se1 = strel('line',3,0)

```
se1 =

Flat STREL object containing 3 neighbors. Neighborhood:
\(\begin{array}{lll}1 & 1 & 1\end{array}\)
se2 = strel('line',3,90)
se2 =

Flat STREL object containing 3 neighbors. Neighborhood:

1
1
1
```

composition = imdilate(1,[se1 se2],'full')

```
composition =
\(1 \quad 1 \quad 1\)
\(\begin{array}{lll}1 & 1 & 1\end{array}\)

\section*{Algorithms}

\section*{References}

See Also
bwpack | bwunpack | conv2 | filter2 | imclose | imerode | imopen | strel
imdilate automatically takes advantage of the decomposition of a structuring element object (if it exists). Also, when performing binary dilation with a structuring element object that has a decomposition, imdilate automatically uses binary image packing to speed up the dilation.

Dilation using bit packing is described in [3].
[1] Gonzalez, R. C., R. E. Woods, and S. L. Eddins, Digital Image Processing Using MATLAB, Gatesmark Publishing, 2009.
[2] Haralick, R. M., and L. G. Shapiro, Computer and Robot Vision, Vol. I, Addison-Wesley, 1992, pp. 158-205.
[3] van den Boomgard, R, and R. van Balen, "Methods for Fast Morphological Image Transforms Using Bitmapped Images," Computer Vision, Graphics, and Image Processing: Graphical Models and Image Processing, Vol. 54, Number 3, pp. 254-258, May 1992.

\section*{imdisplayrange}

\author{
Purpose \\ Description
}

Display Range tool
Syntax \(\quad \begin{aligned} & \text { imdisplayrange } \\ & \text { imdisplayrange }(\mathrm{h}) \\ & \text { imdisplayrange }(\text { hparent }, \text { himage }) \\ & \\ & \text { hpanel }=\text { imdisplayrange (...) }\end{aligned}\)
imdisplayrange creates a Display Range tool in the current figure. The Display Range tool shows the display range of the intensity image or images in the figure.

The tool is a uipanel object, positioned in the lower-right corner of the figure. It contains the text string Display range: followed by the display range values for the image, as shown in the following figure.

\section*{Display range: [0 255]}

Varies with image type
For an indexed, truecolor, or binary image, the display range is not applicable and is set to empty ([]).
imdisplayrange (h) creates a Display Range tool in the figure specified by the handle h , where h is a handle to an image, axes, uipanel, or figure object. Axes, uipanel, or figure objects must contain at least one image object.
imdisplayrange(hparent, himage) creates a Display Range tool in hparent that shows the display range of himage. himage is a handle to an image or an array of image handles. hparent is a handle to the figure or uipanel object that contains the display range tool.
hpanel \(=\) imdisplayrange(...) returns a handle to the Display Range tool uipanel.

\section*{Note}

The Display Range tool can work with multiple images in a figure. When the pointer is not in an image in a figure, the Display Range tool displays the text string [black white].

Examples \(\quad \begin{aligned} & \text { Display an image and include the Display Range tool. } \\ & \begin{array}{l}\text { imshow( 'bag.png' ) ; } \\ \text { imdisplayrange ; }\end{array}\end{aligned}\)
Import a 16 -bit DICOM image and display it with its default range and scaled range in the same figure.
```

dcm = dicomread('CT-MONO2-16-ankle.dcm');
subplot(1,2,1), imshow(dcm);
subplot(1,2,2), imshow(dcm,[]);
imdisplayrange;

```

See also imtool

Purpose Distance tool
Syntax \(\quad\)\begin{tabular}{l}
\(h=\) imdistline \\
\\
\\
\(h=\) imdistline \((h p a r e n t)\) \\
\\
\end{tabular}

\section*{Description}
\(\mathrm{h}=\) imdistline creates a Distance tool on the current axes. The function returns h , a handle to an imdistline object.

The Distance tool is a draggable, resizable line, superimposed on an axes, that measures the distance between the two endpoints of the line. The Distance tool displays the distance in a text label superimposed over the line. The tools specifies the distance in data units determined by the XData and YData properties, which is pixels, by default. The following figure shows a Distance tool on an axes.


To move the Distance tool, position the pointer over the line, the shape changes to the fleur, \(\stackrel{\leftrightarrows}{\ddagger}\). Click and drag the line using the mouse. To resize the Distance tool, move the pointer over either of the endpoints of the line, the shape changes to the pointing finger, dory. Click and drag the endpoint of the line using the mouse. The line also supports a context menu that allows you to control various aspects of its functioning and appearance. See Context Menu for more information. Right-click the line to access the context menu.
\(\mathrm{h}=\) imdistline(hparent) creates a draggable Distance tool on the object specified by hparent. hparent specifies the Distance tool's parent, which is typically an axes object, but can also be any other object that can be the parent of an hggroup object.
\(\mathrm{h}=\) imdistline(..., x, y) creates a Distance tool with endpoints located at the locations specified by the vectors \(x\) and \(y\), where \(x=[x 1\) \(\mathrm{x} 2]\) and \(\mathrm{y}=[\mathrm{y} 1 \mathrm{y} 2]\).

\section*{Context Menu}
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Distance Tool \\
Behavior
\end{tabular} & Context Menu Item \\
\hline \begin{tabular}{l} 
Export endpoint and \\
distance data to the \\
workspace
\end{tabular} & \begin{tabular}{l} 
Select Export to Workspace from the \\
context menu.
\end{tabular} \\
\hline \begin{tabular}{l} 
Toggle the distance \\
label on/off.
\end{tabular} & \begin{tabular}{l} 
Select Show Distance Label from the \\
context menu.
\end{tabular} \\
\hline \begin{tabular}{l} 
Specify horizontal \\
and vertical drag \\
constraints
\end{tabular} & \begin{tabular}{l} 
Select Constrain Drag from the context \\
menu.
\end{tabular} \\
\hline \begin{tabular}{l} 
Change the color \\
used to display the \\
line.
\end{tabular} & Select Set Color from the context menu. \\
\hline \begin{tabular}{l} 
Delete the Distance \\
tool object
\end{tabular} & Select Delete from the context menu. \\
\hline
\end{tabular}

\section*{API \\ Functions}

The Distance tool contains a structure of function handles, called an API, that can be used to retrieve distance information and control other aspects of Distance tool behavior. To retrieve this structure from the Distance tool, use the iptgetapi function, where h is a handle to the Distance tool.
```

api = iptgetapi(h)

```

\section*{imdistline}

The following table lists the functions in the API, with their syntax and brief descriptions.
\begin{tabular}{l|l}
\hline Function & Description \\
\hline getDistance & \begin{tabular}{l} 
Returns the distance between the endpoints of the \\
Distance tool. \\
dist = getDistance()
\end{tabular} \\
\hline getAngleFromHorizontal & \begin{tabular}{l} 
The value returned is in data units determined by the \\
XData and YData properties, which is pixels, by default.
\end{tabular} \\
\hline \begin{tabular}{l} 
Returns the angle in degrees between the line defined \\
by the Distance tool and the horizontal axis. The \\
angle returned is between 0 and 180 degrees. (For \\
information about how this angle is calculated, see \\
"Tips" on page 3-341.) \\
angle = getAngleFromHorizontal()
\end{tabular} \\
\hline setLabelTextFormatter & \begin{tabular}{l} 
Sets the format string used in displaying the distance \\
label. \\
setLabelTextFormatter(str) \\
str is a character array specifying a format string in \\
the form expected by sprintf.
\end{tabular} \\
\hline getLabelTextFormatter & \begin{tabular}{l} 
Returns a character array specifying the format string \\
used to display the distance label.
\end{tabular} \\
str = getLabelTextFormatter()
\end{tabular}
\begin{tabular}{l|l}
\hline Function & Description \\
\hline setLabelVisible & \begin{tabular}{l} 
Sets visibility of Distance tool text label. \\
setLabelVisible(h, TF) \\
h is the Distance tool. TF is a logical scalar. When the \\
distance label is visible, TF is true. When the distance \\
label is invisible, TF is false.
\end{tabular} \\
\hline getLabelVisible & \begin{tabular}{l} 
Gets visibility of Distance tool text label. \\
TF = getLabelVisible(h)
\end{tabular} \\
\hline h is the Distance tool. TF is a logical scalar. When TF is \\
true, the distance label is visible. When TF is false, the \\
distance label is invisible.
\end{tabular}, \begin{tabular}{l} 
Sets the endpoint positions of the Distance tool. \\
setPosition(X, Y) \\
setPosition([X1 Y1; X2 Y2])
\end{tabular}

\section*{imdistline}
\begin{tabular}{l|l}
\hline Function & Description \\
\hline setColor & \begin{tabular}{l} 
Sets the color used to draw the Distance tool. \\
setColor (new_color)
\end{tabular} \\
& \begin{tabular}{l} 
new_color can be a three-element vector specifying \\
an RGB triplet, or a text string specifying the long or \\
short names of a predefined color, such as 'white' or \\
'w'. For a complete list of these predefined colors and \\
their short names, see ColorSpec.
\end{tabular} \\
\hline getColor & \begin{tabular}{l} 
Gets the color used to draw the ROI object h. \\
color = getColor (h)
\end{tabular} \\
\hline addNewPositionCallback & \begin{tabular}{l} 
color is a three-element vector that specifies an RGB \\
triplet.
\end{tabular} \\
\hline \begin{tabular}{l} 
Adds the function handle fcn to the list of new-position \\
callback functions. \\
id = addNewPositionCallback(fcn)
\end{tabular} \\
& \begin{tabular}{l} 
Whenever the Distance tool changes its position, each \\
function in the list is called with the following syntax. \\
fcn(pos)
\end{tabular} \\
pos is a 2-by-2 array [X1 Y1; X2 Y2]. \\
The return value, id, is used only with \\
removeNewPositionCallback.
\end{tabular}
\(\left.\begin{array}{l|l}\hline \text { Function } & \text { Description } \\
\hline \text { removeNewPositionCallback } & \begin{array}{l}\text { Removes the corresponding function from the } \\
\text { new-position callback list. } \\
\text { removeNewPositionCallback(id) } \\
\text { id is the identifier returned by } \\
\text { addNewPositioncallback. }\end{array} \\
\hline \text { setPositionConstraintFcn } & \begin{array}{l}\text { Sets the position constraint function to be the specified } \\
\text { function handle, fcn. Use this function to control } \\
\text { where the Distance tool can be moved and resized. }\end{array} \\
\text { setPositionConstraintFcn(fcn) } \\
\text { Whenever the Distance tool is moved or resized because } \\
\text { of a mouse drag, the constraint function is called using } \\
\text { the following syntax. }\end{array}\right\}\)\begin{tabular}{l} 
constrained_position = fcn(new_position)
\end{tabular}

\footnotetext{
Tips
If you use imdistline with an axes that contains an image object, and do not specify a drag constraint function, users can drag the line outside the extent of the image. When used with an axes created by the plot function, the axes limits automatically expand to accommodate the movement of the line.

To understand how imdistline calculates the angle returned by getAngleToHorizontal, draw an imaginary horizontal vector from the bottom endpoint of the distance line, extending to the right. The value
}

\section*{imdistline}
returned by getAngleToHorizontal is the angle from this horizontal vector to the distance line, which can range from 0 to 180 degrees.

\section*{Examples Example 1}

Insert a Distance tool into an image. Use makeConstrainToRectFen to specify a drag constraint function that prevents the Distance tool from being dragged outside the extent of the image. Right-click the Distance tool and explore the context menu options.
```

figure, imshow('pout.tif');
h = imdistline(gca);
api = iptgetapi(h);
fcn = makeConstrainToRectFcn('imline',...
get(gca,'XLim'),get(gca,'YLim'));
api.setDragConstraintFcn(fcn);

```

\section*{Example 2}

Position endpoints of the Distance tool at the specified locations.
```

close all, imshow('pout.tif');
h = imdistline(gca,[10 100],[10 100]);

```

Delete the Distance tool.
```

api = iptgetapi(h);
api.delete();

```

\section*{Example 3}

Use the Distance tool with XData and YData of associated image in non-pixel units. This example requires the boston.tif image from the Mapping Toolbox software, which includes material copyrighted by GeoEye \({ }^{\mathrm{TM}}\), all rights reserved.
```

start_row = 1478;
end_row = 2246;
meters_per_pixel = 1;
rows = [start_row meters_per_pixel end_row];

```
```

start_col = 349;
end_col = 1117;
cols = [start_col meters_per_pixel end_col];
img = imread('boston.tif','PixelRegion',{rows,cols});
figure;
hImg = imshow(img);
title('1 meter per pixel');
% Specify initial position of distance tool on Harvard Bridge.
hline = imdistline(gca,[271 471],[108 650]);
api = iptgetapi(hline);
api.setLabelTextFormatter('%02.Of meters');
% Repeat process but work with a 2 meter per pixel sampled image. Verify
% that the same distance is obtained.
meters_per_pixel = 2;
rows = [start_row meters_per_pixel end_row];
cols = [start_col meters_per_pixel end_col];
img = imread('boston.tif','PixelRegion',{rows,cols});
figure;
hImg = imshow(img);
title('2 meters per pixel');

```
\% Convert XData and YData to meters using conversion factor.
XDataInMeters = get(hImg,'XData')*meters_per_pixel;
YDataInMeters = get(hImg,'YData')*meters_per_pixel;
\% Set XData and YData of image to reflect desired units.
set (hImg, 'XData', XDataInMeters, 'YData', YDataInMeters) ;
set (gca, 'XLim', XDataInMeters, 'YLim', YDataInMeters);
\% Specify initial position of distance tool on Harvard Bridge.
hline = imdistline(gca,[271 471],[108 650]);
api \(=\) iptgetapi(hline);
api.setLabelTextFormatter('\%02.Of meters');
iptgetapi | makeConstrainToRectFcn

\section*{imdivide}

Purpose Divide one image into another or divide image by constant
Syntax \(\quad Z=\operatorname{imdivide}(X, Y)\)
Description
\(Z=\) imdivide \((X, Y)\) divides each element in the array \(X\) by the corresponding element in array \(Y\) and returns the result in the corresponding element of the output array \(Z\). \(X\) and \(Y\) are real, nonsparse numeric arrays with the same size and class, or \(Y\) can be a scalar double. \(Z\) has the same size and class as \(X\) and \(Y\).

If \(X\) is an integer array, elements in the output that exceed the range of integer type are truncated, and fractional values are rounded.

Note On Intel architecture processors, imdivide can take advantage of the Intel Integrated Performance Primitives (Intel IPP) library, thus accelerating its execution time. The Intel IPP library is activated only if arrays \(X\) and \(Y\) are of class uint8, int16, or single and are of the same size and class.

Examples Divide two uint8 arrays. Note that fractional values greater than or equal to 0.5 are rounded up to the nearest integer.

X = uint8([ 255 10 75; 44 225 100]);
\(Y=\) uint8([ \(502050 ; 505050\) ]);
Z = imdivide(X,Y)
Z =
\(\begin{array}{lll}5 & 1 & 2 \\ 1 & 5 & 2\end{array}\)
Estimate and divide out the background of the rice image.
```

I = imread('rice.png');
background = imopen(I,strel('disk',15));
Ip = imdivide(I,background);
imshow(Ip,[])

```

Divide an image by a constant factor.
```

I = imread('rice.png');
J = imdivide(I,2);
subplot(1,2,1), imshow(I)
subplot(1,2,2), imshow(J)

```

See Also
imabsdiff | imadd | imcomplement | imlincomb | immultiply |
imsubtract | ippl

\section*{imellipse}

Purpose Create draggable ellipse
Syntax
Description
h = imellipse
h = imellipse(hparent)
h = imellipse(hparent, position)
H = imellipse(..., param1, val1, ...)
\(h=\) imellipse begins interactive placement of an ellipse on the current axes. The function returns h, a handle to an imellipse object. The ellipse has a context menu associated with it that controls aspects of its appearance and behavior-see "Interactive Behavior" on page 3-347. Right-click on the line to access this context menu.
\(\mathrm{h}=\) imellipse(hparent) begins interactive placement of an ellipse on the object specified by hparent. hparent specifies the HG parent of the ellipse graphics, which is typically an axes but can also be any other object that can be the parent of an hggroup.
\(\mathrm{h}=\) imellipse(hparent, position) creates a draggable ellipse on the object specified by hparent. position is a four-element vector that specifies the initial location of the ellipse in terms of a bounding rectangle. position has the form [xmin ymin width height].

H = imellipse(..., param1, val1, ...) creates a draggable ellipse, specifying parameters and corresponding values that control the behavior of the ellipse. The following table lists the parameter available. Parameter names can be abbreviated, and case does not matter.
\begin{tabular}{l|l}
\hline Parameter & Value \\
\hline 'PositionConstraintFcn' & \begin{tabular}{l} 
Function handle that is called whenever \\
the mouse is dragged. You can use \\
this to control where the ellipse may \\
be dragged. See the help for the \\
setPositionConstraintFcn method \\
for information about valid function \\
handles.
\end{tabular} \\
\hline
\end{tabular}

\section*{Interactive Behavior}

When you call imellipse with an interactive syntax, the pointer changes to a cross hairs \(T_{\text {when over an image. Click and drag the }}\) mouse to specify the size and position of the ellipse. The ellipse also supports a context menu that you can use to control aspects of its appearance and behavior. The following figure illustrates the ellipse with its context menu.


The following table lists the interactive behavior supported by imellipse.
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} & Description \\
\hline \begin{tabular}{l} 
Moving the entire \\
ellipse.
\end{tabular} & \begin{tabular}{l} 
Move the pointer inside the ellipse. The \\
pointer changes to a fleur shape \(\stackrel{\leftrightarrows}{\leftrightarrows}\). Click \\
and drag the mouse to move the ellipse.
\end{tabular} \\
\hline Resizing the ellipse. & \begin{tabular}{l} 
Move the pointer over a resizing handle on the \\
ellipse. The pointer changes to a double-ended \\
arrow shape \\
to resize the ellipse.
\end{tabular} \\
\hline
\end{tabular}

\section*{imellipse}
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} & Description \\
\hline \begin{tabular}{l} 
Changing the color \\
used to display the \\
ellipse.
\end{tabular} & \begin{tabular}{l} 
Move the pointer inside the ellipse. Right-click \\
and select Set Color from the context menu.
\end{tabular} \\
\hline \begin{tabular}{l} 
Retrieving the \\
current position \\
of the ellipse.
\end{tabular} & \begin{tabular}{l} 
Move the pointer inside the ellipse. Right-click \\
and select Copy Position from the context \\
menu. imellipse copies a four-element \\
position vector [xmin ymin width height] \\
to the clipboard.
\end{tabular} \\
\hline \begin{tabular}{l} 
Preserving the \\
current aspect ratio \\
of the ellipse during \\
resizing.
\end{tabular} & \begin{tabular}{l} 
Move the pointer inside the ellipse. Right-click \\
and select Fix Aspect Ratio from the context \\
menu.
\end{tabular} \\
\hline
\end{tabular}

\section*{Methods}

Each imellipse object supports a number of methods. Type methods imellipse to see a complete list.

\section*{addNewPositionCallback - Add new-position callback to ROI object}

See imroi for information.

\section*{createMask - Create mask within image}

See imroi for information.

\section*{delete - Delete ROI object}

See imroi for information.

\section*{getColor - Get color used to draw ROI object}

See imroi for information.

\section*{getPosition - Return current position of ellipse}

See imrect for information.

\section*{getPositionConstraintFcn - Return function handle to current position constraint function}

See imroi for information.

\section*{getVertices - Return vertices on perimeter of ellipse}
vert \(=\) getVertices ( h ) returns a set of vertices which lie along the perimeter of the ellipse \(h\). vert is a N-by- 2 array.
removeNewPositionCallback - Remove new-position callback from ROI object.
See imroi for information.

\section*{resume - Resume execution of MATLAB command line}

See imroi for information.

\section*{setColor - Set color used to draw ROI object}

See imroi for information.

\section*{setConstrainedPosition - Set ROI object to new position}

See imroi for information.

\section*{setFixedAspectRatioMode - Control whether aspect ratio preserved during resize}

See imrect for information.

\section*{setPosition - Set ellipse to new position}

See imrect for information.

\section*{setPositionConstraintFcn - Set position constraint function of ROI object.}

See imroi for information.

\section*{setResizable - Set resize behavior of ellipse}

See imrect for information.
wait - Block MATLAB command line until ROI creation is finished
vert \(=\) wait ( h ) blocks execution of the MATLAB command line until you finish positioning the ROI object h . You indicate completion by double-clicking on the ROI object. The returned vertices, vert, is of the form returned by the getVertices method.

Tips
If you use imellipse with an axes that contains an image object, and do not specify a position constraint function, users can drag the ellipse outside the extent of the image and lose the ellipse. When used with an axes created by the plot function, the axes limits automatically expand to accommodate the movement of the ellipse.

\section*{imellipse}

\section*{Examples Example 1}

Create an ellipse, using callbacks to display the updated position in the title of the figure. The example illustrates using the makeConstrainToRectFen to keep the ellipse inside the original xlim and ylim ranges.
```

figure, imshow('cameraman.tif');
h = imellipse(gca, [10 10 100 100]);
addNewPositionCallback(h,@(p) title(mat2str(p,3)));
fcn = makeConstrainToRectFcn('imellipse',get(gca,'XLim'),get(gca,'YLim'));
setPositionConstraintFcn(h,fcn);

```

\section*{Example 2}

Interactively place an ellipse by clicking and dragging. Use wait to block the MATLAB command line. Double-click on the ellipse to resume execution of the MATLAB command line.
```

figure, imshow('pout.tif');
h = imellipse;
position = wait(h);

```

See Also imfreehand | imline | impoint | impoly | imrect | imroi | iptgetapi | makeConstrainToRectFen

\section*{Purpose \\ Syntax \\ Description}

Erode image

IM2 = imerode(IM, SE)
IM2 = imerode(IM,NHOOD)
IM2 = imerode(...,PACKOPT,M)
IM2 = imerode(...,SHAPE)

IM2 = imerode(IM, SE) erodes the grayscale, binary, or packed binary image IM, returning the eroded image IM2. The argument SE is a structuring element object or array of structuring element objects returned by the strel function.

If IM is logical and the structuring element is flat, imerode performs binary erosion; otherwise it performs grayscale erosion. If SE is an array of structuring element objects, imerode performs multiple erosions of the input image, using each structuring element in SE in succession.

IM2 = imerode(IM,NHOOD) erodes the image IM, where NHOOD is an array of 0's and 1's that specifies the structuring element neighborhood. This is equivalent to the syntax imerode(IM, strel(NHOOD)). The imerode function determines the center element of the neighborhood by floor((size(NHOOD)+1)/2).

IM2 = imerode(...,PACKOPT,M) specifies whether IM is a packed binary image and, if it is, provides the row dimension \(M\) of the original unpacked image. PACKOPT can have either of the following values. Default value is enclosed in braces ( \(\}\) ).
\begin{tabular}{l|l}
\hline Value & Description \\
\hline 'ispacked' & \begin{tabular}{l} 
IM is treated as a packed binary image as \\
produced by bwpack. IM must be a 2-D uint32 \\
array and SE must be a flat 2-D structuring \\
element.
\end{tabular} \\
\hline \{'notpacked' \(\}\) & IM is treated as a normal array. \\
\hline
\end{tabular}

If PACKOPT is 'ispacked', you must specify a value for M.

\section*{imerode}

IM2 \(=\) imerode(...,SHAPE) specifies the size of the output image. SHAPE can have either of the following values. Default value is enclosed in braces (\{\}).
\begin{tabular}{ll}
\hline Value & Description \\
\{'same' \} & \begin{tabular}{l} 
Make the output image the same size as the input \\
image. If the value of PACKOPT is 'ispacked ',
\end{tabular} \\
'full' & \begin{tabular}{l} 
SHAPE must be 'same'
\end{tabular} \\
\hline
\end{tabular}

\section*{Definitions}

The binary erosion of \(A\) by \(B\), denoted \(A \ominus B\), is defined as the set operation \(A \ominus B=\left\{z \mid\left(B_{z} \subseteq A\right\}\right.\). In other words, it is the set of pixel locations \(z\), where the structuring element translated to location \(z\) overlaps only with foreground pixels in \(A\).

In the general form of gray-scale erosion, the structuring element has a height. The gray-scale erosion of \(A(x, y)\) by \(B(x, y)\) is defined as:
\[
(A \ominus B)(x, y)=\min \left\{A\left(x+x^{\prime}, y+y^{\prime}\right)-B\left(x^{\prime}, y^{\prime}\right) \mid\left(x^{\prime}, y^{\prime}\right) \in D_{B}\right\}
\]
where \(D_{B}\) is the domain of the structuring element \(B\) and \(A(x, y)\) is assumed to be \(+\infty\) outside the domain of the image. To create a structuring element with nonzero height values, use the syntax strel(nhood, height), where height gives the height values and nhood corresponds to the structuring element domain, \(D_{B}\).

Most commonly, gray-scale erosion is performed with a flat structuring element \((B(x, y)=0)\). Gray-scale erosion using such a structuring element is equivalent to a local-minimum operator:
\[
(A \ominus B)(x, y)=\min \left\{A\left(x+x^{\prime}, y+y^{\prime}\right) \mid\left(x^{\prime}, y^{\prime}\right) \in D_{B}\right\}
\]

All of the strel syntaxes except for strel(nhood, height), strel('arbitrary', nhood, height), and strel('ball', ...) produce flat structuring elements.

For more information on binary erosion, see [1].

Class
Support

Examples

IM can be numeric or logical and it can be of any dimension. If IM is logical and the structuring element is flat, the output image is logical; otherwise the output image has the same class as the input. If the input is packed binary, then the output is also packed binary.

Erode a binary image with a disk structuring element.
```

originalBW = imread('circles.png');
se = strel('disk',11);
erodedBW = imerode(originalBW,se);
imshow(originalBW), figure, imshow(erodedBW)

```


Erode a grayscale image with a rolling ball.
```

I = imread('cameraman.tif');
se = strel('ball',5,5);
I2 = imerode(I,se);
imshow(I), title('Original')
figure, imshow(I2), title('Eroded')

```


\section*{Algorithms}

References
imerode automatically takes advantage of the decomposition of a structuring element object (if a decomposition exists). Also, when performing binary dilation with a structuring element object that has a decomposition, imerode automatically uses binary image packing to speed up the dilation.

Erosion using bit packing is described in [3].
[1] Gonzalez, R. C., R. E. Woods, and S. L. Eddins, Digital Image Processing Using MATLAB, Gatesmark Publishing, 2009.
[2] Haralick, Robert M., and Linda G. Shapiro, Computer and Robot Vision, Vol. I, Addison-Wesley, 1992, pp. 158-205.
[3] van den Boomgard, R, and R. van Balen, "Methods for Fast Morphological Image Transforms Using Bitmapped Images," Computer Vision, Graphics, and Image Processing: Graphical Models and Image Processing, Vol. 54, Number 3, pp. 254-258, May 1992.

See Also bwpack | bwunpack | conv2 | filter2 | imclose | imdilate | imopen | strel

Purpose
Syntax

Description

Extended-maxima transform

BW = imextendedmax(I, H)
BW = imextendedmax(I,H,conn)
\(B W=\) imextendedmax \((I, H)\) computes the extended-maxima transform, which is the regional maxima of the H-maxima transform. H is a nonnegative scalar.

Regional maxima are connected components of pixels with a constant intensity value, and whose external boundary pixels all have a lower value.

By default, imextendedmax uses 8-connected neighborhoods for 2-D images and 26 -connected neighborhoods for 3-D images. For higher dimensions, imextendedmax uses conndef(ndims(I), 'maximal').

BW = imextendedmax (I, H, conn) computes the extended-maxima transform, where conn specifies the connectivity. conn can have any of the following scalar values.
\begin{tabular}{l|l}
\hline Value & Meaning \\
\hline Two-dimensional connectivities \\
\hline 4 & 4-connected neighborhood \\
\hline 8 & 8 -connected neighborhood \\
\hline Three-dimensional connectivities \\
\hline 6 & 6 -connected neighborhood \\
\hline 18 & 18 -connected neighborhood \\
\hline 26 & 26 -connected neighborhood \\
\hline
\end{tabular}

Connectivity can be defined in a more general way for any dimension by using for conn a 3 -by- 3 -by- ...-by-3 matrix of 0's and 1's. The 1 -valued elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

Class
Support
Examples

I can be of any nonsparse numeric class and any dimension. BW has the same size as I and is always logical.
```

I = imread('glass.png');
BW = imextendedmax(I,80);
imshow(I), figure, imshow(BW)

```


Original Image


Extended Maximu Image

References

See Also
[1] Soille, P., Morphological Image Analysis: Principles and Applications, Springer-Verlag, 1999, pp. 170-171.
conndef | imextendedmin | imhmax | imreconstruct | imregionalmax

\section*{Purpose \\ Syntax \\ Description}

Extended-minima transform
\(B W=\) imextendedmin( \(I, h\) )
\(B W=\) imextendedmin(I, h, conn)
\(B W=\) imextendedmin( \(I, h\) ) computes the extended-minima transform, which is the regional minima of the H-minima transform. \(h\) is a nonnegative scalar.
Regional minima are connected components of pixels with a constant intensity value, and whose external boundary pixels all have a higher value.

By default, imextendedmin uses 8-connected neighborhoods for 2-D images, and 26-connected neighborhoods for 3-D images. For higher dimensions, imextendedmin uses conndef(ndims(I), 'maximal').
BW = imextendedmin(I, h, conn) computes the extended-minima transform, where conn specifies the connectivity. conn can have any of the following scalar values.
\begin{tabular}{l|l}
\hline Value & Meaning \\
\hline Two-dimensional connectivities \\
\hline 4 & 4 -connected neighborhood \\
\hline 8 & 8 -connected neighborhood \\
\hline \multicolumn{1}{l}{ Three-dimensional connectivities } \\
\hline 6 & 6 -connected neighborhood \\
\hline 18 & 18 -connected neighborhood \\
\hline 26 & 26 -connected neighborhood \\
\hline
\end{tabular}

Connectivity can be defined in a more general way for any dimension by using for conn a 3 -by-3-by-...-by-3 matrix of 0's and 1's. The 1 -valued elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

\section*{imextendedmin}

Class
Support
Examples

References

See Also

I can be of any nonsparse numeric class and any dimension. BW has the same size as I and is always logical.

I = imread('glass.png');
BW = imextendedmin(I,50); imshow(I), figure, imshow(BW)


Original Image


Extended Minima Image
[1] Soille, P., Morphological Image Analysis: Principles and Applications, Springer-Verlag, 1999, pp. 170-171.
conndef | imextendedmax | imhmin | imreconstruct | imregionalmin
Purpose Fill image regions and holes
Syntax

BW2 = imfill(BW)
[BW2,locations] = imfill(BW)
BW2 = imfill(BW,locations)
BW2 = imfill(BW,'holes')
I2 = imfill(I)
BW2 = imfill(BW, locations,conn)

\section*{Description}
BW2 = imfill(BW) displays the binary image BW on the screen and lets you define the region to fill by selecting points interactively by using the mouse. To use this interactive syntax, BW must be a 2 -D image. Press Backspace or Delete to remove the previously selected point. A shift-click, right-click, or double-click selects a final point and starts the fill operation. Pressing Return finishes the selection without adding a point.
[BW2,locations] = imfill(BW) returns the locations of points selected interactively in locations. locations is a vector of linear indices into the input image. To use this interactive syntax, BW must be a 2-D image.
BW2 = imfill(BW, locations) performs a flood-fill operation on background pixels of the binary image BW, starting from the points specified in locations. If locations is a P-by-1 vector, it contains the linear indices of the starting locations. If locations is a P-by-ndims (BW) matrix, each row contains the array indices of one of the starting locations.
BW2 = imfill(BW,'holes') fills holes in the binary image BW. A hole is a set of background pixels that cannot be reached by filling in the background from the edge of the image.
I2 = imfill(I) fills holes in the grayscale image I. In this syntax, a hole is defined as an area of dark pixels surrounded by lighter pixels.
BW2 = imfill(BW, locations, conn) fills the area defined by locations, where conn specifies the connectivity. conn can have any of the following scalar values.
\begin{tabular}{l|l}
\hline Value & Meaning \\
\hline Two-dimensional connectivities \\
\hline 4 & 4-connected neighborhood \\
\hline 8 & 8 -connected neighborhood \\
\hline Three-dimensional connectivities \\
\hline 6 & 6 -connected neighborhood \\
\hline 18 & 18 -connected neighborhood \\
\hline 26 & 26 -connected neighborhood \\
\hline
\end{tabular}

Connectivity can be defined in a more general way for any dimension by using for conn a 3 -by- 3 -by- ... -by- 3 matrix of 0 's and 1's. The 1 -valued elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

\section*{Specifying Connectivity}

By default, imfill uses 4-connected background neighbors for 2-D inputs and 6 -connected background neighbors for 3-D inputs. For higher dimensions the default background connectivity is determined by using conndef (NUM_DIMS, 'minimal'). You can override the default connectivity with these syntaxes:
```

BW2 = imfill(BW,locations,conn)
BW2 = imfill(BW,conn,'holes')
I2 = imfill(I,conn)

```

To override the default connectivity and interactively specify the starting locations, use this syntax:

BW2 = imfill(BW,0,conn)

The input image can be numeric or logical, and it must be real and nonsparse. It can have any dimension. The output image has the same class as the input image.

Examples

Fill in the background of a binary image from a specified starting location.
```

BW1 = logical([[1 0 0 0 0 0 0 0
1}1101141101000
10}000001001
1 0}0000111110

```

```

    1}000011%1001
    10}000001001
    1 0 0 0 1 1 1 0]);
    ```
BW2 \(=\) imfill(BW1,[3 3], 8)

Fill in the holes of a binary image.
```

BW4 = im2bw(imread('coins.png'));
BW5 = imfill(BW4,'holes');
imshow(BW4), figure, imshow(BW5)

```


Original Image


Filled Image

Fill in the holes of a grayscale image.
```

I = imread('tire.tif');
I2 = imfill(I,'holes');
figure, imshow(I), figure, imshow(I2)

```


Original Image


Filled Image

Algorithms

\section*{References}

See Also
imfill uses an algorithm based on morphological reconstruction [1].
[1] Soille, P., Morphological Image Analysis: Principles and Applications, Springer-Verlag, 1999, pp. 173-174.
bwselect | imreconstruct | roifill

\section*{Purpose}
\(\mathrm{N}-\mathrm{D}\) filtering of multidimensional images
Syntax
\(B=\) imfilter (A, H)
\(B\) = imfilter (A, H, option1, option2,...)
\(B=\operatorname{imfilter}(A, H)\) filters the multidimensional array \(A\) with the multidimensional filter \(H\). The array A can be logical or a nonsparse numeric array of any class and dimension. The result B has the same size and class as A.

Each element of the output B is computed using double-precision floating point. If \(A\) is an integer or logical array, then output elements that exceed the range of the integer type are truncated, and fractional values are rounded.
\(B=\) imfilter (A, H, option1, option2,...) performs multidimensional filtering according to the specified options. Option arguments can have the following values.

\section*{Boundary Options}
\begin{tabular}{l|l}
\hline Option & Description \\
\hline X & \begin{tabular}{l} 
Input array values outside the bounds of the array \\
are implicitly assumed to have the value X . When no \\
boundary option is specified, imfilter uses \(\mathrm{X}=0\).
\end{tabular} \\
\hline 'symmetric' & \begin{tabular}{l} 
Input array values outside the bounds of the array are \\
computed by mirror-reflecting the array across the \\
array border.
\end{tabular} \\
\hline 'replicate' & \begin{tabular}{l} 
Input array values outside the bounds of the array are \\
assumed to equal the nearest array border value.
\end{tabular} \\
\hline 'circular' & \begin{tabular}{l} 
Input array values outside the bounds of the array \\
are computed by implicitly assuming the input array \\
is periodic.
\end{tabular} \\
\hline
\end{tabular}

\section*{imfilter}

\section*{Output Size Options}
\begin{tabular}{l|l}
\hline Option & Description \\
\hline 'same' & \begin{tabular}{l} 
The output array is the same size as the input array. \\
This is the default behavior when no output size \\
options are specified.
\end{tabular} \\
\hline 'full' & \begin{tabular}{l} 
The output array is the full filtered result, and so is \\
larger than the input array.
\end{tabular} \\
\hline
\end{tabular}

\section*{Correlation and Convolution Options}
\begin{tabular}{l|l}
\hline Option & Description \\
\hline 'corr' & \begin{tabular}{l} 
imfilter performs multidimensional filtering using \\
correlation, which is the same way that filter2 \\
performs filtering. When no correlation or convolution \\
option is specified, imfilter uses correlation.
\end{tabular} \\
\hline 'conv' & \begin{tabular}{l} 
imfilter performs multidimensional filtering using \\
convolution.
\end{tabular} \\
\hline
\end{tabular}
\(\mathrm{N}-\mathrm{D}\) convolution is related to N - D correlation by a reflection of the filter matrix.

On Intel architecture processors, imfilter can take advantage of the Intel Integrated Performance Primitives (Intel IPP) library, thus accelerating its execution time. The Intel IPP library is activated only if \(A\) and \(H\) are both two-dimensional and \(A\) is of class uint8, uint16, int16, single, or double.

When the Intel IPP library is used, imfilter has different rounding behavior on some processors. Normally, when A is an integer class, filter outputs such as \(1.5,4.5\), etc are rounded away from zero. However, when the Intel IPP library is used, these values are rounded toward zero.

Also, a special case exists if A is of class single or double, your input image contains NaN values, and your filtering kernel contains zero values. In this situation, you will receive different results if the Intel IPP library is enabled versus if it is not enabled. If you write code that depends on output values in the same neighborhood as NaN values in an input image, be aware that your code may behave differently on different machines, depending on the availability of the Intel IPP library.

To disable the Intel IPP library, use this command:
```

iptsetpref('UseIPPL', false)

```

\section*{Example}

This example shows the different results obtained with the Intel IPP library enabled versus not enabled in the special case when you are filtering an array containing NaN elements with a filter containing zero values.

First, consider the case in which the Intel IPP library is enabled (the default case).
```

A = [2 2 2 2; 2 NaN 2 2; 2 2 2 2; 2 2 2 2];
h = [1 0; 0 1];
imfilter(A, h)
ans =

| NaN | NaN | 4 | 2 |
| ---: | ---: | ---: | ---: |
| NaN | NaN | 4 | 2 |
| 4 | 4 | 4 | 2 |
| 2 | 2 | 2 | 2 |

```

Now, compare this result to that obtained when you disable the Intel IPP library.
```

iptsetpref('UseIPPL', false);
imfilter(A, h)

```
ans =
\begin{tabular}{rrrr}
NaN & 4 & 4 & 2 \\
4 & NaN & 4 & 2 \\
4 & 4 & 4 & 2 \\
2 & 2 & 2 & 2
\end{tabular}

As you can see, your output is not the same.
Examples Read a color image into the workspace and view it.
originalRGB = imread('peppers.png');
imshow(originalRGB)


\section*{Original Image}

Create a filter, h , that can be used to approximate linear camera motion.
h = fspecial('motion', 50, 45);
Apply the filter, using imfilter, to the image originalRGB to create a new image, filteredRGB.
filteredRGB = imfilter(originalRGB, h);
```

figure, imshow(filteredRGB)

```


\section*{Filtered Image}

Note that imfilter is more memory efficient than some other filtering operations in that it outputs an array of the same data type as the input image array. In this example, the output is an array of uint8.
\begin{tabular}{llrl} 
whos & & \\
Name & Size & Bytes & Class \\
& & \\
filteredRGB & \(384 \times 512 \times 3\) & 589824 & uint8 \\
h & \(37 \times 37\) & 10952 & double \\
originalRGB & \(384 \times 512 \times 3\) & 589824 & uint8
\end{tabular}

Specify the replicate boundary option.
```

boundaryReplicateRGB = imfilter(originalRGB, h, 'replicate');

```
figure, imshow(boundaryReplicateRGB)

\section*{imfilter}


\section*{Image with Replicate Boundary}

See Also

\author{
conv2 | convn | filter2 | fspecial | ippl
}

\section*{Purpose Find circles using circular Hough transform}

\author{
Syntax \\ Description
}

\section*{Input Arguments}
```

centers = imfindcircles(A,radius)
[centers,radii] = imfindcircles(A,radiusRange)
[centers,radii,metric] = imfindcircles(A,radiusRange)
[centers,radii,metric] = imfindcircles(___,Name,Value)

```
centers = imfindcircles(A, radius) finds the circles in image \(A\) whose radii are approximately equal to radius. The output, centers, is a two-column matrix containing the \(x, y\) coordinates of the circles centers in the image.
[centers, radii] = imfindcircles(A,radiusRange) finds circles with radii in the range specified by radiusRange. The additional output argument, radii, contains the estimated radii corresponding to each circle center in centers.
[centers,radii,metric] = imfindcircles(A,radiusRange) also returns a column vector, metric, containing the magnitudes of the accumulator array peaks for each circle (in descending order). The rows of centers and radii correspond to the rows of metric.
[centers,radii,metric] = imfindcircles( , Name, Value) specifies additional options with one or more Name, Value pair arguments, using any of the previous syntaxes.

\section*{A - Input image}
grayscale image | truecolor image | binary image
Input image is the image in which to detect circular objects, specified as a grayscale, truecolor, or binary image.

\author{
Data Types \\ single | double | int16 | uint8 | uint16 | logical \\ radius - Circle radius
}

\section*{imfindcircles}

\section*{scalar integer}

Circle radius is the approximate radius of the circular objects you want to detect, specified as a scalar integer of any numeric type.

\section*{Data Types}
single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32 | uint64

\section*{radiusRange - Range of radii}
two-element vector of integers
Range of radii for the circular objects you want to detect, specified as a two-element vector, [rmin rmax], of integers of any numeric type.

\section*{Data Types}
single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32 | uint64

\section*{Name-Value Pair Arguments}

Specify 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 and value pair arguments in any order as Name1, Value1, . . . , NameN, ValueN.

Example: 'ObjectPolarity','bright' specifies bright circular objects on a dark background.

\section*{ObjectPolarity - Object polarity}
'bright' (default) | 'dark'
Object polarity indicates whether the circular objects are brighter or darker than the background, specified as the comma-separated pair consisting of 'ObjectPolarity' and either of the text strings in the following table.
\begin{tabular}{ll} 
'bright' & \begin{tabular}{l} 
The circular objects are brighter than the \\
background.
\end{tabular} \\
'dark' & The circular objects are darker than the background.
\end{tabular}

Example: 'ObjectPolarity','bright' specifies bright circular objects on a dark background.

\section*{Method - Computation method}
'PhaseCode' (default) | 'TwoStage'
Computation method is the technique used to compute the accumulator array, specified as the comma-separated pair consisting of 'Method' and either of the text strings in the following table.
\begin{tabular}{ll} 
'PhaseCode ' & \begin{tabular}{l} 
Atherton and Kerbyson's [1] phase coding method . \\
This is the default.
\end{tabular} \\
'TwoStage ' & \begin{tabular}{l} 
The method used in two-stage circular Hough \\
transform [2], [3].
\end{tabular}
\end{tabular}

Example: 'Method', 'PhaseCode' specifies the Atherton and Kerbyson's phase coding method.

\section*{Sensitivity - Sensitivity factor \\ nonnegative scalar between 0 and 1 | 0.85 (default)}

Sensitivity factor is the sensitivity for the circular Hough transform accumulator array, specified as the comma-separated pair consisting of 'Sensitivity' and a nonnegative scalar value in the range \([0,1]\). As you increase the sensitivity factor, imfindcircles detects more circular objects, including weak and partially obscured circles. Higher sensitivity values also increase the risk of false detection.
Example: 'Sensitivity', 0.3 sets the sensitivity factor to 0.3 .

\section*{EdgeThreshold - Edge gradient threshold}
nonnegative scalar between 0 and 1

\section*{imfindcircles}

Edge gradient threshold sets the gradient threshold for determining edge pixels in the image, specified as the comma-separated pair consisting of 'EdgeThreshold' and a nonnegative scalar value in the range \([0,1]\). Specify 0 to set the threshold to zero-gradient magnitude. Specify 1 to set the threshold to the maximum gradient magnitude. imfindcircles detects more circular objects (with both weak and strong edges) when you set the threshold to a lower value. It detects fewer circles with weak edges as you increase the value of the threshold. By default, imfindcircles chooses the edge gradient threshold automatically using the function graythresh.

\section*{Example: 'EdgeThreshold', 0.5 sets the edge gradient threshold to 0.5 .}

\section*{Output \\ Arguments}

\section*{centers - Coordinates of circle centers}
two-column matrix
Coordinates of the circle centers, returned as a P-by-2 matrix containing the \(x\)-coordinates of the circle centers in the first column and the \(y\)-coordinates in the second column. The number of rows, P , is the number of circles detected. centers is sorted based on the strength of the circles.

\section*{radii - Estimated radii}
column vector
The estimated radii for the circle centers, returned as a column vector. The radius value at radii(j) corresponds to the circle centered at centers(j,:).

\section*{metric - Circle strengths}
column vector
Circle strengths is the relative strengths for the circle centers, returned as a vector. The value at metric(j) corresponds to the circle with radius radii(j) centered at centers(j,:).

\section*{Tips}

\section*{Examples}
- Specify a relatively small radiusRange for better accuracy. A good rule of thumb is to choose radiusRange such that rmax < \(3^{*} \mathrm{rmin}\) and (rmax-rmin) < 100.
- The accuracy of imfindcircles is limited when the value of radius (or rmin) is less than 10 .
- The radius estimation step is typically faster if you use the (default) 'PhaseCode' method instead of 'TwoStage'.
- Both computation methods, 'PhaseCode' and 'TwoStage' are limited in their ability to detect concentric circles. The results for concentric circles can vary depending on the input image.
- imfindcircles does not find circles with centers outside the domain of the image.
- imfindcircles preprocesses binary (logical) images to improve the accuracy of the result. It converts truecolor images to grayscale using the function rgb2gray before processing them.

\section*{Detection of Five Strongest Circles in an Image}

Read the image into the workspace and display it.
```

A = imread('coins.png');
imshow(A)

```


Find all the circles with radius \(r\) such that \(15 \leq r \leq 30\).
```

[centers, radii, metric] = imfindcircles(A,[15 30]);

```

Retain the five strongest circles according to the metric values.
```

centersStrong5 = centers(1:5,:);
radiiStrong5 = radii(1:5);
metricStrong5 = metric(1:5);

```

Draw the five strongest circle perimeters.
viscircles(centersStrong5, radiiStrong5,'EdgeColor','b');


\section*{Detection of Bright and Dark Circles in an Image}

Read the image into the workspace and display it.
A = imread('circlesBrightDark.png');
imshow(A)

\section*{imfindcircles}


Define the radius range.
Rmin = 30;
Rmax \(=65\);
Find all the bright circles in the image within the radius range.
[centersBright, radiiBright] = imfindcircles(A,[Rmin Rmax],'ObjectPolarit
Find all the dark circles in the image within the radius range.
[centersDark, radiiDark] = imfindcircles(A,[Rmin Rmax],'ObjectPolarity','
Plot bright circles in blue.

\section*{imfindcircles}
viscircles(centersBright, radiiBright,'EdgeColor','b');


Plot dark circles in dashed red boundaries.
```

viscircles(centersDark, radiiDark,'LineStyle','--');

```

\section*{imfindcircles}


\section*{Algorithm}

Function imfindcircles uses a Circular Hough Transform (CHT) based algorithm for finding circles in images. This approach is used because of its robustness in the presence of noise, occlusion and varying illumination.

The CHT is not a rigorously specified algorithm, rather there are a number of different approaches that can be taken in its implementation. However, by and large, there are three essential steps which are common to all.

1 Accumulator Array Computation.

Foreground pixels of high gradient are designated as being candidate pixels and are allowed to cast 'votes' in the accumulator array. In a classical CHT implementation, the candidate pixels vote in pattern around them that forms a full circle of a fixed radius. Figure 1a shows an example of a candidate pixel lying on an actual circle (solid circle) and the classical CHT voting pattern (dashed circles) for the candidate pixel.

\section*{imfindcircles}

(a)

Figure 1: classical CHT voting pattern

\section*{2 Center Estimation}

The votes of candidate pixels belonging to an image circle tend to accumulate at the accumulator array bin corresponding to the circle's center. Therefore, the circle centers are estimated by detecting the peaks in the accumulator array. Figure 1b shows an example of the candidate pixels (solid dots) lying on an actual circle (solid circle), and their voting patterns (dashed circles) which coincide at the center of the actual circle.

\section*{3 Radius Estimation}

If the same accumulator array is used for more than one radius value, as is commonly done in CHT algorithms, radii of the detected circles have to be estimated as a separate step.

Function imfindcircles provides two algorithms for finding circles in images: Phase-Coding (default) and Two-Stage. Both share some common computational steps, but each has its own unique aspects as well.

The common computational features shared by both algorithms are as follow:
- Use of 2-D Accumulator Array:

The classical Hough Transform requires a 3-D array for storing votes for multiple radii, which results in large storage requirements and long processing times. Both the Phase-Coding and Two-Stage methods solve this problem by using a single 2-D accumulator array for all the radii. Although this approach requires an additional step of radius estimation, the overall computational load is typically lower, especially when working over large radius range. This is a widely adopted practice in modern CHT implementations.
- Use of Edge Pixels

Overall memory requirements and speed is strongly governed by the number of candidate pixels. To limit their number, the gradient magnitude of the input image is threshold so that only pixels of high gradient are included in tallying votes.
- Use of Edge Orientation Information:

Another way to optimize performance is to restrict the number of bins available to candidate pixels. This is accomplished by utilizing locally available edge information to only permit voting in a limited interval along direction of the gradient (Figure 2).


Figure 2: Voting mode: multiple radii, along direction of the gradient
\begin{tabular}{c|l}
\hline \(\mathrm{r}_{\min }\) & Minimum search radius \\
\hline \(\mathrm{r}_{\max }\) & Maximum search radius \\
\hline \(\mathrm{r}_{\text {actual }}\) & \begin{tabular}{l} 
Radius of the circle that the candidate pixel \\
helongs to
\end{tabular} \\
\hline \(\mathrm{c}_{\min }\) & Center of the circle of radius \(\mathrm{r}_{\min }\) \\
\hline \(\mathrm{c}_{\ldots}\) & Center of the circle of radius r \\
\hline \(\mathrm{c}_{\text {actual }}\) & Center of the circle of radius \(\mathrm{r}_{\text {actual }}\) \\
\hline
\end{tabular}

The two CHT methods employed by function imfindcircles fundamentally differ in the manner by which the circle radii are computed.
- Two-Stage

Radii are explicitly estimated utilizing the estimated circle centers along with image information. The technique is based on computing radial histograms; see references \(1 \& 2\) for a detailed explanation.
- Phase-Coding

The key idea in Phase Coding is the use of complex values in the accumulator array with the radius information encoded in the phase of the array entries. The votes cast by the edge pixels contain information not only about the possible center locations but also about the radius of the circle associated with the center location. Unlike the Two-Stage method where radius has to be estimated explicitly using radial histograms, in Phase Coding the radius can be estimated by simply decoding the phase information from the estimated center location in the accumulator array. (see reference 3).

\section*{References}
[1] T.J Atherton, D.J. Kerbyson. "Size invariant circle detection." Image and Vision Computing. Volume 17, Number 11, 1999, pp. 795-803.
[2] H.K Yuen, .J. Princen, J. Illingworth, and J. Kittler. "Comparative study of Hough transform methods for circle finding." Image and Vision Computing. Volume 8, Number 1, 1990, pp. 71-77.

\section*{imfindcircles}
[3] E.R. Davies, Machine Vision: Theory, Algorithms, Practicalities. Chapter 10. 3rd Edition. Morgan Kauffman Publishers, 2005,

\section*{See Also \\ hough | houghpeaks | houghlines | viscircles}

\section*{Purpose}

Create draggable freehand region
Syntax
h = imfreehand
h = imfreehand(hparent)
h = imfreehand(..., param1, val1,...)

\section*{Description}
\(h=\) imfreehand begins interactive placement of a freehand region of interest on the current axes. The function returns \(h\), a handle to an imfreehand object. A freehand region of interest can be dragged interactively using the mouse and supports a context menu that controls aspects of its appearance and behavior. See "Interactive Behavior" on page 3-386.
\(\mathrm{h}=\) imfreehand(hparent) begins interactive placement of a freehand region of interest on the object specified by hparent. hparent specifies the HG parent of the freehand region graphics, which is typically an axes, but can also be any other object that can be the parent of an hggroup.
h = imfreehand(..., param1, val1,...) creates a freehand ROI, specifying parameters and corresponding values that control the behavior of the tool. The following table lists the parameters available. Parameter names can be abbreviated, and case does not matter.
\begin{tabular}{l|l}
\hline Parameter & Description \\
\hline 'Closed ' & \begin{tabular}{l} 
Scalar logical that controls whether the \\
freehand region is closed. When set to \\
true (the default), imfreehand draws a \\
straight line to connect the endpoints of the \\
freehand line to create a closed region. If \\
set to false, imfreehand leaves the region \\
open.
\end{tabular} \\
\hline 'PositionConstraintFc & \begin{tabular}{l} 
Function handle specifying the function \\
that is called whenever the freehand region \\
is dragged using the mouse. Use this \\
parameter to control where the freehand \\
region can be dragged. See the help for
\end{tabular} \\
\hline
\end{tabular}

\section*{imfreehand}
\begin{tabular}{l|l}
\hline Parameter & Description \\
\hline
\end{tabular}
the setPositionConstraintFcn method for information about valid function handles.

\section*{Interactive Behavior}

When you call imfreehand with an interactive syntax, the pointer changes to a cross hairs \(\mathcal{F}_{\text {when positioned over an image. Click and }}\) drag the mouse to draw the freehand region. By default, imfreehand draws a straight line connecting the last point you drew with the first point, but you can control this behavior using the 'Closed' parameter. The following figure illustrates a freehand region with its context menu.


The following table lists the interactive features supported by imfreehand.
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} & Description \\
\hline Moving the region. & \begin{tabular}{l} 
Move the pointer inside the freehand region. \\
The pointer changes to a fleur shape \\
Click and hold the left mouse button to move \\
the region.
\end{tabular} \\
\hline \begin{tabular}{l} 
Changing the color \\
used to draw the \\
region.
\end{tabular} & \begin{tabular}{l} 
Move the pointer inside the freehand region. \\
Right-click and select Set Color from the \\
context menu.
\end{tabular} \\
\hline \begin{tabular}{l} 
Retrieving the \\
current position of \\
the freehand region.
\end{tabular} & \begin{tabular}{l} 
Move the pointer inside the freehand region. \\
Right-click and select Copy Position from \\
the context menu. imfreehand copies an \\
\(n\)-by-2 array of coordinates on the boundary of \\
the ROI to the clipboard..
\end{tabular} \\
\hline
\end{tabular}

\section*{Methods}

The imfreehand object supports the following methods. Type methods imfreehand to see a complete list of all methods.
addNewPositionCallback - Add new-position callback to ROI object
See imroi for information.

\section*{createMask - Create mask within image}

See imroi for information.

\section*{delete - Delete ROI object}

See imroi for information.

\section*{getColor - Get color used to draw ROI object}

See imroi for information.

\section*{getPosition - Return current position of freehand region}
pos \(=\) getPosition(h) returns the current position of the freehand region \(h\). The returned position, pos, is an N -by- 2 array [ X 1 Y 1 ; ...; XN YN].

\section*{getPositionConstraintFen - Return function handle to current position constraint function}

See imroi for information.
removeNewPositionCallback - Remove new-position callback from ROI object.
See imroi for information.
resume - Resume execution of MATLAB command line
See imroi for information.
setClosed - Set geometry of freehand region
setClosed (h, TF) sets the geometry of the freehand region h. TF is a logical scalar. True means that the freehand region is closed. False means that the freehand region is open.
setColor - Set color used to draw ROI object
See imroi for information.
setConstrainedPosition - Set ROI object to new position
See imroi for information.
setPositionConstraintFen - Set position constraint function of ROI object.
See imroi for information.
wait - Block MATLAB command line until ROI creation is finished
See imroi for information.

Examples Interactively place a closed freehand region of interest by clicking and dragging over an image.
figure, imshow('pout.tif');
h = imfreehand(gca);
If you use imfreehand with an axes that contains an image object, and do not specify a position constraint function, users can drag the freehand region outside the extent of the image and lose the freehand region. When used with an axes created by the plot function, the axes limits automatically expand to accommodate the movement of the freehand region.

Interactively place a freehand region by clicking and dragging. Use the wait method to block the MATLAB command line. Double-click on the freehand region to resume execution of the MATLAB command line.
```

figure, imshow('pout.tif');
h = imfreehand;
position = wait(h);

```

See Also
imellipse | imline | impoint | impoly | imrect | iptgetapi | makeConstrainToRectFcn

\section*{Purpose Composite of two images}
```

Syntax $\quad C=\operatorname{imfuse}(A, B)$
$C=$ imfuse(A, B, method)
C = imfuse( __, Name, Value)

```

\section*{Description}

\section*{Input Arguments}
\(C=\) imfuse \((A, B)\) creates a composite image from two images, \(A\) and \(B\). If \(A\) and \(B\) are different sizes, the smaller dimensions are padded with zeros so that both images are the same size before creating the composite.
\(C=\) imfuse (A, B, method) uses the visualization method specified by method.

C = imfuse (__ , Name, Value) specifies additional options with one or more Name, Value pair arguments, using any of the previous syntaxes.

\section*{A,B - Input images}
grayscale images | truecolor images | binary images
Input images to be combined into a composite image, specified as any combination of grayscale, truecolor, or binary images.

\section*{Data Types}
single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32 | uint64 | logical

\section*{method - Visualization method}
'falsecolor' (default) | 'blend' | 'diff' | 'montage'
Visualization method for creating the composite image, specified as one of the text strings in the following table.
\begin{tabular}{l|l}
\hline Method & Description \\
\hline 'falsecolor' & \begin{tabular}{l} 
Creates a composite RGB image showing \\
A and B overlaid in different color bands. \\
Gray regions in the composite image show \\
where the two images have the same \\
intensities. Magenta and green regions \\
show where the intensities are different. \\
This is the default method.
\end{tabular} \\
\hline 'blend ' & Overlays A and B using alpha blending. \\
\hline 'diff' & Creates a difference image from A and B. \\
\hline 'montage' & \begin{tabular}{l} 
Places A and B next to each other in the \\
same image.
\end{tabular} \\
\hline
\end{tabular}

Example: C = imfuse(A, B,'montage') places A and B next to each other in the output image.

\section*{Name-Value Pair Arguments}

Specify 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 and value pair arguments in any order as Name1, Value1, . . . , NameN, ValueN.
Example: 'Scaling', 'joint' scales the intensity values of A and B together as a single data set.

\section*{Scaling - Image data scaling option}

\author{
'independent' (default) | 'joint' | 'none'
}

Image data scaling option that controls the intensity scaling of the pixels representing the input images in the output image, specified as a comma-separated pair consisting of 'Scaling' and 'independent', 'joint', or 'none'. These options are described in the table below.
\(\left.\begin{array}{ll}\text { 'independent' } & \begin{array}{l}\text { Scales the intensity values of A and B } \\ \text { independently when C is created. }\end{array} \\ \text { 'joint' } & \begin{array}{l}\text { Scales the intensity values in the images } \\ \text { jointly as if they were together in the }\end{array} \\ \text { same image. This option is useful when } \\ \text { you want to visualize registrations of } \\ \text { monomodal images, where one image } \\ \text { contains fill values that are outside the } \\ \text { dynamic range of the other image. }\end{array}\right\}\)

\section*{ColorChannels - Output color channel for each input image}
[R G B] | 'red-cyan' | 'green-magenta' (default)
Output color channel for each input image, specified as the comma-separated pair consisting of 'ColorChannels ' and one of the text strings in the following table. `ColorChannels' can only be used with the 'falsecolor' visualization method.
\begin{tabular}{|c|c|}
\hline [ R G B] & A three element vector that specifies which image to assign to the red, green, and blue channels. The R, G, and B values must be 1 (for the first input image), 2 (for the second input image), and 0 (for neither image). \\
\hline 'red-cyan' & A shortcut for the vector [ \(\left.\begin{array}{lll}1 & 2 & 2\end{array}\right]\), which is suitable for red/cyan stereo anaglyphs. \\
\hline 'green-magenta' & A shortcut for the vector [1 2 2 2], which is a high contrast option, ideal for people with many kinds of color blindness. \\
\hline
\end{tabular}

\section*{Output Arguments}

\section*{Tips}

\section*{Examples Create Overlay Image of Two Images}

Load an image into the workspace. Create a copy and apply a rotation and offset.

A = imread('cameraman.tif');
\(B=\) imrotate(A,5,'bicubic','crop');
Create blended overlay image, scaling the intensities of A and B jointly as a single data set.
```

C = imfuse(A,B,'blend','Scaling','joint');

```

Save the resulting image as a .png file.
imwrite(C,'my_blend_overlay.png');
See Also imregister | imshowpair | imtransform

Purpose Get handle to current axes containing image
Syntax
h = imgca
h = imgca(hfig)

Description

Note

\section*{Examples}
\(\mathrm{h}=\) imgca returns the handle of the current axes that contains an image. The current axes can be in a regular figure window or in an Image Tool window.

If no figure contains an axes that contains an image, imgca creates a new axes.
\(\mathrm{h}=\) imgca(hfig) returns the handle to the current axes that contains an image in the specified figure. (It need not be the current figure.)
imgca can be useful in returning the handle to the Image Tool axes. Because the Image Tool turns graphics object handle visibility off, you cannot retrieve a handle to the tool figure using gca.

Compute the centroid of each coin, and superimpose its location on the image. View the results using imtool and imgca:

I = imread('coins.png');
figure, imshow(I)


\section*{Original Image}
```

bw = im2bw(I, graythresh(getimage));

```
figure, imshow(bw)


Binary Image
```

bw2 = imfill(bw,'holes');
s = regionprops(bw2, 'centroid');
centroids = cat(1, s.Centroid);

```

Display original image I and superimpose centroids:
```

imtool(I)
hold(imgca,'on')
plot(imgca,centroids(:,1), centroids(:,2), 'r*')
hold(imgca,'off')

```


\section*{Centroids of Coins}

\section*{See also}
gca, gcf, imgcf, imhandles

Purpose Get handle to current figure containing image

\section*{Syntax \\ hfig = imgcf}

Description hfig = imgcf returns the handle of the current figure that contains an image. The figure may be a regular figure window that contains at least one image or an Image Tool window.

If none of the figures currently open contains an image, imgcf creates a new figure.

Note
imgcf can be useful in getting the handle to the Image Tool figure window. Because the Image Tool turns graphics object handle visibility off, you cannot retrieve a handle to the tool figure using gcf.
```

Examples imtool rice.png
cmap $=$ copper(256);
set(imgcf,'Colormap', cmap)

```

See also gca, gcf, imgca, imhandles

\section*{Purpose}

Open Image dialog box

\section*{Syntax}

Description
[filename, user_canceled] = imgetfile
[filename, user_canceled] = imgetfile displays the Open Image dialog box. You can use this dialog box in imaging applications to get the name of the image file a user wants to open. The Open Image dialog box includes only files using supported image file formats (listed in imformats) and DICOM files. When the user selects a file and clicks Open, imgetfile returns the full path of the file in the return value filename and sets the user_canceled return value to FALSE. If the user clicks Cancel, imgetfile returns an empty string in filename and sets the user_canceled return value to TRUE.

Note The Open Image dialog box is modal; it blocks the MATLAB command line until the user responds.

See Also
imformats | imtool | uigetfile

Purpose Gradient magnitude and direction of an image
```

Syntax [Gmag,Gdir] = imgradient(I)
[Gmag,Gdir] = imgradient(I,method)
[Gmag,Gdir] = imgradient(Gx,Gy)
[Gmag,Gdir] = imgradient(I)
[Gmag,Gdir] = imgradient(I,method)
[Gmag,Gdir] = imgradient(Gx,Gy)

```

\section*{Description}

\section*{Input Arguments}
[Gmag, Gdir] = imgradient(I) returns the gradient magnitude, Gmag, and the gradient direction, Gdir, for input image I.
- Gmag and Gdir are the same size as input image I
- Gdir contains angles in degrees within the range [-180 180]
[Gmag,Gdir] = imgradient(I,method) returns the gradient magnitude and direction using specified method.
[Gmag,Gdir] = imgradient(Gx,Gy) returns the gradient magnitude and direction using directional gradients.

\section*{I- Input image}
grayscale image | binary image

Input image, specified as a grayscale or binary image.

\section*{Data Types}
single | double | int8 | int32 | uint8 | uint16 | uint32 | logical

\section*{method - Gradient operator}
'Sobel' (default) | 'Prewitt' | 'CentralDifference' |
'IntermediateDifference' | `Roberts'
Gradient operator, specified as one of the text strings 'Sobel',
'Prewitt', 'CentralDifference', 'IntermediateDifference', or
'Roberts'.
- Central difference gradient \((\mathrm{dI} / \mathrm{dx}=(\mathrm{I}(\mathrm{x}+1)-\mathrm{I}(\mathrm{x}-1)) / 2)\)
- Intermediate difference gradient \((\mathrm{dI} / \mathrm{dx}=\mathrm{I}(\mathrm{x}+1)-\mathrm{I}(\mathrm{x}))\)

\section*{Data Types \\ char}

\section*{Gx, Gy - Directional gradients along \(\mathbf{x}\)-axis (horizontal) and \(y\)-axis (vertical)}
matrix
Directional gradients along \(x\)-axis (horizontal) and \(y\)-axis (vertical), specified as non-sparse matrices equal in size to image I. Typically they are obtained from function imgradientxy which returns them as output arguments.

\author{
Data Types \\ single | double | int8 | int32 | uint8 | uint16 | uint32
}

\section*{Output Arguments}

\section*{Gmag - Gradient magnitude}
matrix
Gradient magnitude, returned as a non-sparse matrix the same size as image I. Gmag is of class double, unless the input image I to function imgradientxy is of class single, in which case it is of class single.

Data Types
double | single

\section*{Gdir - Gradient direction}
matrix
Gradient direction, returned as a non-sparse matrix the same size as image I. Gdir contains angles in degrees within the range [-180 180] measured counterclockwise from the positive x -axis (horizontal). Gdir is of class double, unless the input image I to function gradientxy is of class single, in which case it is of class single.

\section*{Data Types \\ double | single}

\section*{imgradient}

\section*{Examples Display gradient magnitude and gradient direction}

Read image and compute gradient magnitude and gradient direction using Prewitt's gradient operator.

I = imread('coins.png');
[Gmag, Gdir] = imgradient(I,'prewitt');
figure
imshowpair(Gmag, Gdir, 'montage');
title('Gradient Magnitude, Gmag (left), and Gradient Direction, Gdir (rig axis off;

Gradient Magnitude, Gmag (left), and Gradient Direction, Gdir (right), usi


\section*{Display directional gradients in addition to gradient magnitude and direction}

Read in image and return directional gradients, Gx and Gx, as well as gradient magnitude and direction, Gmag and Gdir, utilizing default Sobel gradient operator.
```

I = imread('coins.png');
[Gx, Gy] = imgradientxy(I);
[Gmag, Gdir] = imgradient(Gx, Gy);
figure; imshowpair(Gmag, Gdir, 'montage'); axis off;
title('Gradient Magnitude (Gmag) and Gradient Direction (Gdir) using
figure; imshowpair(Gx, Gy, 'montage'); axis off;
title('Directional Gradients, Gx and Gy, using Sobel method')

```

Gradient Magnitude, Gmag (left), and Gradient Direction, Gdir (right.


\section*{imgradient}

Directional Gradients, Gx and Gy, using Sobel methoo


Tips

Algorithms

See Also
- When applying the gradient operator at the boundaries of the image, values outside the bounds of the image are assumed to equal the nearest image border value.

The algorithmic approach taken in imgradient for each of the listed gradient methods is to first compute directional gradients,Gx and Gy, with respect to the x -axis and y -axis. The x -axis is defined along the columns going right and the y -axis is defined along the rows going down. The gradient magnitude and direction are then computed from their orthogonal components Gx and Gy.
```

imgradientxy | edge | fspecial

```
Purpose Directional gradients of an image
Syntax [Gx,Gy] = imgradientxy(I)[Gx,Gy] = imgradientxy(I,method)
Description [Gx, Gy] = imgradientxy(I) returns the directional gradients, Gxand Gy.
- Gx and Gy. are the same size as input image I- When applying the gradient operator at the boundaries of the image,values outside the bounds of the image are assumed to equal thenearest image border value.
[Gx,Gy] = imgradientxy(I,method) returns the directional gradients using specified method

\section*{Input \\ Arguments}

\section*{I-Input image}
grayscale image | binary image
Input image, specified as a grayscale or binary image.

\section*{Data Types}
single | double | int8 | int32 | uint8 | uint16 | uint32 | logical

\section*{method - Gradient operator}
`Sobel' (default) | `Prewitt' | 'CentralDifference' |
'IntermediateDifference'
Gradient operator, specified as one of the text strings 'Sobel', 'Prewitt', 'CentralDifference', or 'IntermediateDifference'.
- Central difference gradient ( \(\mathrm{dI} / \mathrm{dx}=(\mathrm{I}(\mathrm{x}+1)-\mathrm{I}(\mathrm{x}-1)) / 2)\)
- Intermediate difference gradient \((\mathrm{dI} / \mathrm{dx}=\mathrm{I}(\mathrm{x}+1)-\mathrm{I}(\mathrm{x}))\)

\section*{Data Types}
char

\section*{imgradientxy}

\section*{Output Arguments}

\section*{Gx, Gy - Directional gradients along x-axis (horizontal) and \(y\)-axis (vertical) \\ matrix}

Directional gradients along \(x\)-axis (horizontal) and \(y\)-axis (vertical), returned as non-sparse matrices equal in size to image I. The output matrices are of class double, unless the input image is of class single, in which case they are of class single.
```

Data Types
single | double

```

\section*{Examples}

\section*{Display directional gradients}

Read image and compute gradient magnitude and gradient direction using Prewitt's gradient operator.
```

I = imread('coins.png');
[Gx, Gy] = imgradientxy(I,'prewitt');
figure
imshowpair(Gx, Gy, 'montage');
title('Directional Gradients: x-direction, Gx (left), y-direction, Gy
axis off;

```

Directional Gradients: x-direction, Gx (left), y-direction, Gy (right),


\section*{Display gradient magnitude and direction in addition to directional gradients}

Read in image and return directional gradients, Gx and Gx, as well as gradient magnitude and direction, Gmag and Gdir, utilizing default Sobel gradient operator.
```

I = imread('coins.png');
[Gx, Gy] = imgradientxy(I);
[Gmag, Gdir] = imgradient(Gx, Gy);
figure; imshowpair(Gmag, Gdir, 'montage'); axis off;
title('Gradient Magnitude, Gmag (left), and Gradient Direction, Gdir
figure; imshowpair(Gx, Gy, 'montage'); axis off;
title('Directional Gradients, Gx and Gy, using Sobel method')

```

\section*{imgradientxy}

Gradient Magnitude, Gmag (left), and Gradient Direction, Gdir (right), us


Directional Gradients, Gx and Gy, using Sobel me


Tips
- When applying the gradient operator at the boundaries of the image, values outside the bounds of the image are assumed to equal the nearest image border value.

\section*{Algorithms}

See Also
The algorithmic approach is to compute directional gradients, \(G x\) and Gy, with respect to the x -axis and y -axis. The x -axis is defined along the columns going right and the \(y\)-axis is defined along the rows going down.
```

edge | fspecial | imgradient

```

Purpose Get all image handles
Syntax himage \(=\) imhandles \((\mathrm{h})\)
Description

Note

Examples Return the handle to the image object in the current axes.
```

figure, imshow('moon.tif');
himage = imhandles(gca)

```

Display two images in a figure and uses imhandles to get handles to both of the image objects in the figure.
```

subplot(1,2,1), imshow('autumn.tif');
subplot(1,2,2), imshow('glass.png');
himages = imhandles(gcf)

```

\section*{See Also imgca | imgcf}

Purpose
Display histogram of image data
Syntax
imhist(I)
imhist(I, n\()\)
imhist(X, map)
[counts,x] = imhist(...)

\section*{Description}
imhist(I) displays a histogram for the image I above a grayscale colorbar. The number of bins in the histogram is specified by the image type. If I is a grayscale image, imhist uses a default value of 256 bins. If \(I\) is a binary image, imhist uses two bins.
imhist(I, n) displays a histogram where n specifies the number of bins used in the histogram. n also specifies the length of the colorbar. If \(I\) is a binary image, \(n\) can only have the value 2 .
imhist ( \(X\), map) displays a histogram for the indexed image \(X\). This histogram shows the distribution of pixel values above a colorbar of the colormap map. The colormap must be at least as long as the largest index in X . The histogram has one bin for each entry in the colormap.
[counts, \(x\) ] = imhist(...) returns the histogram counts in counts and the bin locations in \(x\) so that stem ( \(x\), counts) shows the histogram. For indexed images, imhist returns the histogram counts for each colormap entry; the length of counts is the same as the length of the colormap.

Note The maximum value on the \(y\)-axis may be automatically reduced, so outlier spikes do not dominate. To show the full range of \(y\)-axis values, call imhist with the following syntax:
```

[counts,x] = imhist(...)

```

Then call stem:
```

stem(x,counts)

```

Tips

\section*{Class Support}

\section*{Examples}

For intensity images, the n bins of the histogram are each half-open intervals of width \(A /(n-1)\). In particular, for intensity images that are not int16, the \(p\) th bin is the half-open interval
\[
\frac{A(p-1.5)}{(n-1)} \leq x<\frac{A(p-0.5)}{(n-1)}
\]
where \(x\) is the intensity value. For int16 intensity images, the \(p\) th bin is the half-open interval
\[
\frac{A(p-1.5)}{(n-1)}-32768 \leq x<\frac{A(p-0.5)}{(n-1)}-32768
\]
where \(x\) is the intensity value. The scale factor \(A\) depends on the image class. \(A\) is 1 if the intensity image is double or single, \(A\) is 255 if the intensity image is uint8, and \(A\) is 65535 if the intensity image is uint16 or int16.

An input intensity image can be of class uint8, int8, uint16, int16, uint32, int32, single, double, or logical. An input indexed image can be of class uint8, uint16, single, double, or logical.
```

I = imread('pout.tif');
imhist(I)

```


See Also histeq | hist

\section*{imhistmatch}

Purpose
Syntax
\(\mathrm{B}=\) imhistmatch(A, Ref)
\(B=\) imhistmatch(A,Ref,N)
[B,hgram] = imhistmatch( __ )

Adjust histogram of image to match N -bin histogram of reference image
Lo
\(B=\) imhistmatch (A, Ref) image \(A\) is transformed so that the histogram of the returned image \(B\) approximately matches the histogram of reference image Ref built with 64 (default value) equally spaced histogram bins. The returned image \(B\) will have no more than 64 discrete levels.
- Images A and Ref can be any of the permissible data types.
- If both A and Ref are truecolor RGB images, then each color channel of \(A\) is matched independently to the corresponding color channel of Ref.
- If \(A\) is a truecolor RGB image and Ref is a grayscale image, then each channel of \(A\) is matched against the single histogram derived from Ref.
- If A is a grayscale image, then Ref must also be a grayscale image.
- Images A and Ref need not be equal in size.
\(B=\) imhistmatch (A, Ref, \(N\) ) image \(A\) is transformed using a histogram derived from image Ref consisting of \(N\) equally spaced bins within the appropriate range for the given image data type. The returned image B will have no more than \(N\) discrete levels. The default value for \(N\) is 64.
- If the data type of the image is either single or double, then the histogram range is \([0,1]\).
- If the data type of the image is uint8, then the histogram range is [0, 255]
- If the data type of the image is uint16, then the histogram range is [0, 65535]
- If the data type of the image is int16, then the histogram range is \([-32768,32767]\)
[ \(B\), hgram] = imhistmatch (__ ) returns hgram, a vector of length \(N\), containing the histogram counts derived from reference image Ref, using either of the previous two syntaxes.

\section*{Input Arguments}

\section*{A - Input image}
truecolor image | grayscale image
Input image to be transformed, specified as a truecolor or grayscale image. The returned image will take the data type class of the input image.

Data Types
single | double | int16 | uint8 | uint16

\section*{Ref - Reference image whose histogram is the reference histogram}
truecolor image | grayscale image
Reference image whose histogram is the reference histogram, specified as truecolor or grayscale image. The reference image provides the equally spaced \(N\) bin reference histogram which output image \(B\) is trying to match.

\section*{Data Types}
single | double | int16 | uint8 | uint16

\section*{\(\mathbf{N}\) - Number of equally spaced bins in reference histogram}

64 (default) | scalar
Number of equally spaced bins in reference histogram, specified as a scalar value. In addition to specifying the number of equally spaced bins in the histogram for image Ref, \(N\) also represents the upper limit of the number of discrete data levels present in output image B.

\section*{Data Types \\ double}

\section*{imhistmatch}
Output B-Output imageArgumentstruecolor RGB image | grayscale image
Output image, returned as a truecolor or grayscale image. The output image is derived from image A whose histogram is an approximate match to the histogram of input image Ref built with \(N\) equally spaced bins. Image \(B\) is of the same size and data type as input image \(A\). Input argument \(N\) represents the upper limit of the number of discrete levels contained in image B.
```

Data Types
single | double | int16 | uint8 | uint16

```

\section*{hgram - Histogram counts derived from reference image Ref}
vector | matrix
Histogram counts derived from reference image Ref, specified as a vector or matrix. When Ref is a truecolor image, hgram is a \(3 \times N\) matrix. When Ref is a grayscale image, hgram is a 1 xN vector.

\section*{Data Types}
double

\section*{Examples \\ Examples Histogram matching of aerial images}
These aerial images, taken at different times, represent overlapping views of the same terrain in Concord, Massachusetts. This example demonstrates that input images A and Ref can be of different sizes and image types.
Load both images.
```

A = imread('concordaerial.png');
Ref = imread('concordorthophoto.png');

```
Querying for the size of the images reveals that both are different in size and type; image A is a truecolor RGB image, while image Ref is a grayscale image. Both images are of data type uint8.
size (A)

2036
size(Ref)
ans =

2215
2956

Generate the histogram matched output image; each channel of \(A\) is matched against the single histogram of Ref built with 64 (default value) equally spaced bins. Output image B takes on the characteristics of image \(A\); it is an RGB image whose size and data type is the same as image A. The number of distinct levels present in each RGB channel of image \(B\) is determined by the number of bins in the single aim histogram built from grayscale image Ref which in this case is 64 .
\(B=i m h i s t m a t c h(A, R e f) ;\)

RGB image with color cast


Reference grayscale image


\section*{imhistmatch}

\section*{Multiple N values applied to RGB Images}

In this example, you will see the effect on output image \(B\) of varying \(N\), the number of equally spaced bins in the aim histogram of image Ref, from its default value 64 to the maximum value of 256 for uint8 pixel data.

The following images were taken with a digital camera and represent two different exposures of the same scene.
```

A = imread('office_2.jpg'); % Dark Image
Ref = imread('office_4.jpg'); % Reference image

```

Image \(A\), being the darker image, has a preponderance of its pixels in the lower bins. The reference image, Ref, is a properly exposed image and fully populates all of the available bins values in all three RGB channels: as shown in the table below, all three channels have 256 unique levels for 8 -bit pixel values.


RGB Histograms: 256 bins


Ref: Reference Image


RGB Histograms: 256 bins


\section*{imhistmatch}

\section*{Unique 8-bit level values in each RGB Channel}
\begin{tabular}{l|c|c}
\hline & Image A & Image Ref \\
\hline Red Channel & 205 & 256 \\
\hline Green Channel & 193 & 256 \\
\hline Blue Channel & 224 & 256 \\
\hline
\end{tabular}

Output image B is generated using three different values of N : 64,128 and 256. The objective of function imhistmatch is to transform image \(A\) such that the histogram of output image \(B\) is a match to the histogram of Ref built with N equally spaced bins. As a result, N represents the upper limit of the number of discrete data levels present in image \(B\).
```

[B64, hgram] = imhistmatch(A, Ref, 64);
[B128, hgram] = imhistmatch(A, Ref, 128);
[B256, hgram] = imhistmatch(A, Ref, 256);

```

Output Image B64


RGB Histograms: 64 bins




Output Image B128


RGB Histograms: 128 bins




15000 10000 5000 0 15000 10000 5000 0 15000 10000 5000 0

\section*{imhistmatch}
\begin{tabular}{l|c|c|c}
\hline \multicolumn{4}{|c}{ Unique 8-bit level values in each RGB Channel } \\
for \(\mathbf{N}=\left[\begin{array}{cc}\mathbf{6 4} \mathbf{1 2 8} \mathbf{2 5 6}\end{array}\right.\) \\
\hline & \begin{tabular}{c} 
output Image \\
B64
\end{tabular} & \begin{tabular}{c} 
output image \\
B128
\end{tabular} & \begin{tabular}{c} 
output image \\
B256
\end{tabular} \\
\hline & 57 & 101 & 134 \\
\hline \begin{tabular}{l} 
Red Channel
\end{tabular} & 60 & 104 & 135 \\
\hline \begin{tabular}{l} 
Green \\
Channel
\end{tabular} & 58 & 104 & 136 \\
\hline \begin{tabular}{l} 
Blue \\
Channel
\end{tabular} & & & \\
\hline
\end{tabular}

Note that as \(N\) increases, the number of levels in each RGB channel of output image B also increases.

\section*{Histogram matching a 16-bit grayscale MRI image}

In this example, a 16 bit grayscale MRI image is loaded, darkened and histogram matched at two values of \(N\).

A 16-bit DICOM image of a knee imaged via MRI is loaded into the workspace.
```

K = dicomread('knee1.dcm'); % read in original image
K = dicomread('knee1.dcm'); % read in original 16-bit image
LevelsK = unique(K(:)); % determine number of unique code values
disp(['image K: \# levels: ' num2str(length(LevelsK))]);
disp(['max level = ' num2str( max(LevelsK) )]);
disp(['min level = ' num2str( min(LevelsK) )]);
image K: \# levels = 448
max level = 473
min level = 0

```

Since it appears that all 448 discrete values are at low code values (darker), the image data will be scaled to span the entire 16 -bit range of [0 65535]
```

% Scale it to full 16-bit range

```
```

Kdouble = double(K); % cast uint16 to double
kmult = 65535/(max(max(Kdouble(:)))); % full range multiplier
Ref = uint16(kmult*Kdouble); % full range 16-bit reference image

```

The reference image is darkened to yield the input A image argument to imhistmatch
\% build concave bow-shaped curve for darkening Reference image ramp = [0:65535]/65535;
ppconcave = spline([0 .1 . 50 . 72 . 87 1],[0 . 025 . 25 . 5 . 75 1]);
Ybuf = ppval( ppconcave, ramp);
Lut16bit = uint16( round ( 65535*Ybuf ) );
\% pass image Ref through LUT to darken image A = intlut(Ref,Lut16bit);

The two images contain the same number of discrete code values, but differ in overall brightness.


Ref: Reference Image


\section*{imhistmatch}

Next, the histogram matched output image, B, is generated at two values of \(N\). The first is the default value of 64 , the second is the number of values present in image \(A\) of 448.

B16bit64 \(=\) imhistmatch(A(:,:,1), Ref(:,:,1)); \% default \# bins: N = 64
\(N=\) length(LevelsA); \(\quad\) \% number of unique 16 -bit code values in image B16bitUniq = imhistmatch(A(:,:,1),Ref(:,:,1),N);


The following figure shows the 16 bit histograms of all four images; the y -axis scaling is the same for plots.


\section*{imhistmatch}
\begin{tabular}{l|c|c|}
\hline \multicolumn{2}{|c|}{ Unique 16-bit code values in output B Images } \\
\hline & Levels & N \\
\hline B16bit64 & 63 & 64 \\
\hline B16bitUniq & 222 & 448 \\
\hline
\end{tabular}

N also represents the upper limit of discrete levels in the output image which is shown above; the number of levels increases from 63 to 222 when the number of histogram bins increases from 64 to 448 . But note, in the above histogram plots, there are rapid fluctuations in adjacent histogram bins for the B image containing 222 levels, especially in the upper portion of the histogram range. By comparison, the 63 level B histogram has a relatively smooth and continuous progression of peaks in this region.

\section*{Algorithms}

The objective of imhistmatch is to transform image A such the the histogram of image \(B\) matches the histogram derived from image Ref. It consists of \(N\) equally spaced bins which span the full range of the image data type. A consequence of matching histograms in this way is that \(N\) also represents the upper limit of the number of discrete data levels present in image \(B\).

An important behavioral aspect of this algorithm to note is that as \(N\) increases in value, the degree of rapid fluctuations between adjacent populated peaks in the histogram of image \(B\) tends to increase. This can be seen in the following histogram plots taken from the 16 -bit grayscale MRI example.

Histogram of output image B16bit64: \(N=64\)


Histogram of output image B16bitUniq: \(N=448\)


An optimal value for N represents a trade-off between more output levels (larger values of N ) while minimizing peak fluctuations in the histogram (smaller values of N ).

See Also histeq | imadjust | imhist

\section*{imhmax}

\section*{Purpose H-maxima transform}

Syntax \(\quad I 2=\operatorname{imhmax}(I, h)\)
I2 \(=\) imhmax (I, h, conn \()\)

\section*{Description}

I2 \(=i m h m a x(I, h)\) suppresses all maxima in the intensity image \(I\) whose height is less than \(h\), where \(h\) is a scalar.
Regional maxima are connected components of pixels with a constant intensity value, and whose external boundary pixels all have a lower value.

By default, imhmax uses 8-connected neighborhoods for 2-D images, and 26 -connected neighborhoods for 3-D images. For higher dimensions, imhmax uses conndef(ndims(I), 'maximal').
\(\mathrm{I} 2=\) imhmax ( \(\mathrm{I}, \mathrm{h}\), conn \()\) computes the H -maxima transform, where conn specifies the connectivity. conn can have any of the following scalar values.
\begin{tabular}{l|l}
\hline Value & Meaning \\
\hline \multicolumn{2}{|c}{ Two-dimensional connectivities } \\
\hline 4 & 4 -connected neighborhood \\
\hline 8 & 8 -connected neighborhood \\
\hline \multicolumn{2}{|c}{ Three-dimensional connectivities } \\
\hline 6 & 6 -connected neighborhood \\
\hline 18 & 18 -connected neighborhood \\
\hline 26 & 26 -connected neighborhood \\
\hline
\end{tabular}

Connectivity can be defined in a more general way for any dimension by using for conn a 3 -by- 3 -by- ...-by-3 matrix of 0's and 1's. The 1 -valued elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.
Class
Support
I can be of any nonsparse numeric class and any dimension. I2 has the same size and class as I.
```

Examples a = zeros(10,10);
a(2:4,2:4) = 3; % maxima 3 higher than surround
a(6:8,6:8) = 8; % maxima 8 higher than surround
b = imhmax(a,4); % only the maxima higher than 4 survive.

```

\author{
References [1] Soille, P., Morphological Image Analysis: Principles and Applications, Springer-Verlag, 1999, pp. 170-171. \\ See Also conndef \| imextendedmax | imhmin | imreconstruct | imregionalmax
}

\section*{imhmin}
\[
\begin{array}{ll}
\text { Purpose } & \text { H-minima transform } \\
\text { Syntax } & \text { I2 }=\operatorname{imhmin}(I, h) \\
& \text { I2 }=\operatorname{imhmin}(I, h, \text { conn })
\end{array}
\]

Description \(\quad \mathrm{I} 2=\operatorname{imhmin}(\mathrm{I}, \mathrm{h})\) suppresses all minima in I whose depth is less than h. I is a grayscale image and h is a scalar.

Regional minima are connected components of pixels with a constant intensity value, and whose external boundary pixels all have a higher value.

By default, imhmin uses 8-connected neighborhoods for 2-D images, and 26 -connected neighborhoods for 3-D images. For higher dimensions, imhmin uses conndef(ndims(I), 'maximal').

I2 \(=\) imhmin( \(\mathrm{I}, \mathrm{h}, \mathrm{conn}\) ) computes the H-minima transform, where conn specifies the connectivity. conn can have any of the following scalar values.
\begin{tabular}{l|l}
\hline Value & Meaning \\
\hline \multicolumn{2}{l}{ Two-dimensional connectivities } \\
\hline 4 & 4-connected neighborhood \\
\hline 8 & 8 -connected neighborhood \\
\hline Three-dimensional connectivities \\
\hline 6 & 6 -connected neighborhood \\
\hline 18 & 18 -connected neighborhood \\
\hline 26 & 26 -connected neighborhood \\
\hline
\end{tabular}

Connectivity can be defined in a more general way for any dimension by using for conn a 3 -by- 3 -by- ...-by-3 matrix of 0's and 1's. The 1 -valued elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

Class
Support
Examples

I can be of any nonsparse numeric class and any dimension. I2 has the same size and class as I.

Create a sample image with two regional minima.
\begin{tabular}{|c|c|c|c|c|c|c|c|c|c|}
\hline \multicolumn{10}{|l|}{\[
\begin{aligned}
& \mathrm{a}=10 * \text { ones }(10,10) ; \\
& \mathrm{a}(2: 4,2: 4)=7 ; \\
& \mathrm{a}(6: 8,6: 8)=2
\end{aligned}
\]} \\
\hline \multicolumn{10}{|l|}{\(\mathrm{a}=\)} \\
\hline 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 7 & 7 & 7 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 7 & 7 & 7 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 7 & 7 & 7 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 2 & 2 & 2 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 2 & 2 & 2 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 2 & 2 & 2 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline
\end{tabular}

Suppress all minima below a specified value. Note how the region with pixel valued 7 disappears in the transformed image.
b \(=\) imhmin \((a, 4)\)
b =
\begin{tabular}{rrrrrrrrrr}
10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
10 & 10 & 10 & 10 & 10 & 6 & 6 & 6 & 10 & 10 \\
10 & 10 & 10 & 10 & 10 & 6 & 6 & 6 & 10 & 10 \\
10 & 10 & 10 & 10 & 10 & 6 & 6 & 6 & 10 & 10
\end{tabular}

\section*{imhmin}
\begin{tabular}{llllllllll}
10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10
\end{tabular}

\author{
References [1] Soille, P., Morphological Image Analysis: Principles and Applications, Springer-Verlag, 1999, pp. 170-171. \\ See Also conndef | imextendedmin | imhmax | imreconstruct | imregionalmin
}

Purpose
Impose minima
Syntax

Description
\(\mathrm{I} 2=\operatorname{imimposemin}(\mathrm{I}, \mathrm{BW})\)

\section*{Class Support}

I2 \(=\) imimposemin(I, BW, conn)
I2 = imimposemin( \(\mathrm{I}, \mathrm{BW}\) ) modifies the intensity image I using morphological reconstruction so it only has regional minima wherever \(B W\) is nonzero. BW is a binary image the same size as I.

By default, imimposemin uses 8 -connected neighborhoods for 2-D images and 26 -connected neighborhoods for 3-D images. For higher dimensions, imimposemin uses conndef(ndims(I), 'minimum').

I2 \(=\) imimposemin( \(\mathrm{I}, \mathrm{BW}\), conn \()\) specifies the connectivity, where conn can have any of the following scalar values.
\begin{tabular}{l|l}
\hline Value & Meaning \\
\hline \multicolumn{2}{|c}{ Two-dimensional connectivities } \\
\hline 4 & 4-connected neighborhood \\
\hline 8 & 8 -connected neighborhood \\
\hline \multicolumn{2}{|c}{ Three-dimensional connectivities } \\
\hline 6 & 6 -connected neighborhood \\
\hline 18 & 18 -connected neighborhood \\
\hline 26 & 26 -connected neighborhood \\
\hline
\end{tabular}

Connectivity can also be defined in a more general way for any dimension by using for conn a 3-by-3-by-...-by-3 matrix of 0's and 1's. The 1 -valued elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

I can be of any nonsparse numeric class and any dimension. BW must be a nonsparse numeric array with the same size as I. I2 has the same size and class as I.

\section*{imimposemin}

Examples Modify an image so that it only has regional minima at one location.
1 Read an image and display it. This image is called the mask image.
```

mask = imread('glass.png');
imshow(mask)

```


2 Create the marker image that will be used to process the mask image.
The example creates a binary image that is the same size as the mask image and sets a small area of the binary image to 1 . These pixels define the location in the mask image where a regional minimum will be imposed.
```

marker = false(size(mask));
marker(65:70,65:70) = true;

```

To show where these pixels of interest fall on the original image, this code superimposes the marker over the mask. The small white square marks the spot. This code is not essential to the impose minima operation.
```

J = mask;
J(marker) = 255;
figure, imshow(J); title('Marker Image Superimposed on Mask');

```


3 Impose the regional minimum on the input image using the imimposemin function.

The imimposemin function uses morphological reconstruction of the mask image with the marker image to impose the minima at the specified location. Note how all the dark areas of the original image, except the marked area, are lighter.

K = imimposemin(mask,marker);
figure, imshow(K);


4 To illustrate how this operation removes all minima in the original image except the imposed minimum, compare the regional minima in the original image with the regional minimum in the processed image. These calls to imregionalmin return binary images that specify the locations of all the regional minima in both images.
```

BW = imregionalmin(mask);
figure, imshow(BW);

```

\section*{imimposemin}
```

title('Regional Minima in Original Image');
BW2 = imregionalmin(K);
figure, imshow(BW2);
title('Regional Minima After Processing');

```


Regional Minima in Original Image


Regional Minima After Processing

Algorithms
See Also
imimposemin uses a technique based on morphological reconstruction.
conndef | imreconstruct | imregionalmin
\[
\begin{array}{ll}
\text { Purpose } & \text { Linear combination of images } \\
\text { Syntax } & Z=\operatorname{imlincomb}(\mathrm{K} 1, \mathrm{~A} 1, \mathrm{~K} 2, \mathrm{~A} 2, \ldots, \mathrm{Kn}, \mathrm{An}) \\
& \mathrm{Z}=\operatorname{imlincomb}(\mathrm{K} 1, \mathrm{~A} 1, \mathrm{~K} 2, \mathrm{~A} 2, \ldots, \mathrm{Kn}, \mathrm{An}, \mathrm{~K}) \\
& \mathrm{Z}=\operatorname{imlincomb}(\ldots, \text { output_class }) \\
\text { Description } & \mathrm{Z}=\operatorname{imlincomb}(\mathrm{K} 1, \mathrm{~A} 1, \mathrm{~K} 2, \mathrm{~A} 2, \ldots, \mathrm{Kn}, \mathrm{An}) \mathrm{co} \\
& \mathrm{~K} 1 * \mathrm{~A} 1+\mathrm{K} 2 * \mathrm{~A} 2+\ldots+\mathrm{Kn} * \mathrm{An}
\end{array}
\]
where K1, K2, through Kn are real, double scalars and A1, A2, through An are real, nonsparse, numeric arrays with the same class and size. Z has the same class and size as A1.

Z = imlincomb(K1,A1,K2,A2,...,Kn,An,K) computes
K1*A1 + K2*A2 + ... + Kn*An + K
where imlincomb adds K, a real, double scalar, to the sum of the products of K1 through Kn and A1 through An.

Z = imlincomb(...,output_class) lets you specify the class of Z. output_class is a string containing the name of a numeric class.

When performing a series of arithmetic operations on a pair of images, you can achieve more accurate results if you use imlincomb to combine the operations, rather than nesting calls to the individual arithmetic functions, such as imadd. When you nest calls to the arithmetic functions, and the input arrays are of an integer class, each function truncates and rounds the result before passing it to the next function, thus losing accuracy in the final result. imlincomb computes each element of the output \(Z\) individually, in double-precision floating point. If \(Z\) is an integer array, imlincomb truncates elements of \(Z\) that exceed the range of the integer type and rounds off fractional values.

On Intel architecture processors, imlincomb can take advantage of the Intel Integrated Performance Primitives (Intel IPP) library, thus accelerating its execution time. The Intel IPP library is activated only in the following cases:

\section*{imlincomb}
```

Z = imlincomb( 1.0, A1, 1.0, A2)
Z = imlincomb( 1.0, A1,-1.0, A2)
Z = imlincomb(-1.0, A1, 1.0, A2)
Z = imlincomb( 1.0 , A1, K)

```
where A1, A2, and Z are of class uint8, int16, or single and are of the same class.

\section*{Examples}

\section*{Example 1}

Scale an image by a factor of 2 .
I = imread('cameraman.tif');
\(J=\) imlincomb(2,I);
imshow(J)

\section*{Example 2}

Form a difference image with the zero value shifted to 128.
```

I = imread('cameraman.tif');
J = uint8(filter2(fspecial('gaussian'), I));
K = imlincomb(1,I,-1,J,128); % K(r,c) = I(r,c) - J(r,c) + 128
figure, imshow(K)

```

\section*{Example 3}

Add two images with a specified output class.
```

I = imread('rice.png');
J = imread('cameraman.tif');
K = imlincomb(1, I,1,J,'uint16');
figure, imshow(K,[])

```

\section*{Example 4}

To illustrate how imlincomb performs all the arithmetic operations before truncating the result, compare the results of calculating the average of two arrays, \(X\) and \(Y\), using nested arithmetic functions and then using imlincomb.
In the version that uses nested arithmetic functions, imadd adds 255 and 50 and truncates the result to 255 before passing it to imdivide. The average returned in \(Z(1,1)\) is 128 .
\(\mathrm{X}=\) uint8([ \(2551075 ; 44225\) 100]);
\(\mathrm{Y}=\) uint8([ \(502050 ; 505050\) ]);
Z = imdivide(imadd(X,Y),2)
Z =
\(128 \quad 15 \quad 63\)
\(\begin{array}{lll}47 & 128 & 75\end{array}\)
imlincomb performs the addition and division in double precision and only truncates the final result. The average returned in \(\mathrm{Z2}(1,1)\) is 153 .
```

Z2 = imlincomb(.5, X, .5, Y)
Z2 =
$153 \quad 15 \quad 63$
$47 \quad 138 \quad 75$

```

\footnotetext{
See Also
imadd | imcomplement | imdivide | immultiply | imsubtract
}

\section*{imline}

Purpose Create draggable, resizable line
```

Syntax h = imline
h = imline(hparent)
h = imline(hparent, position)
h = imline(hparent, x, y)
H = imline(..., param1, val1,...)

```

\section*{Description}
\(\mathrm{h}=\) imline begins interactive placement of a line on the current axes. The function returns h , a handle to an imline object. The line has a context menu associated with it that controls aspects of its appearance and behavior-see "Interactive Behavior" on page 3-439. Right-click on the line to access this context menu.
\(\mathrm{h}=\) imline(hparent) begins interactive placement of a line on the object specified by hparent. hparent specifies the HG parent of the line graphics, which is typically an axes but can also be any other object that can be the parent of an hggroup
h = imline(hparent, position) creates a draggable, resizable line on the object specified by hparent. position is a 2 -by- 2 array that specifies the initial endpoint positions of the line in the form [ X 1 Y 1 ; X2 Y2].
\(\mathrm{h}=\) imline(hparent, \(\mathrm{x}, \mathrm{y})\) creates a line on the object specified by hparent. \(x\) and \(y\) are two-element vectors that specify the initial endpoint positions of the line in the form \(x=\left[\begin{array}{ll}\mathrm{X} 1 & \mathrm{X} 2\end{array}\right], \mathrm{y}=\left[\begin{array}{ll}\mathrm{Y} 1 & \mathrm{Y} 2\end{array}\right]\).
H = imline(..., param1, val1,...) creates a draggable, resizable line, specifying parameters and corresponding values that control the behavior of the line. The following tables lists the parameter available. Parameter names can be abbreviated, and case does not matter.
\begin{tabular}{l|l}
\hline Parameter & Description \\
\hline 'PositionConstraintFcn & \begin{tabular}{l} 
Function handle fon that is called \\
whenever the object is dragged using \\
the mouse. You can use this function to \\
control where the line can be dragged. See \\
the help for the setPositionConstraintFcn \\
method for information about valid \\
function handles.
\end{tabular} \\
\hline
\end{tabular}

\section*{Interactive Behavior}

When you call imline with an interactive syntax, the pointer changes to a cross hairs \(+_{\text {when over the image. Click and drag the mouse to }}\) specify the position and length of the line, such as \(\square \square\). The line supports a context menu that you can use to control aspects of its appearance and behavior. For more information about these interactive features, see the following table.
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} & Description \\
\hline Moving the line. & \begin{tabular}{l} 
Move the pointer over the line. The pointer \\
changes to a fleur shape \\
the mouse to move the line.
\end{tabular} \\
\hline \begin{tabular}{l} 
Moving the \\
endpoints of the \\
line.
\end{tabular} & \begin{tabular}{l} 
Move the pointer over either end of the line. \\
The pointer changes to the pointing finger, \\
drom. Click and drag the mouse to resize the \\
line.
\end{tabular} \\
\hline
\end{tabular}

\section*{imline}
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} & Description \\
\hline \begin{tabular}{l} 
Changing the color \\
used to display the \\
line.
\end{tabular} & \begin{tabular}{l} 
Move the pointer over the line. Right-click \\
and select Set Color from the context menu.
\end{tabular} \\
\hline \begin{tabular}{l} 
Retrieving the \\
coordinates of the \\
endpoints of the line.
\end{tabular} & \begin{tabular}{l} 
Move the pointer over the line. Right-click and \\
select Copy Position from the context menu. \\
imline copies a 2-by-2 array to the clipboard \\
specifying the coordinates of the endpoints of \\
the line in the form [X1 Y1; X2 Y2].
\end{tabular} \\
\hline
\end{tabular}

\section*{Methods}

Each imline object supports a number of methods. Type methods imline to see a list of the methods.

\section*{addNewPositionCallback - Add new-position callback to ROI object}

See imroi for information.

\section*{delete - Delete ROI object}

See imroi for information.

\section*{getColor - Get color used to draw ROI object.}

See imroi for information.

\section*{getPosition - Return current position of line}

Returns the endpoint positions of the line.
pos = api.getPosition()
pos is a 2-by-2 array [X1 Y1; X2 Y2].

\section*{getPositionConstraintFen - Return function handle to current position constraint function}

See imroi for information.

\section*{removeNewPositionCallback - Remove new-position callback from ROI object.}

See imroi for information.

\section*{resume - Resume execution of MATLAB command line}

See imroi for information.

\section*{setColor - Set color used to draw ROI object}

See imroi for information.

\section*{setConstrainedPosition - Set ROI object to new position}

See imroi for information.

\section*{setPosition - Set line to new position}
setPosition( \(\mathrm{h}, \mathrm{pos}\) ) sets the line h to a new position. The new position, pos, has the form, [ X 1 Y 1 ; X2 Y2].
setPosition ( \(\mathrm{h}, \mathrm{x}, \mathrm{y}\) ) sets the line h to a new position. x and y specify the endpoint positions of the line in the form \(x=\left[\begin{array}{ll}x 1 & x 2\end{array}\right], y=[y 1\) \(\mathrm{y} 2]\).
setPositionConstraintFen - Set position constraint function of ROI object.
See imroi for information.
wait - Block MATLAB command line until ROI creation is finished
See imroi for information.
Tips

\section*{Examples Example 1}

Use a custom color for displaying the line. Use addNewPositionCallback method. Move the line, note that the 2 -by- 2 position vector of the line is displayed in the title above the image. Explore the context menu of the line by right clicking on the line.
```

figure, imshow('pout.tif');

```
figure, imshow('pout.tif');
h = imline(gca,[10 100], [100 100]);
h = imline(gca,[10 100], [100 100]);
setColor(h,[0 1 0]);
setColor(h,[0 1 0]);
id = addNewPositionCallback(h,@(pos) title(mat2str(pos,3)));
```

id = addNewPositionCallback(h,@(pos) title(mat2str(pos,3)));

```

\section*{imline}
\% After observing the callback behavior, remove the callback. \% using the removeNewPositionCallback API function. removeNewPositionCallback(h,id);

\section*{Example 2}

Interactively place a line by clicking and dragging. Use wait to block the MATLAB command line. Double-click on the line to resume execution of the MATLAB command line
figure, imshow('pout.tif');
h = imline;
position = wait(h);

\section*{See Also}
imellipse | imfreehand | impoint | impoly | imrect | imroi | makeConstrainToRectFcn

Purpose Magnification box for scroll panel
Syntax hbox \(=\) immagbox (hparent, himage)
Description
hbox = immagbox(hparent, himage) creates a Magnification box for the image displayed in a scroll panel created by imscrollpanel. hparent is a handle to the figure or uipanel object that will contain the Magnification box. himage is a handle to the target image (the image in the scroll panel). immagbox returns hbox, which is a handle to the Magnification box uicontrol object

A Magnification box is an editable text box uicontrol that contains the current magnification of the target image. When you enter a new value in the magnification box, the magnification of the target image changes. When the magnification of the target image changes for any reason, the magnification box updates the magnification value.

API A Magnification box contains a structure of function handles, called an Functions API. You can use the functions in this API to manipulate magnification box. To retrieve this structure, use the iptgetapi function.
api \(=\) iptgetapi(hbox)
The API for the Magnification box includes the following function.
\begin{tabular}{l|l}
\hline Function & Description \\
\hline setMagnification & \begin{tabular}{l} 
Sets the magnification in units of screen pixels per image pixel. \\
setMagnification(new_mag)
\end{tabular} \\
& \begin{tabular}{l} 
where new_mag is a scalar magnification factor. Multiply \\
new_mag by 100 to get percent magnification. For example \\
if you call setMagnification(2), the magnification box will \\
show the string '200\%'.
\end{tabular} \\
\hline
\end{tabular}

\section*{Examples}

Add a magnification box to a scrollable image. Because the toolbox scrollable navigation is incompatible with standard MATLAB figure

\section*{immagbox}
window navigation tools, the example suppresses the toolbar and menu bar in the figure window. The example positions the scroll panel in the figure window to allow room for the magnification box.
```

hFig = figure('Toolbar','none',...
'Menubar','none');
hIm = imshow('pears.png');
hSP = imscrollpanel(hFig,hIm);
set(hSP,'Units','normalized',...
'Position',[0 .1 1 .9])
hMagBox = immagbox(hFig,hIm);
pos = get(hMagBox,'Position');
set(hMagBox,'Position',[0 0 pos(3) pos(4)])

```

Change the magnification of the image in the scroll panel, using the scroll panel API function setMagnification. Notice how the magnification box updates.
apiSP = iptgetapi(hSP); apiSP.setMagnification(2)
```

See also imscrollpanel, iptgetapi

```

\section*{Purpose Make movie from multiframe image}

Note immovie(D,size) is an obsolete syntax and is no longer supported. Use immovie (X, map) instead.
```

Syntax mov = immovie(X,map)
mov = immovie(RGB)

```

Description

Tips
\(\begin{array}{ll}\text { Class } & \text { An indexed image can be uint8, uint16, single, double, or logical. } \\ \text { Support } & \text { A truecolor image can be uint8, uint16, single, or double. mov is a } \\ & \text { MATLAB movie structure. }\end{array}\)
Examples
load mri
mov = immovie(D,map);
implay(mov)
See Also
mov = immovie(X,map) returns the movie structure array mov from the images in the multiframe indexed image \(X\) with the colormap map. For details about the movie structure array, see the reference page for getframe. To play the movie, call implay.

X comprises multiple indexed images, all having the same size and all using the colormap map. X is an m -by-n-by-1-by-k array, where k is the number of images.
mov = immovie(RGB) returns the movie structure array mov from the images in the multiframe, truecolor image RGB.

RGB comprises multiple truecolor images, all having the same size. RGB is an m-by-n-by-3-by-k array, where \(k\) is the number of images.

You can also use the MATLAB function avifile to make movies from images. The avifile function creates AVI files. To convert an existing MATLAB movie into an AVI file, use the movie2avi function.
v
avifile | getframe | montage | movie | movie2avi

\section*{immultiply}

\section*{Purpose}

Multiply two images or multiply image by constant
Syntax \(\quad Z=\) immultiply \((X, Y)\)
\(Z=\) immultiply \((X, Y)\) multiplies each element in array \(X\) by the corresponding element in array Y and returns the product in the corresponding element of the output array Z .
If \(X\) and \(Y\) are real numeric arrays with the same size and class, then \(Z\) has the same size and class as \(X\). If \(X\) is a numeric array and \(Y\) is a scalar double, then \(Z\) has the same size and class as \(X\).

If \(X\) is logical and \(Y\) is numeric, then \(Z\) has the same size and class as \(Y\). If \(X\) is numeric and \(Y\) is logical, then \(Z\) has the same size and class as \(X\).
immultiply computes each element of \(Z\) individually in double-precision floating point. If \(X\) is an integer array, then elements of \(Z\) exceeding the range of the integer type are truncated, and fractional values are rounded.

Note On Intel architecture processors, immultiply can take advantage of the Intel Integrated Performance Primitives (Intel IPP) library, thus accelerating its execution time. The Intel IPP library is activated only if arrays \(X, Y\), and \(Z\) are of class logical, uint8, or single, and are of the same class.

\section*{Examples}

Multiply an image by itself. Note how the example converts the class of the image from uint 8 to uint 16 before performing the multiplication to avoid truncating the results.
```

I = imread('moon.tif');
I16 = uint16(I);
J = immultiply(I16,I16);
imshow(I), figure, imshow(J)

```

Scale an image by a constant factor:
```

I = imread('moon.tif');
J = immultiply(I,0.5);
subplot(1,2,1), imshow(I)
subplot(1,2,2), imshow(J)

```

See Also
imabsdiff | imadd | imcomplement | imdivide | imlincomb | imsubtract | ippl

\section*{imnoise}

Purpose Add noise to image
Syntax \(\quad J=\) imnoise(I,type)
J = imnoise(I,type,parameters)
J = imnoise(I, 'gaussian',m,v)
J = imnoise(I, 'localvar', V)
J = imnoise(I,'localvar',image_intensity,var)
J = imnoise(I,'poisson')
\(J\) = imnoise(I,'salt \& pepper',d)
J = imnoise(I,'speckle', v)

\section*{Description}
\(J=\) imnoise (I, type) adds noise of a given type to the intensity image I. type is a string that can have one of these values.
\begin{tabular}{l|l}
\hline Value & Description \\
\hline 'gaussian' & \begin{tabular}{l} 
Gaussian white noise with constant mean and \\
variance
\end{tabular} \\
\hline 'localvar' & \begin{tabular}{l} 
Zero-mean Gaussian white noise with an \\
intensity-dependent variance
\end{tabular} \\
\hline 'poisson' & Poisson noise \\
\hline \begin{tabular}{l} 
'salt \& \\
pepper'
\end{tabular} & On and off pixels \\
\hline 'speckle' & Multiplicative noise \\
\hline
\end{tabular}
\(J\) = imnoise(I,type,parameters) Depending on type, you can specify additional parameters to imnoise. All numerical parameters are normalized; they correspond to operations with images with intensities ranging from 0 to 1 .
\(J=\) imnoise(I, 'gaussian', m, v) adds Gaussian white noise of mean \(m\) and variance \(v\) to the image \(I\). The default is zero mean noise with 0.01 variance.

J = imnoise(I, 'localvar', V) adds zero-mean, Gaussian white noise of local variance V to the image I . V is an array of the same size as I .

J = imnoise(I,'localvar',image_intensity,var) adds zero-mean, Gaussian noise to an image I, where the local variance of the noise, var, is a function of the image intensity values in I. The image_intensity and var arguments are vectors of the same size, and plot(image_intensity, var) plots the functional relationship between noise variance and image intensity. The image_intensity vector must contain normalized intensity values ranging from 0 to 1 .
\(J=\) imnoise(I,'poisson') generates Poisson noise from the data instead of adding artificial noise to the data. If I is double precision, then input pixel values are interpreted as means of Poisson distributions scaled up by 1e12. For example, if an input pixel has the value \(5.5 \mathrm{e}-12\), then the corresponding output pixel will be generated from a Poisson distribution with mean of 5.5 and then scaled back down by 1 e 12 . If I is single precision, the scale factor used is 1 e 6 . If I is uint8 or uint16, then input pixel values are used directly without scaling. For example, if a pixel in a uint8 input has the value 10 , then the corresponding output pixel will be generated from a Poisson distribution with mean 10.
\(J=\) imnoise(I,'salt \& pepper',d) adds salt and pepper noise to the image I, where \(d\) is the noise density. This affects approximately \(d *\) numel (I) pixels. The default for \(d\) is 0.05 .
\(J=\) imnoise(I, 'speckle', v) adds multiplicative noise to the image I, using the equation \(J=I+n * I\), where \(n\) is uniformly distributed random noise with mean 0 and variance \(v\). The default for \(v\) is 0.04 .

Note The mean and variance parameters for 'gaussian', 'localvar', and 'speckle' noise types are always specified as if the image were of class double in the range [ 0,1 ]. If the input image is of class uint8 or uint16, the imnoise function converts the image to double, adds noise according to the specified type and parameters, and then converts the noisy image back to the same class as the input.

\section*{imnoise}
Class
Support
Examples
I = imread('eight.tif');
I = imread('eight.tif');
J = imnoise(I,'salt & pepper',0.02);
J = imnoise(I,'salt & pepper',0.02);
figure, imshow(I)
figure, imshow(I)
figure, imshow(J)
figure, imshow(J)

See Also
rand | randn

\section*{Purpose}

Morphologically open image
Syntax
IM2 = imopen(IM,SE)
IM2 \(=\) imopen(IM,NHOOD)

Class
Support

\section*{Examples}

IM2 = imopen(IM, SE) performs morphological opening on the grayscale or binary image IM with the structuring element SE. The argument SE must be a single structuring element object, as opposed to an array of objects. The morphological open operation is an erosion followed by a dilation, using the same structuring element for both operations.

IM2 = imopen(IM,NHOOD) performs opening with the structuring element strel(NHOOD), where NHOOD is an array of 0's and 1's that specifies the structuring element neighborhood.

IM can be any numeric or logical class and any dimension, and must be nonsparse. If IM is logical, then SE must be flat. IM2 has the same class as IM.

Remove the smaller objects in an image.
1 Read the image into the MATLAB workspace and display it.
```

I = imread('snowflakes.png');
imshow(I)

```


2 Create a disk-shaped structuring element with a radius of 5 pixels.
```

se = strel('disk',5);

```

\section*{imopen}

3 Remove snowflakes having a radius less than 5 pixels by opening it with the disk-shaped structuring element created in step 2.

I_opened = imopen(I,se);
figure, imshow(I_opened,[])


\section*{See Also}
imclose | imdilate | imerode | strel

\section*{Purpose Overview tool for image displayed in scroll panel}

\section*{Syntax imoverview(himage)}
hfig = imoverview(...)
Description
imoverview(himage) creates an Overview tool associated with the image specified by the handle himage, called the target image. The target image must be contained in a scroll panel created by imscrollpanel.

The Overview tool is a navigation aid for images displayed in a scroll panel. imoverview creates the tool in a separate figure window that displays the target image in its entirety, scaled to fit. Over this scaled version of the image, the tool draws a rectangle, called the detail rectangle, that shows the portion of the target image that is currently visible in the scroll panel. To view portions of the image that are not currently visible in the scroll panel, move the detail rectangle in the Overview tool.

The following figure shows the Image Tool with the Overview tool.

\section*{imoverview}

hfig = imoverview(...) returns a handle to the Overview tool figure.

Note

\section*{Examples}

To create an Overview tool that can be embedded in an existing figure or uipanel object, use imoverviewpanel.

Create a figure, disabling the toolbar and menubar, because the toolbox navigation tools are not compatible with the standard MATLAB zoom and pan tools. Then create a scroll panel in the figure and use scroll panel API functions to set the magnification.
```

hFig = figure('Toolbar','none',...
'Menubar','none');
hIm = imshow('tape.png');
hSP = imscrollpanel(hFig,hIm);
api = iptgetapi(hSP);

```
```

api.setMagnification(2) % 2X = 200%
imoverview(hIm)

```

See Also imoverviewpanel | imscrollpanel

\section*{imoverviewpanel}
\begin{tabular}{|c|c|}
\hline Purpose & Overview tool panel for image displayed in scroll panel \\
\hline Syntax & hpanel = imoverviewpanel(hparent, himage) \\
\hline \multirow[t]{2}{*}{Description} & hpanel = imoverviewpanel(hparent, himage) creates an Overview tool panel associated with the image specified by the handle himage, called the target image. himage must be contained in a scroll panel created by imsrollpanel. hparent is a handle to the figure or uipanel object that will contain the Overview tool panel. imoverviewpanel returns hpanel, a handle to the Overview tool uipanel object. \\
\hline & The Overview tool is a navigation aid for images displayed in a scroll panel. imoverviewpanel creates the tool in a uipanel object that can be embedded in a figure or uipanel object. The tool displays the target image in its entirety, scaled to fit. Over this scaled version of image, the tool draws a rectangle, called the detail rectangle, that shows the portion of the target image that is currently visible in the scroll panel. To view portions of the image that are not currently visible in the scroll panel, move the detail rectangle in the Overview tool. \\
\hline Note & To create an Overview tool in a separate figure, use imoverview. When created using imoverview, the Overview tool includes zoom-in and zoom-out buttons. \\
\hline \multirow[t]{2}{*}{Examples} & Create an Overview tool that is embedded in the same figure that contains the target image. \\
\hline & ```
hFig = figure('Toolbar','none','Menubar','none');
hIm = imshow('tissue.png');
hSP = imscrollpanel(hFig,hIm);
set(hSP,'Units','normalized','Position',[0 . 5 1 .5])
hOvPanel = imoverviewpanel(hFig,hIm);
set(hOvPanel,'Units','Normalized',...
'Position',[0 0 1 .5])
``` \\
\hline See Also & imoverview | imscrollpanel \\
\hline
\end{tabular}

See Also imoverview \| imscrollpanel

\section*{Purpose Pixel color values}

Syntax \(\quad P=\operatorname{impixel}(I)\)
P = impixel(X,map)
\(P=\) impixel(RGB)
\(\mathrm{P}=\) impixel( \(\mathrm{I}, \mathrm{c}, \mathrm{r})\)
\(P=i m p i x e l(X\), map, \(c, r)\)
\(P=i m p i x e l(R G B, c, r)\)
\([\mathrm{c}, \mathrm{r}, \mathrm{P}]=\operatorname{impixel}(\ldots)\)
P = impixel( \(x, y, I, x i, y i)\)
\(P=\) impixel( \(x, y, X, m a p, x i, y i)\)
P = impixel(x,y,RGB,xi,yi)
[xi,yi,P] = impixel(x,y,...)

\section*{Description}
impixel returns the red, green, and blue color values of specified image pixels. In the syntax below, impixel displays the input image and waits for you to specify the pixels with the mouse.
```

P = impixel(I)
P = impixel(X,map)
P = impixel(RGB)

```

If you omit the input arguments, impixel operates on the image in the current axes.

Use normal button clicks to select pixels. Press Backspace or Delete to remove the previously selected pixel. A shift-click, right-click, or double-click adds a final pixel and ends the selection; pressing Return finishes the selection without adding a pixel.
When you finish selecting pixels, impixel returns an m-by-3 matrix of RGB values in the supplied output argument. If you do not supply an output argument, impixel returns the matrix in ans.

You can also specify the pixels noninteractively, using these syntax.
```

P = impixel(I,c,r)

```

\section*{impixel}
\(P=i m p i x e l(X, \operatorname{map}, c, r)\)
\(P=i m p i x e l(R G B, c, r)\)
\(r\) and \(c\) are equal-length vectors specifying the coordinates of the pixels whose RGB values are returned in \(P\). The kth row of \(P\) contains the RGB values for the pixel ( \(\mathrm{r}(\mathrm{k}), \mathrm{c}(\mathrm{k})\) ).

If you supply three output arguments, impixel returns the coordinates of the selected pixels. For example,
\([c, r, P]=\) impixel(...)

To specify a nondefault spatial coordinate system for the input image, use these syntax.
```

P = impixel(x,y,I,xi,yi)
P = impixel(x,y,X,map,xi,yi)
P = impixel(x,y,RGB,xi,yi)

```
\(x\) and \(y\) are two-element vectors specifying the image XData and YData. xi and yi are equal-length vectors specifying the spatial coordinates of the pixels whose RGB values are returned in P. If you supply three output arguments, impixel returns the coordinates of the selected pixels.
```

[xi,yi,P] = impixel(x,y,...)

```

\section*{Class Support}

Tips

The input image can be of class uint8, uint16, int16, single, double, or logical. All other inputs are of class double.

If the input is double, the output \(P\) is double. For all other input classes the output is single. The rest of the outputs are double.
impixel works with indexed, intensity, and RGB images. impixel always returns pixel values as RGB triplets, regardless of the image type:
- For an RGB image, impixel returns the actual data for the pixel. The values are either uint8 integers or double floating-point numbers, depending on the class of the image array.
- For an indexed image, impixel returns the RGB triplet stored in the row of the colormap that the pixel value points to. The values are double floating-point numbers.
- For an intensity image, impixel returns the intensity value as an RGB triplet, where \(\mathrm{R}=\mathrm{G}=\mathrm{B}\). The values are either uint8 integers or double floating-point numbers, depending on the class of the image array.
Examples \(\quad R G B=\) imread('peppers.png');
c = [12 146 410];
\(r=[104156\) 129];
pixels \(=\) impixel( \(\mathrm{RGB}, \mathrm{c}, \mathrm{r})\)
pixels =
\(62 \quad 34 \quad 63\)
    \(16654 \quad 60\)
    \(\begin{array}{lll}59 & 28 & 47\end{array}\)
See Also improfile

\section*{impixelinfo}
\begin{tabular}{ll} 
Purpose & Pixel Information tool \\
Syntax & \begin{tabular}{l} 
impixelinfo \\
impixelinfo \((\mathrm{h})\) \\
impixelinfo(hparent, himage) \\
hpanel \(=\) impixelinfo(...)
\end{tabular}
\end{tabular}

\section*{Description}
impixelinfo creates a Pixel Information tool in the current figure. The Pixel Information tool displays information about the pixel in an image that the pointer is positioned over. The tool can display pixel information for all the images in a figure.

The Pixel Information tool is a uipanel object, positioned in the lower-left corner of the figure. The tool contains the text string Pixel info: followed by the pixel information. Before you move the pointer over the image, the tool contains the default pixel information text string \((X, Y)\) Pixel Value. Once you move the pointer over the image, the information displayed varies by image type, as shown in the following table. If you move the pointer off the image, the pixel information tool displays the default pixel information string for that image type.
\begin{tabular}{|c|c|c|}
\hline Image Type & Pixel Information & Example \\
\hline Intensity & ( \(\mathrm{X}, \mathrm{Y}\) ) Intensity & \((13,30) 82\) \\
\hline Indexed & \[
\begin{aligned}
& (\mathrm{X}, \mathrm{Y})<\text { index }>[\mathrm{R} \mathrm{G} \\
& \mathrm{B}]
\end{aligned}
\] & \[
\begin{aligned}
& (2,6)<4>[0.29 \\
& 0.050 .32]
\end{aligned}
\] \\
\hline Binary & (X,Y) BW & \((12,1) 0\) \\
\hline Truecolor & (X,Y) [R G B] & \[
\begin{aligned}
& (19,10)[15255 \\
& 10]
\end{aligned}
\] \\
\hline Floating point image with CDataMapping property set to direct & \begin{tabular}{l}
(X,Y) value \\
<index> [R G B]
\end{tabular} & \[
\begin{aligned}
& (19,10) 82<4>[15 \\
& 25510]
\end{aligned}
\] \\
\hline
\end{tabular}

For example, for grayscale (intensity) images, the pixel information tool displays the \(x\) and \(y\) coordinates of the pixel and its value, as shown in the following figure.


If you want to display the pixel information without the "Pixel Info" label, use the impixelinfoval function.
impixelinfo(h) creates a Pixel Information tool in the figure specified by h , where h is a handle to an image, axes, uipanel, or figure object. Axes, uipanel, or figure objects must contain at least one image object.
impixelinfo(hparent, himage) creates a Pixel Information tool in hparent that provides information about the pixels in himage. himage is a handle to an image or an array of image handles. hparent is a handle to the figure or uipanel object that contains the pixel information tool.
hpanel \(=\) impixelinfo(...) returns a handle to the Pixel Information tool uipanel.

Note

\section*{Examples}

To copy the pixel information string to the clipboard, right-click while the pointer is positioned over a pixel. In the context menu displayed, choose Copy pixel info.

Display an image and add a Pixel Information tool to the figure. The example shows how you can change the position of the tool in the figure using properties of the tool uipanel object.
```

h = imshow('hestain.png');
hp = impixelinfo;
set(hp,'Position',[5 1 300 20]);

```

Use the Pixel Information tool in a figure containing multiple images of different types.

\section*{impixelinfo}
```

figure
subplot(1,2,1), imshow('liftingbody.png');
subplot(1,2,2), imshow('autumn.tif');
impixelinfo;

```

See Also impixelinfoval | imtool

\section*{Purpose Pixel Information tool without text label}
```

Syntax hcontrol = impixelinfoval(hparent,himage)

```

Description

\section*{Examples}

Add a Pixel Information tool to a figure. Note how you can change the style and size of the font used to display the value in the tool using standard Handle Graphics commands.
```

ankle = dicomread('CT-MONO2-16-ankle.dcm');
h = imshow(ankle,[]);

```

\section*{impixelinfoval}

> hText = impixelinfoval(gcf,h); set(hText,'FontWeight', 'bold') set(hText,'FontSize', 10)

See also impixelinfo

\section*{impixelregion}

\section*{Purpose Pixel Region tool}
```

Syntax impixelregion
impixelregion(h)
hfig = impixelregion(...)

```

Description impixelregion creates a Pixel Region tool associated with the image displayed in the current figure, called the target image. The Pixel Region tool opens a separate figure window containing an extreme close-up view of a small region of pixels in the target image, as shown in the following figure.

\section*{impixelregion}


The Pixel Region rectangle defines the area of the target image that is displayed in the Pixel Region tool. You can move this rectangle over the target image using the mouse to view different regions. To get a closer view of the pixels displayed in the tool, use the zoom buttons on the Pixel Region tool toolbar or change the size of the Pixel Region rectangle using the mouse. You can also resize the Pixel Region tool itself to view more or fewer pixels. If the size of the pixels allows, the tool superimposes the numeric value of the pixel over each pixel.

To get the current position of the Pixel Region rectangle, right-click on the rectangle and select Copy Position from the context menu. The Pixel Region tool copies a four-element position vector to the clipboard.

To change the color of the Pixel Region rectangle, right-click and select Set Color.
impixelregion (h) creates a Pixel Region tool associated with the object specified by the handle h . h can be a handle to a figure, axes, uipanel, or image object. If h is a handle to an axes or figure, impixelregion associates the tool with the first image found in the axes or figure.
hfig = impixelregion(...) returns hfig, a handle of the Pixel Region tool figure.

\section*{Note}

Examples Display an image and then create a Pixel Region tool associated with the image.
```

imshow peppers.png
impixelregion

```

See Also
impixelinfo | impixelregionpanel | imtool

\section*{impixelregionpanel}
\begin{tabular}{|c|c|}
\hline Purpose & Pixel Region tool panel \\
\hline Syntax & hpanel = impixelregionpanel(hparent, himage) \\
\hline \multirow[t]{2}{*}{Description} & hpanel = impixelregionpanel(hparent,himage) creates a Pixel Region tool panel associated with the image specified by the handle himage, called the target image. This is the image whose pixels are to be displayed. hparent is the handle to the figure or uipanel object that will contain the Pixel Region tool panel. hpanel is the handle to the Pixel Region tool scroll panel. \\
\hline & The Pixel Region tool is a uipanel object that contains an extreme close-up view of a small region of pixels in the target image. If the size of the pixels allows, the tool superimposes the numeric value of the pixel over each pixel. To define the region being examined, the tool overlays a rectangle on the target image, called the pixel region rectangle. To view pixels in a different region, click and drag the rectangle over the target image. See impixelregion for more information. \\
\hline Note & To create a Pixel Region tool in a separate figure window, use impixelregion. \\
\hline \multirow[t]{2}{*}{Examples} & ```
himage = imshow('peppers.png');
hfigure = figure;
hpanel = impixelregionpanel(hfigure, himage);
``` \\
\hline & \begin{tabular}{l}
Set the panel's position to the lower-left quadrant of the figure. \\
set(hpanel, 'Position', [0 0 . 5 .5])
\end{tabular} \\
\hline See Also & impixelregion | imrect | imscrollpanel \\
\hline
\end{tabular}

Purpose
Syntax

Play movies, videos, or image sequences
```

implay

```
implay
implay(filename)
implay(filename)
implay(I)
implay(I)
implay(..., FPS)
```

implay(..., FPS)

```
implay opens a Movie Player for showing MATLAB movies, videos, or image sequences (also called image stacks). Use the implay File menu to select the movie or image sequence that you want to play. Use implay toolbar buttons or menu options to play the movie, jump to a specific frame in the sequence, change the frame rate of the display, or perform other exploration activities. You can open multiple implay movie players to view different movies simultaneously.

The following figure shows the Movie Player containing an image sequence.


\section*{implay}
implay(filename) opens the implay movie player, displaying the content of the file specified by filename. The file can be an Audio Video Interleaved (AVI) file. implay reads one frame at a time, conserving memory during playback. implay does not play audio tracks.
implay (I) opens the implay movie player, displaying the first frame in the multiframe image array specified by I. I can be a MATLAB movie structure, or a sequence of binary, grayscale, or truecolor images. A binary or grayscale image sequence can be an M-by-N-by-1-by-K array or an M-by-N-by-K array. A truecolor image sequence must be an M-by-N-by-3-by-K array.
implay (..., FPS) specifies the rate at which you want to view the movie or image sequence. The frame rate is specified as frames-per-second. If omitted, implay uses the frame rate specified in the file or the default value 20 .
\begin{tabular}{ll} 
Class & \begin{tabular}{l} 
I can be numeric but uint8 is preferred. The actual data type used to \\
display pixels may differ from the source data type.
\end{tabular} \\
Support & - You can access implay through the Plot Selector workspace tool, \\
which is represented by this icon: \\
In your workspace, select the data to plot want to display. The Plot
\end{tabular}.

\section*{Examples Animate a sequence of images.}
load cellsequence
implay (cellsequence,10);
Visually explore a stack of MRI images.
```

load mristack
implay(mristack);

```

Play an AVI file.
implay('rhinos.avi');

\section*{impoint}

Purpose Create draggable point
```

Syntax $\quad h=$ impoint
h = impoint (hparent)
$\mathrm{p}=$ impoint(hparent, position)
p = impoint(hparent, $x, y)$
$\mathrm{p}=$ impoint(..., param, val)

```

\section*{Description}
\(\mathrm{h}=\) impoint begins interactive placement of a draggable point on the current axes. The function returns h , a handle to an impoint object. The point has a context menu associated with it that controls aspects of its appearance and behavior-see "Interactive Behavior" on page 3-473. Right-click on the point to access this context menu.
\(\mathrm{h}=\) impoint (hparent) begins interactive placement of a point on the object specified by hparent. hparent specifies the HG parent of the point graphics, which is typically an axes but can also be any other object that can be the parent of an hggroup.
p = impoint(hparent, position) creates a draggable point on the object specified by hparent. position is a 1-by-2 array of the form [ x \(y]\) that specifies the initial position of the point.
\(\mathrm{p}=\) impoint (hparent, \(x, y\) ) creates a draggable point on the object specified by hparent. \(x\) and \(y\) are both scalars that together specify the initial position of the point.
p = impoint(..., param, val) creates a draggable point, specifying parameters and corresponding values that control the behavior of the point. The following table lists the parameter available. Parameter names can be abbreviated, and case does not matter.
\begin{tabular}{l|l}
\hline Parameter & Description \\
\hline 'PositionConstraintFcn & \begin{tabular}{l} 
Function handle fon that is called \\
whenever the point is dragged \\
using the mouse. You can use this \\
function to control where the point \\
can be dragged. See the help for the \\
setPositionConstraintFcn method for \\
information about valid function handles.
\end{tabular} \\
\hline
\end{tabular}

\section*{Interactive Behavior}

When you call impoint with an interactive syntax, the pointer changes to a cross hairs \(+_{\text {when over the image. Click and drag the mouse }}\) to specify the position of the point, such as \(\$\). The following table describes the interactive behavior of the point, including the right-click context menu options.
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} & Description \\
\hline Moving the point. & \begin{tabular}{l} 
Move the mouse pointer over the point. The \\
mouse pointer changes to a fleur shape \\
Click and drag the mouse to move the point.
\end{tabular} \\
\hline \begin{tabular}{l} 
Changing the color \\
used to display the \\
point.
\end{tabular} & \begin{tabular}{l} 
Move the mouse pointer over the point. \\
Right-click and select Set Color from the \\
context menu and specify the color you want \\
to use.
\end{tabular} \\
\hline \begin{tabular}{l} 
Retrieving the \\
coordinates of the \\
point.
\end{tabular} & \begin{tabular}{l} 
Move the mouse pointer over the point. \\
Right-click and select Copy Position from \\
the context menu to copy a 1-by-2 array to the \\
llipboard specifying the coordinates of the \\
point [X Y].
\end{tabular} \\
\hline
\end{tabular}

\section*{impoint}

\section*{Methods}

The following lists the methods supported by the impoint object. Type methods impoint to see a complete list of all the methods.
addNewPositionCallback - Add new-position callback to ROI object
See imroi for information.
delete - Delete ROI object
See imroi for information.

\section*{getColor - Get color used to draw ROI object}

See imroi for information.

\section*{getPosition - Return current position of point}
pos \(=\) getPosition( \(h\) ) returns the current position of the point \(h\). The returned position, pos, is a two-element vector [x y].
getPositionConstraintFcn - Return function handle to current position constraint function
See imroi for information.

\section*{removeNewPositionCallback - Remove new-position callback from ROI object.}

See imroi for information.
resume - Resume execution of MATLAB command line
See imroi for information.
setColor - Set color used to draw ROI object
See imroi for information.
setConstrainedPosition - Set ROI object to new position
See imroi for information.
setPosition - Set point to new position
setPosition(h,pos) sets the pointh to a new position. The new position, pos, has the form, \([\mathrm{x} y]\).
setPosition(h, new_x, new_y) sets the point \(h\) to a new position. new_x and new_y are both scalars that together specify the position of the point.

\section*{setPositionConstraintFen - Set position constraint function of ROI object.}

See imroi for information.

\section*{setString - Set text label for point}
setString (h,s) sets a text label for the point \(h\). The string, \(s\), is placed to the lower right of the point.
wait - Block MATLAB command line until ROI creation is finished
See imroi for information.

\section*{Tips}

\section*{Examples Example 1}

Use impoint methods to set custom color, set a label, enforce a boundary constraint, and update position in title as point moves.
```

figure, imshow rice.png
h = impoint(gca, 100, 200);
% Update position in title using newPositionCallback
addNewPositionCallback(h,@(h) title(sprintf('(%1.Of,%1.0f)',h(1),h(2))));
% Construct boundary constraint function
fcn = makeConstrainToRectFcn('impoint',get(gca,'XLim'),get(gca,'YLim'));
% Enforce boundary constraint function using setPositionConstraintFen
setPositionConstraintFcn(h,fcn);
setColor(h,'r');
setString(h,'Point label');

```

\section*{Example 2}

Interactively place a point. Use wait to block the MATLAB command line. Double-click on the point to resume execution of the MATLAB command line.
```

figure, imshow('pout.tif');

```

\section*{impoint}
```

p = impoint(gca,[]);
p = wait(p);

```

See Also
imellipse | imfreehand | imline | impoly | imrect | imroi | makeConstrainToRectFcn

\section*{Purpose Create draggable, resizable polygon}

Syntax
h = impoly
h = impoly(hparent)
h = impoly(hparent, position)
h = impoly(..., param1, val1, ...)
\(\mathrm{h}=\) impoly begins interactive placement of a polygon on the current axes. The function returns h , a handle to an impoly object. The polygon has a context menu associated with it that controls aspects of its appearance and behavior-see "Interactive Behavior" on page 3-478. Right-click on the polygon to access this context menu.
\(\mathrm{h}=\) impoly(hparent) begins interactive placement of a polygon on the object specified by hparent. hparent specifies the HG parent of the polygon graphics, which is typically an axes but can also be any other object that can be the parent of an hggroup.
h = impoly(hparent, position) creates a draggable, resizable polygon on the object specified by hparent. position is an \(n\)-by- 2 array that specifies the initial position of the vertices of the polygon. position has the form [ \(\mathrm{X} 1, \mathrm{Y} 1 ; \ldots ; \mathrm{XN}, \mathrm{YN}\) ].
h = impoly(..., param1, val1, ...) creates a draggable, resizable polygon, specifying parameters and corresponding values that control the behavior of the polygon. The following table lists available parameters. Parameter names can be abbreviated, and case does not matter.
\begin{tabular}{l|l}
\hline Parameter & Description \\
\hline 'Closed ' & \begin{tabular}{l} 
Scalar logical that controls whether the \\
polygon is closed. When set to true \\
(the default), impoly creates a closed \\
polygon, that is, it draws a straight line \\
between the last vertex specified and the \\
first vertex specified to create a closed \\
region. When Closed is false, impoly \\
does not connect the last vertex with the \\
first vertex, creating an open polygon (or \\
polyline).
\end{tabular} \\
\hline 'PositionConstraintFcn & \begin{tabular}{l} 
Function handle fcn that is called \\
whenever the object is dragged using \\
the mouse. You can use this function to \\
control where the line can be dragged. See \\
the help for the setPositionConstraintFcn \\
method for information about valid \\
function handles.
\end{tabular} \\
\hline
\end{tabular}

\section*{Interactive Behavior}

When you call impoly with an interactive syntax, the pointer changes to a cross hairs \(+_{\text {when over the image. Click and drag the mouse }}\) to define the vertices of the polygon and adjust the size, shape, and position of the polygon. The polygon also supports a context menu that you can use to control aspects of its appearance and behavior. The choices in the context menu vary whether you position the pointer on an edge of the polygon (or anywhere inside the region) or on one of the vertices. The following figure shows a polygon being created.


The following table lists the interactive behaviors supported by impoly.
\begin{tabular}{|l|l|}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} \\
\hline Closing the polygon. \\
\hline
\end{tabular}

\section*{Description}

Use any of the following mechanisms:
- Move the pointer over the initial vertex of the polygon that you selected. The pointer changes to a circle \(\bigcirc\). Click either mouse button.
- Double-click the left mouse button. This action creates a vertex at the point under the mouse and draws a straight line connecting this vertex with the initial vertex.
- Click the right mouse button. This action draws a line connecting the last vertex
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} & Description \\
\hline & \begin{tabular}{l} 
selected with the initial vertex; it does not \\
create a new vertex.
\end{tabular} \\
\hline Adding a new vertex. & \begin{tabular}{l} 
Move the pointer over an edge of the polygon \\
and press the A key. The shape of the pointer \\
changes \(\uparrow\). Click the left mouse button to \\
create a new vertex at that position on the \\
line.
\end{tabular} \\
\hline \begin{tabular}{l} 
Moving a vertex. \\
(Reshaping the \\
polygon.)
\end{tabular} & \begin{tabular}{l} 
Move the pointer over a vertex. The pointer \\
changes to a circle \(\bigcirc\). Click and drag the \\
vertex to its new position.
\end{tabular} \\
\hline Deleting a vertex. & \begin{tabular}{l} 
Move the pointer over a vertex. The shape \\
changes to a circle \(\bigcirc\). Right-click and select \\
Delete Vertex from the vertex context menu. \\
This action deletes the vertex and adjusts \\
the shape of the polygon, drawing a new \\
straight line between the two vertices that \\
were neighbors of the deleted vertex.
\end{tabular} \\
\hline Moving the polygon. & \begin{tabular}{l} 
Move the pointer inside the polygon. The \\
pointer changes to a fleur shape \(\ddagger \mathbf{~}\) \\
and drag the mouse to move the polygon.
\end{tabular} \\
\hline \begin{tabular}{l} 
Changing the color of
\end{tabular} \\
the polygon & \begin{tabular}{l} 
Move the pointer inside the polygon. \\
Right-click and select Set Color from the \\
context menu.
\end{tabular} \\
\hline \begin{tabular}{l} 
Retrieving the \\
coordinates of the \\
vertices
\end{tabular} & \begin{tabular}{l} 
Move the pointer inside the polygon. \\
Right-click and select Copy Position from \\
the context menu. impoly copies an \(n\)-by-2 \\
array containing the \(x\) - and \(y\)-coordinates of \\
each vertex to the clipboard. \(n\) is the number \\
of vertices you specified.
\end{tabular} \\
\hline
\end{tabular}

\section*{Methods}

Each impoly object supports a number of methods, listed below. Methods inherited from the base class are links to that class.
addNewPositionCallback - Add new-position callback to ROI object
See imroi for information.
createMask - Create mask within image
See imroi for information.

\section*{delete - Delete ROI object}

See imroi for information.

\section*{getColor - Get color used to draw ROI object}

See imroi for information.

\section*{getPosition - Return current position of polygon}
pos \(=\) getPosition( \(h\) ) returns the current position of the polygon \(h\). The returned position, pos, is an N-by-2 array [ \(\mathrm{X} 1 \mathrm{Y} 1 ; \ldots\); XN YN].
getPositionConstraintFen - Return function handle to current position constraint function
See imroi for information.
removeNewPositionCallback - Remove new-position callback from ROI object.
See imroi for information.
resume - Resume execution of MATLAB command line
See imroi for information.
setClosed - Set geometry of polygon
setClosed (TF) sets the geometry of the polygon. TF is a logical scalar. true means that the polygon is closed. false means that the polygon is an open polyline.
setColor - Set color used to draw ROI object
See imroi for information.
setConstrainedPosition - Set ROI object to new position
See imroi for information.

\section*{setPosition - Set polygon to new position}
setPosition(h,pos) sets the polygon \(h\) to a new position. The new position, pos, is an \(n\)-by- 2 array, [x1 y1; ..; xn yn] where each row specifies the position of a vertex of the polygon.

\section*{setPositionConstraintFcn - Set position constraint function of ROI object.}

See imroi for information.

\section*{setVerticesDraggable - Control whether vertices may be dragged}
setVerticesDraggable(h,TF) sets the interactive behavior of the vertices of the polygon \(h\). TF is a logical scalar. True means that the vertices of the polygon are draggable. False means that the vertices of the polygon are not draggable.
wait - Block MATLAB command line until ROI creation is finished
See imroi for information.

Tips

\section*{Examples}

If you use impoly with an axes that contains an image object, and do not specify a position constraint function, users can drag the polygon outside the extent of the image and lose the polygon. When used with an axes created by the plot function, the axes limits automatically expand when the polygon is dragged outside the extent of the axes.

\section*{Example 1}

Display updated position in the title. Specify a position constraint function using makeConstrainToRectFen to keep the polygon inside the original xlim and ylim ranges.
```

figure, imshow('gantrycrane.png');
h = impoly(gca, [188,30; 189,142; 93,141; 13,41; 14,29]);
setColor(h, 'yellow');
addNewPositionCallback(h,@(p) title(mat2str(p,3)));
fcn = makeConstrainToRectFcn('impoly',get(gca,'XLim'),...
get(gca,'YLim'));
setPositionConstraintFcn(h,fcn);

```

\section*{Example 2}

Interactively place a polygon by clicking to specify vertex locations. Double-click or right-click to finish positioning the polygon. Use wait to block the MATLAB command line. Double-click on the polygon to resume execution of the MATLAB command line.
figure, imshow('pout.tif');
h = impoly;
position = wait(h);

\section*{See also}
imellipse, imfreehand, imline, impoint, imrect, imroi, makeConstrainToRectFcn

\section*{impositionrect}
\begin{tabular}{ll} 
Purpose & Create draggable position rectangle \\
Syntax & \(H=\) impositionrect (hparent, position)
\end{tabular}

Note This function is obsolete and may be removed in future versions. Use imrect instead.

\section*{Description}

Tips

API
Function
Syntaxes

H = impositionrect(hparent, position) creates a position rectangle on the object specified by hparent. The function returns H , a handle to the position rectangle, which is an hggroup object. hparent specifies the hggroup's parent, which is typically an axes object, but can also be any other object that can be the parent of an hggroup. position is a four-element position vector that specifies the initial location of the rectangle. position has the form [XMIN YMIN WIDTH HEIGHT].

All measurements are in units specified by the Units property axes object.When you do not specify the position argument, impositionrect uses [ \(\left.\begin{array}{llll}0 & 0 & 1 & 1\end{array}\right]\) as the default value.

A position rectangle can be dragged interactively using the mouse. When the position rectangle occupies a small number of screen pixels, its appearance changes to aid visibility.
The position rectangle has a context menu associated with it that you can use to copy the current position to the clipboard and change the color used to display the rectangle.

A position rectangle contains a structure of function handles, called an API, that can be used to manipulate it. To retrieve this structure from the position rectangle, use the iptgetapi function.

API = iptgetapi(H)
The following lists the functions in the position rectangle API in the order they appear in the API structure.
\begin{tabular}{l|l}
\hline Function & Description \\
\hline setPosition & \begin{tabular}{l} 
Sets the position rectangle to a new position. \\
api.setPosition(new_position) \\
where new_position is a four-element position vector.
\end{tabular} \\
\hline getPosition & \begin{tabular}{l} 
Returns the current position of the position rectangle. \\
position = api.getPosition()
\end{tabular} \\
\hline delete & position is a four-element position vector.
\end{tabular}, \begin{tabular}{l} 
Deletes the position rectangle associated with the API. \\
api.delete()
\end{tabular}, \begin{tabular}{l} 
Sets the color used to draw the position rectangle. \\
api.setColor(new_color) \\
setColor \\
where new_color can be a three-element vector \\
specifying an RGB triplet, or a text string specifying \\
the long or short names of a predefined color, such as \\
'white' or 'w . For a complete list of these predefined \\
colors and their short names, see ColorSpec.
\end{tabular}

\section*{impositionrect}
\begin{tabular}{l|l}
\hline Function & Description \\
\hline & \begin{tabular}{l} 
The return value, id, is used only with \\
removeNewPositionCallback.
\end{tabular} \\
\hline removeNewPositionCallback & \begin{tabular}{l} 
Removes the corresponding function from the \\
new-position callback list.
\end{tabular} \\
& api.removeNewPositionCallback(id) \\
setDragConstraintCallback & \begin{tabular}{l} 
where id is the identifier returned by \\
api.addNewPositionCallback
\end{tabular} \\
\hline & \begin{tabular}{l} 
Sets the drag constraint function to be the specified \\
function handle, fcn.
\end{tabular} \\
api.setDragConstraintCallback(fcn) \\
& \begin{tabular}{l} 
Whenever the position rectangle is moved because of \\
a mouse drag, the constraint function is called using \\
the syntax: \\
constrained_position = fcn(new_position) \\
anere new_position is a four-element position vector.
\end{tabular} \\
\hline
\end{tabular}

Examples Display in the command window the updated position of the position rectangle as it moves in the axes.
close all, plot(1:10)
h = impositionrect(gca, [4 4 2 2]);
api = iptgetapi(h);
api.addNewPositionCallback(@(p) disp(p));
Constrain the position rectangle to move only up and down.
```

close all, plot(1:10)
h = impositionrect(gca, [4 4 2 2]);
api = getappdata(h, 'API');
api.setDragConstraintCallback(@(p) [4 p(2:4)]);

```

Specify the color of the position rectangle.
```

close all, plot(1:10)
h = impositionrect(gca, [4 4 2 2]);
api = iptgetapi(h, 'API');
api.setColor([1 0 0]);

```

When the position rectangle occupies only a few pixels on the screen, the rectangle is drawn in a different style to increase its visibility.
close all, imshow cameraman.tif h = impositionrect(gca, [100 100 10 10]);

\section*{See Also iptgetapi}

Purpose Pixel-value cross-sections along line segments
```

Syntax $\quad c=$ improfile
c = improfile(n)
c = improfile(I,xi,yi)
c = improfile(I, xi,yi,n)
[cx,cy,c] = improfile(...)
[cx,cy,c,xi,yi] = improfile(...)
[...] = improfile(x,y,I,xi,yi)
[...] = improfile(x,y,I,xi,yi,n)
[...] = improfile(..., method)

```

\section*{Description}
improfile computes the intensity values along a line or a multiline path in an image. improfile selects equally spaced points along the path you specify, and then uses interpolation to find the intensity value for each point. improfile works with grayscale images and RGB images.

If you call improfile with one of these syntax, it operates interactively on the image in the current axes.
c = improfile
c = improfile(n)
n specifies the number of points to compute the intensity value for. If you do not provide this argument, improfile chooses a value for \(n\), roughly equal to the number of pixels the path traverses.

You specify the line or path using the mouse, by clicking points in the image. Press Backspace or Delete to remove the previously selected point. A shift-click, right-click, or double-click adds a final point and ends the selection; pressing Return finishes the selection without adding a point. When you finish selecting points, improfile returns the interpolated data values in c. c is an n-by- 1 vector if the input is
a grayscale intensity image, or an n-by-1-by-3 array if the input is an RGB image.
If you omit the output argument, improfile displays a plot of the computed intensity values. If the specified path consists of a single line segment, improfile creates a two-dimensional plot of intensity values versus the distance along the line segment; if the path consists of two or more line segments, improfile creates a three-dimensional plot of the intensity values versus their \(x\) - and \(y\)-coordinates.
You can also specify the path non-interactively, using these syntax.
c = improfile(I,xi,yi)
c = improfile(I,xi,yi,n)
xi and yi are equal-length vectors specifying the spatial coordinates of the endpoints of the line segments.

You can use these syntax to return additional information.
[cx,cy,c] = improfile(...)
[cx,cy,c,xi,yi] = improfile(...)
cx and cy are vectors of length \(n\), containing the spatial coordinates of the points at which the intensity values are computed.

To specify a non-default spatial coordinate system for the input image, use these syntax.
[...] = improfile(x,y,I,xi,yi)
[...] = improfile(x,y, \(\mathrm{I}, \mathrm{xi}, \mathrm{yi}, \mathrm{n})\)
\(x\) and \(y\) are two-element vectors specifying the image XData and YData.
[...] = improfile (..., method) uses the specified interpolation method. method is a string that can have one of these values. The default value is enclosed in braces (\{\}).
\begin{tabular}{l|l}
\hline Value & Description \\
\hline \{'nearest' \(\}\) & Nearest-neighbor interpolation \\
\hline 'bilinear' & Bilinear interpolation \\
\hline 'bicubic' & Bicubic interpolation \\
\hline
\end{tabular}

\section*{Class} Support

\section*{Examples}

The input image can be uint8, uint16, int16, single, double, or logical. All other inputs and outputs must be double.
```

I = imread('liftingbody.png');
x = [19 427 416 77];
y = [96 462 37 33];
improfile(I,x,y),grid on;

```


\section*{See Also}
impixel | interp2

\section*{Purpose}

Display Save Image dialog box

\section*{Syntax}

Description
[filename, ext, user_canceled] = imputfile
[filename, ext, user_canceled] = imputfile displays the Save Image dialog box (shown below) which you can use to specify the full path and format of a file. Using the dialog box, you can navigate to folders in a file system and select a particular file or specify the name of a new file. imputfile limits the types of files displayed in the dialog box to the image file format selected in the Files of Type menu.


When you click Save, imputfile returns the full path to the file in filenameand the file type selected from the Files of Type menu in ext. imputfile does not automatically add a file name extension (such as . jpg) to the file name.

\section*{imputfile}

If the user clicks Cancel or closes the Save Image dialog box, imputfile returns, setting user_canceled to True (1), and settingfilename and ext to empty strings; otherwise, user_canceled is False (0).

Note The Save Image dialog box is modal; it blocks the MATLAB command line until you click Save or cancel the operation.

\author{
See Also \\ imformats | imtool | imgetfile | imsave
}

\section*{Purpose Image pyramid reduction and expansion}
\[
\text { Syntax } \quad B=\text { impyramid }(A \text {, direction })
\]

Description

\section*{Class \\ support}

Examples
\(B=\) impyramid(A, direction) computes a Gaussian pyramid reduction or expansion of \(A\) by one level. direction can be 'reduce' or 'expand'.

If \(A\) is m-by-n and direction is 'reduce', then the size of \(B\) is ceil(M/2)-by-ceil(N/2). If direction is 'expand', then the size of \(B\) is \((2 * M-1)-\) by \(-(2 * N-1)\).

Reduction and expansion take place only in the first two dimensions. For example, if A is 100 -by-100-by-3 and direction is 'reduce', then \(B\) is 50 -by- 50 -by- 3 .

Note that impyramid uses the kernel specified on page 533 of the Burt and Adelson paper cited below:
\(w=\left[\frac{1}{4}-\frac{a}{2}, \frac{1}{4}, a, \frac{1}{4}, \frac{1}{4}-\frac{a}{2}\right]\), where \(a=0.375\).

The parameter \(a\) is chosen to be 0.375 so that the equivalent weighting function is close to a Gaussian shape and the weights can be readily applied using fixed-point arithmetic.

A can be any numeric class except uint64 or int64, or it can be logical. The class of \(B\) is the same as the class of \(A\).

Compute a four-level multiresolution pyramid of the cameraman image.
```

IO = imread('cameraman.tif');
I1 = impyramid(IO, 'reduce');
I2 = impyramid(I1, 'reduce');
I3 = impyramid(I2, 'reduce');

```
imshow(IO)

\section*{impyramid}
```

figure, imshow(I1)
figure, imshow(I2)
figure, imshow(I3)

```

\section*{References [1] Burt and Adelson, "The Laplacian Pyramid as a Compact Image Code," IEEE Transactions on Communications, vol. COM-31, no. 4, April 1983, pp. 532-540.}
[2] Burt, "Fast Filter Transforms for Image Processing," Computer Graphics and Image Processing, vol. 16, 1981, pp. 20-51

\section*{See Also \\ imresize}

\section*{Purpose}

Quantize image using specified quantization levels and output values

\section*{Syntax}
quant_A = imquantize(A, levels) quant_A = imquantize( \(\qquad\) ,values)
[quant_A,index] = imquantize( __ )

\section*{Description}
quant_A = imquantize( \(A\), levels) quantizes image \(A\) using specified quantization values contained in the \(N\) element vector levels. Output image quant_A is the same size as A and contains \(\mathrm{N}+1\) discrete integer values in the range 1 to \(N+1\) which are determined by the following criteria:
- If \(A(k) \leq\) levels \((1)\), then quant_A \((k)=1\).
- If levels \((m-1)<A(k) \leq \operatorname{levels}(m)\), then quant_A \((k)=m\).
- If \(A(k)>\operatorname{levels}(N)\), then quant_A( \(k)=N+1\).

Note that imquantize assigns values to the two implicitly defined end intervals:
- \(A(k) \leq\) levels \((1)\)
- \(A(k)>\operatorname{levels}(N)\)
quant_A = imquantize( __ , values) adds the \(N+1\) element vector values where \(N=\) length(levels). Each of the \(N+1\) elements of values specify the quantization value for one of the \(N+1\) discrete pixel values in quant_A.
- If \(A(k) \leq\) levels \((1)\), then quant_A \((k)=\operatorname{values}(1)\).
- If levels \((m-1)<A(k) \leq \operatorname{levels}(m)\), then quant_A \((k)=\operatorname{values}(m)\).
- If \(A(k)>\operatorname{levels}(N)\), then quant_ \(A(k)=\operatorname{values}(N+1)\).
[quant_A,index] = imquantize( __ ) returns matrix index such that:
```

quant_A = values(index)

```

\section*{imquantize}

\section*{Input Arguments}

\section*{Output Arguments}

\section*{A - Input image}

\section*{image}

Input image, specified as a numeric array of any dimension.
```

Data Types
single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32
| uint64

```

\section*{levels - Quantization levels}
vector
Quantization levels, specified as an \(N\) element vector. Values of the discrete quantization levels must be in monotonically increasing order.
```

Data Types
single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32
| uint64

```

\section*{values - Quantization values}
vector
Quantization values, specified as an \(N+1\) element vector.
```

Data Types
single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32
| uint64

```

\section*{quant_A - Quantized output image}
image
Quantized output image, returned as a numeric array the same size as \(A\). If input argument values is specified, then quant_ \(A\) is the same data type as values. If values is not specified, then quant_ \(A\) is of class double.

\section*{index - Mapping matrix}
matrix
Mapping matrix, returned as a matrix the same size as input image \(A\). It contains integer indices which access values to construct the
output image: quant_A = values(index). If input argument values is not defined, then index = quant_A.

\section*{Data Types}
double

\section*{Examples Image Threshold}

Compute multiple thresholds for an image using multithresh and apply those thresholds to the image using imquantize to get segment labels.
```

I = imread('circlesBrightDark.png');

```

Computing two thresholds will quantize the image into three discrete levels
```

thresh = multithresh(I,2);
seg_I = imquantize(I,thresh); % apply the thresholds to obtain segmer
RGB = label2rgb(seg_I); % convert to color image
figure;
imshowpair(I,RGB,'montage'); % display images side-by-side
axis off;
title('Original Image RGB Segmented Imas

```

\section*{imquantize}

Original Image


\section*{Two Schemes for RGB Image Quantization}

Quantize truecolor RGB image to 8 levels using multi-level thresholding function multithresh. Compare results between thresholding the entire RGB image versus plane-by-plane thresholding.

Read in truecolor RGB image.

\section*{imquantize}
```

I = imread('peppers.png');
imshow(I); axis off;
title('RGB Image');

```

RGB Image


\section*{imquantize}

Generate thresholds for seven levels from the entire RGB image. then repeat process for each plane in the RGB image.
```

threshRGB = multithresh(I,7) % 7 thresholds from entire RGB image
threshPlanes = zeros(3,7); % initialize
% Compute thresholds for each R, G and B plane
for i = 1:3
threshPlane(i,:) = multithresh(I(:,:,i),7);
end
threshPlane
threshRGB =
24
threshPlane =

| 40 | 69 | 92 | 125 | 159 | 195 | 231 |
| ---: | ---: | ---: | ---: | ---: | ---: | ---: |
| 27 | 49 | 74 | 100 | 128 | 164 | 209 |
| 18 | 38 | 60 | 86 | 127 | 165 | 222 |

```

Process entire image with set of threshold values computed from entire image. Similarly, process each RGB plane separately using threshold vector computed from the given plane. Add black (0) and white (255) to value vector which assigns values to output image.
```

value = [O threshRGB(2:end) 255];
% Quantize entire image using one threshold vector
quantRGB = imquantize(I, threshRGB, value);
quantPlane = zeros( size(I) );
% Quantize each RGB plane using threshold vector generated for that plane
for i = 1:3
value = [0 threshPlane(i,2:end) 255] % output value to assign
quantPlane(:,:,i) = imquantize(I(:,:,i),threshPlane(i,:),value);
end

```

\section*{imquantize}
```

quantPlane = uint8(quantPlane); % convert from double to uint8

```

Display both posterized images and note the visual differences in the two thresholding schemes.

\section*{Full RGB Image Quantization}


The following code snippet computes the number of unique RGB pixel vectors in each output image. Note that the plane-by-plane thresholding scheme yields about \(23 \%\) more colors than the full RGB image scheme.

\section*{imquantize}
```

% convert images to mx3 matrices
dim = size( quantRGB );
quantRGBmx3 = reshape(quantRGB, prod(dim(1:2)), 3);
quantPlanemx3 = reshape(quantPlane, prod(dim(1:2)), 3);
% extract only unique 3 element RGB pixel vectors from each matrix
colorsRGB = unique( quantRGBmx3, 'rows' );
colorsPlane = unique( quantPlanemx3, 'rows' );
disp(['Number of unique colors in RGB image : ' int2str(length
disp(['Number of unique colors in Plane-by-Plane image : ' int2str(lengtr
Number of unique colors in RGB image : 188
Number of unique colors in Plane-by-Plane image : 231

```

\section*{Threshold a Grayscale Image from \(\mathbf{2 5 6}\) to \(\mathbf{8}\) levels}

This example reduces the number of discrete levels in an image from 256 to 8 . It then demonstrates two different schemes for assigning values to each of the eight output levels.
```

I = imread('coins.png');
imshow(I); axis off;
title('Grayscale Image');

```

\section*{imquantize}


Obtain seven thresholds from multithresh to split the image into eight levels.
```

thresh = multithresh(I,7); % 7 thresholds result in 8 image levels

```

Construct the valuesMax vector such that the maximum value in each quantization interval is assigned to the eight levels of the output image.
```

valuesMax = [thresh max(I(:))]
[quant8_I_max,index] = imquantize(I,thresh,valuesMax);
valuesMax =
65

```

\section*{imquantize}

Similarly, construct valuesMin such that the minimum value in each quantization interval is assigned to the eight levels of the output image valuesMin = [min(I(:)) thresh] valuesMin =
\begin{tabular}{llllllll}
23 & 65 & 88 & 119 & 149 & 169 & 189 & 215
\end{tabular}

Instead of calling imquantize again with the vector valuesMin, use the output argument index to assign those values to the output image.
quant8_I_min = valuesMin(index);

Display both eight-level output images side by side.


See Also multithresh | label2rgb | rgb2ind

\section*{imreconstruct}
\begin{tabular}{ll} 
Purpose & Morphological reconstruction \\
Syntax & IM \(=\) imreconstruct (marker, mask) \\
& IM \(=\) imreconstruct (marker, mask, conn)
\end{tabular}

Description IM = imreconstruct(marker, mask) performs morphological reconstruction of the image marker under the image mask. marker and mask can be two intensity images or two binary images with the same size. The returned image IM is an intensity or binary image, respectively. marker must be the same size as mask, and its elements must be less than or equal to the corresponding elements of mask.

By default, imreconstruct uses 8 -connected neighborhoods for 2-D images and 26 -connected neighborhoods for 3-D images. For higher dimensions, imreconstruct uses conndef(ndims(I), 'maximal').

IM = imreconstruct(marker,mask,conn) performs morphological reconstruction with the specified connectivity. conn can have any of the following scalar values.
\begin{tabular}{l|l}
\hline Value & Meaning \\
\hline \multicolumn{1}{|c}{ Two-dimensional connectivities } \\
\hline 4 & 4 -connected neighborhood \\
\hline 8 & 8 -connected neighborhood \\
\hline \multicolumn{2}{|c}{ Three-dimensional connectivities } \\
\hline 6 & 6 -connected neighborhood \\
\hline 18 & 18 -connected neighborhood \\
\hline 26 & 26 -connected neighborhood \\
\hline
\end{tabular}

Connectivity can be defined in a more general way for any dimension by using for conn a 3 -by- 3 -by- ... -by- 3 matrix of 0's and 1's. The 1 -valued elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

Morphological reconstruction is the algorithmic basis for several other Image Processing Toolbox functions, including imclearborder, imextendedmax, imextendedmin, imfill, imhmax, imhmin, and imimposemin.

\section*{Class \\ Support}

\section*{Performance Note}

\section*{Algorithms}

\section*{References}

See Also
marker and mask must be nonsparse numeric (including uint64 or int64) or logical arrays with the same class and any dimension. IM is of the same class as marker and mask.

This function may take advantage of hardware optimization for data types logical, uint8, and single to run faster. Hardware optimization requires marker and mask to be 2-D images and conn to be either 4 or 8 .
imreconstruct uses the fast hybrid grayscale reconstruction algorithm described in [1].
[1] Vincent, L., "Morphological Grayscale Reconstruction in Image Analysis: Applications and Efficient Algorithms," IEEE Transactions on Image Processing, Vol. 2, No. 2, April, 1993, pp. 176-201.
imclearborder | imextendedmax | imextendedmin | imfill | imhmax | imhmin | imimposemin

\section*{imrect}

Purpose Create draggable rectangle
Syntax \(\quad\)\begin{tabular}{rl}
\(H\) & \(=\operatorname{imrect}\) \\
\(h\) & \(=\operatorname{imrect}(\) hparent \()\) \\
\(h\) & \(=\operatorname{imrect}(\) hparent, position \()\) \\
& \(H\)
\end{tabular}

Description
H = imrect begins interactive placement of a rectangle on the current axes. The function returns h , a handle to an imrect object. The rectangle has a context menu associated with it that controls aspects of its appearance and behavior-see "Interactive Behavior" on page 3-509. Right-click on the rectangle to access this context menu.
\(\mathrm{h}=\) imrect(hparent) begins interactive placement of a rectangle on the object specified by hparent. hparent specifies the HG parent of the rectangle graphics, which is typically an axes but can also be any other object that can be the parent of an hggroup.
h = imrect(hparent, position) creates a draggable rectangle on the object specified by hparent. position is a four-element vector that specifies the initial size and location of the rectangle. position has the form [xmin ymin width height].

H = imrect(..., param1, val1,...) creates a draggable rectangle, specifying parameters and corresponding values that control the behavior of the rectangle. The following table lists the parameter available. Parameter names can be abbreviated, and case does not matter.
\begin{tabular}{l|l}
\hline Parameter & Description \\
\hline 'PositionConstraintFcn & \begin{tabular}{l} 
Function handle fon that is called \\
whenever the mouse is dragged. You can \\
use this function to control where the \\
rectangle can be dragged. See the help for \\
the setPositionConstraintFcn method for \\
information about valid function handles.
\end{tabular} \\
\hline
\end{tabular}

\section*{Interactive Behavior}

When you call imrect with an interactive syntax, the pointer changes to a cross hairs \(+_{\text {when over the image. You can create the rectangle }}\) and adjust its size and position using the mouse. The rectangle also supports a context menu that you can use to control aspects of its appearance and behavior. The following figure shows the rectangle.

Draggable, resizable, rectangle


The following table lists the interactive behaviors supported by imrect.
\(\left.\left.\begin{array}{l|l}\hline \begin{array}{l}\text { Interactive } \\ \text { Behavior }\end{array} & \text { Description } \\ \hline \begin{array}{l}\text { Moving the } \\ \text { rectangle. }\end{array} & \begin{array}{l}\text { Move the pointer inside the rectangle. The } \\ \text { pointer changes to a fleur shape } \\ \text { and drag the mouse to move the rectangle. }\end{array} \vec{\leftrightarrows} \text {. Click }\end{array}\right] . \begin{array}{l}\text { Move the pointer over any of the edges or } \\ \text { corners of the rectangle, the shape changes to } \\ \text { a double-ended arrow, } \leftrightarrows \text {. Click and drag } \\ \text { the edge or corner using the mouse. }\end{array}\right\}\)

\section*{imrect}
\begin{tabular}{l|l}
\hline \begin{tabular}{l} 
Interactive \\
Behavior
\end{tabular} & Description \\
\hline \begin{tabular}{l} 
Retrieving the \\
coordinates of the \\
current position
\end{tabular} & \begin{tabular}{l} 
Move the pointer inside the polygon. \\
Right-click and select Copy Position \\
from the context menu. imrect copies a \\
four-element position vector to the clipboard.
\end{tabular} \\
\hline \begin{tabular}{l} 
Preserve the current \\
aspect ratio of the \\
rectangle during \\
interactive resizing.
\end{tabular} & \begin{tabular}{l} 
Move the pointer inside the rectangle. \\
Right-click and select Fix Aspect Ratio from \\
the context menu.
\end{tabular} \\
\hline
\end{tabular}

\section*{Methods}

Each imrect object supports a number of methods, listed below. Type methods imrect to see a list of the methods.

\section*{addNewPositionCallback - Add new-position callback to ROI object}

See imroi for information.

\section*{createMask - Create mask within image}

See imroi for information.

\section*{delete - Delete ROI object}

See imroi for information.

\section*{getColor - Get color used to draw ROI object}

See imroi for information.

\section*{getPosition - Return current position of rectangle}
pos \(=\) getPosition(h) returns the current position of the rectangle h. The returned position, pos, is a 1-by-4 array [xmin ymin width height].

\section*{getPositionConstraintFen - Return function handle to current position constraint function}

See imroi for information.

\section*{removeNewPositionCallback - Remove new-position callback from ROI object.}

See imroi for information.

\section*{resume - Resume execution of MATLAB command line}

See imroi for information.

\section*{setColor - Set color used to draw ROI object}

See imroi for information.

\section*{setConstrainedPosition - Set ROI object to new position}

See imroi for information.

\section*{setFixedAspectRatioMode - Control whether aspect ratio preserved during resize}
setFixedAspectRatioMode(h,TF) sets the interactive resize behavior of the rectangle \(h\). TF is a logical scalar. True means that the current aspect ratio is preserved during interactive resizing. False means that interactive resizing is not constrained.
setPosition - Set rectangle to new position
setPosition(h, pos) sets the rectangle \(h\) to a new position. The new position, pos, has the form [xmin ymin width height].
setPositionConstraintFen - Set position constraint function of ROI object
See imroi for information.
setResizable - Set resize behavior of rectangle
setResizable ( \(\mathrm{h}, \mathrm{TF}\) ) sets whether the rectangle \(h\) may be resized interactively. TF is a logical scalar.
wait - Block MATLAB command line until ROI creation is finished See imroi for information.

If you use imrect with an axes that contains an image object, and do not specify a position constraint function, users can drag the rectangle outside the extent of the image. When used with an axes created by the plot function, the axes limits automatically expand to accommodate the movement of the rectangle.

When the API function setResizable is used to make the rectangle non-resizable, the Fix Aspect Ratio context menu item is not provided.

\section*{imrect}

\section*{Examples Example 1}

Display updated position in the title. Specify a position constraint function using makeConstrainToRectFcn to keep the rectangle inside the original Xlim and Ylim ranges.
```

figure, imshow('cameraman.tif');
h = imrect(gca, [10 10 100 100]);
addNewPositionCallback(h,@(p) title(mat2str(p,3)));
fcn = makeConstrainToRectFcn('imrect',get(gca,'XLim'),get(gca,'YLim'));
setPositionConstraintFcn(h,fcn);

```

Now drag the rectangle using the mouse.

\section*{Example 2}

Interactively place a rectangle by clicking and dragging. Use wait to block the MATLAB command line. Double-click on the rectangle to resume execution of the MATLAB command line.
figure, imshow('pout.tif');
h = imrect;
position = wait(h);

\author{
See Also imellipse | imfreehand | imline | impoint | impoly | imroi | makeConstrainToRectFcn
}

\section*{Purpose Regional maxima}

Syntax \(\quad\) BW \(=\) imregionalmax(I)
BW = imregionalmax(I,conn)
Description
\(B W=\) imregionalmax(I) finds the regional maxima of \(I\).
imregionalmax returns the binary image BW that identifies the locations of the regional maxima in I. BW is the same size as I. In BW, pixels that are set to 1 identify regional maxima; all other pixels are set to 0 .

Regional maxima are connected components of pixels with a constant intensity value, and whose external boundary pixels all have a lower value.

By default, imregionalmax uses 8-connected neighborhoods for 2-D images and 26 -connected neighborhoods for 3-D images. For higher dimensions, imregionalmax uses conndef(ndims(I), 'maximal').
BW = imregionalmax(I, conn) computes the regional maxima of I using the specified connectivity. conn can have any of the following scalar values.
\begin{tabular}{l|l}
\hline Value & Meaning \\
\hline \multicolumn{2}{l}{ Two-dimensional connectivities } \\
\hline 4 & 4 -connected neighborhood \\
\hline 8 & 8 -connected neighborhood \\
\hline Three-dimensional connectivities \\
\hline 6 & 6 -connected neighborhood \\
\hline 18 & 18 -connected neighborhood \\
\hline 26 & 26 -connected neighborhood \\
\hline
\end{tabular}

Connectivity can be defined in a more general way for any dimension by using for conn a 3 -by-3-by- ...-by-3 matrix of 0's and 1's. The 1 -valued

\section*{imregionalmax}
elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

\section*{Class Support}

I can be any nonsparse, numeric class and any dimension. BW is logical.

Examples Create a sample image with several regional maxima.
```

A = 10*ones(10,10);
A(2:4,2:4) = 22;
A(6:8,6:8) = 33;
A(2,7) = 44;
A(3,8) = 45;
A(4,9) = 44;
A =

| 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| 10 | 22 | 22 | 22 | 10 | 10 | 44 | 10 | 10 | 10 |
| 10 | 22 | 22 | 22 | 10 | 10 | 10 | 45 | 10 | 10 |
| 10 | 22 | 22 | 22 | 10 | 10 | 10 | 10 | 44 | 10 |
| 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| 10 | 10 | 10 | 10 | 10 | 33 | 33 | 33 | 10 | 10 |
| 10 | 10 | 10 | 10 | 10 | 33 | 33 | 33 | 10 | 10 |
| 10 | 10 | 10 | 10 | 10 | 33 | 33 | 33 | 10 | 10 |
| 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |

```

Find the regional maxima.
```

regmax = imregionalmax(A)
regmax =

| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 |
| 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 |

```

\section*{imregionalmax}
\begin{tabular}{llllllllll}
0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0
\end{tabular}

See Also
conndef | imextendedmax | imhmax | imreconstruct | imregionalmin

\section*{imregionalmin}

Purpose Regional minima
Syntax \(\quad B W=\) imregionalmin(I)
BW = imregionalmin(I,conn)
Description
BW = imregionalmin(I) computes the regional minima of I. The output binary image BW has value 1 corresponding to the pixels of I that belong to regional minima and 0 otherwise. BW is the same size as I.

Regional minima are connected components of pixels with a constant intensity value, and whose external boundary pixels all have a higher value.

By default, imregionalmin uses 8 -connected neighborhoods for 2-D images and 26 -connected neighborhoods for 3-D images. For higher dimensions, imregionalmin uses conndef(ndims(I), 'maximal').

BW = imregionalmin(I, conn) specifies the desired connectivity. conn can have any of the following scalar values.
\begin{tabular}{l|l}
\hline Value & Meaning \\
\hline Two-dimensional connectivities \\
\hline 4 & 4-connected neighborhood \\
\hline 8 & 8 -connected neighborhood \\
\hline \multicolumn{2}{|l}{ Three-dimensional connectivities } \\
\hline 6 & 6 -connected neighborhood \\
\hline 18 & 18 -connected neighborhood \\
\hline 26 & 26 -connected neighborhood \\
\hline
\end{tabular}

Connectivity can be defined in a more general way for any dimension by using for conn a 3 -by- 3 -by- ...-by-3 matrix of 0's and 1's. The 1 -valued elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

Class
Support
Examples

I can be any nonsparse, numeric class and any dimension. BW is logical.

Create a 10 -by-10 pixel sample image that contains two regional minima.
\begin{tabular}{|c|c|c|c|c|c|c|c|c|c|}
\hline \(\mathrm{A}=10{ }^{*}\) & s(10 & 10) & & & & & & & \\
\hline A(2:4, 2 & \(=\) & & & & & & & & \\
\hline A (6:8,6 & \(=\) & & & & & & & & \\
\hline A \(=\) & & & & & & & & & \\
\hline 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 2 & 2 & 2 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 2 & 2 & 2 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 2 & 2 & 2 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 7 & 7 & 7 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 7 & 7 & 7 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 7 & 7 & 7 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 & 10 \\
\hline
\end{tabular}

Pass the sample image A to imregionalmin. The function returns a binary image, the same size as \(A\), in which pixels with the value 1 represent the regional minima in \(A\). imregionalmin sets all other pixels in to zero ( 0 ).
\(B=\) imregionalmin \((A)\)
\(B=\)
\begin{tabular}{llllllllll}
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0
\end{tabular}

\section*{imregionalmin}
\begin{tabular}{llllllllll}
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0
\end{tabular}

See Also conndef | imextendedmin | imhmin | imimposemin | imreconstruct | imregionalmax

\section*{Purpose Configurations for intensity-based registration}
Description

\section*{Input Arguments}

\section*{Output Arguments}

Tips
```

Syntax
[optimizer,metric] = imregconfig(modality)

```
[optimizer, metric] = imregconfig(modality) creates optimizer and metric configurations that you pass to imregister to perform intensity-based image registration. imregconfig returns optimizer and metric with default settings to provide a basic registration configuration.

\section*{modality - Image capture modality}
'monomodal' | 'multimodal'
Image capture modality describes how your images have been captured, specified as either 'monomodal' (captured on the same device) or 'multimodal' (captured on different devices).

\section*{optimizer - Optimization configuration}
optimizer object
Optimization configuration describes the method for optimizing the similarity metric, returned as one of the optimizer objects, registration.optimizer.RegularStepGradientDescent or registration.optimizer.OnePlusOneEvolutionary

\section*{metric - Metric configuration}
metric object
Metric configuration describes the image similarity metric to be optimized during registration, returned as one of the metric objects, registration.metric.MeanSquares or registration.metric.MattesMutualInformation.
- Your registration results can improve if you adjust the optimizer or metric settings. For example, if you increase the number of iterations in the optimizer, reduce the optimizer step size, or change
the number of samples in a stochastic metric, the registration improves to a point, at the expense of performance.

\section*{Definitions}

\section*{Monomodal}

Images captured on the same device. Monomodal images have similar brightness ranges.

\section*{Multimodal}

Images captured on different devices. Multimodal images usually have different brightness ranges.

\section*{Examples Create Optimizer and Metric Configurations to Register Images Captured on the Same Device}

Load the images into the workspace and display them.
```

fixed = imread('pout.tif');
moving = imrotate(fixed, 5, 'bilinear', 'crop');
imshowpair(fixed, moving,'Scaling','joint');

```


Create the optimizer and metric. The two images in this example were captured on the same device, so we'll set the modality to 'monomodal'.
```

[optimizer, metric] = imregconfig('monomodal')
optimizer =
registration.optimizer.RegularStepGradientDescent
Properties:
GradientMagnitudeTolerance: 1.000000e-04
MinimumStepLength: 1.000000e-05
MaximumStepLength: 6.250000e-02
MaximumIterations: 100
RelaxationFactor: 5.000000e-01

```
metric \(=\)

\section*{imregconfig}
registration.metric.MeanSquares
This class has no properties.
Pass optimizer and metric to imregister to perform the registration.
```

movingRegistered = imregister(moving,fixed,'rigid',optimizer, metric);

```

View the registered images
figure
imshowpair(fixed, movingRegistered,'Scaling','joint');


\section*{See Also}
imshowpair | imregisterregistration.metric.MattesMutualInformation | registration.metric.MeanSquares | registration.optimizer. RegularStepGradientDescent | registration.optimizer.OnePlusOneEvolutionary |

\section*{imregconfig}

\section*{Concepts}

\author{
- "Intensity-Based Automatic Image Registration"
}

\section*{imregister}

Purpose Intensity-based image registration
```

Syntax movingRegistered = imregister(moving,fixed,transformType,
optimizer, metric)
movingRegistered = imregister(moving,fixed,transformType,
optimizer, metric, Name, Value)

```

\section*{Description}

\section*{Input \\ Arguments}

\section*{moving - Moving image}
grayscale image
Moving image is the image to be transformed into alignment with a reference image, specified as a 2-D or 3-D grayscale image.

Data Types
single | double | int8 | int16 | int32 | uint8 | uint16 | uint32

\section*{fixed - Fixed image}
grayscale image
Fixed image is the reference image in the target orientation, specified as a \(2-\mathrm{D}\) or \(3-\mathrm{D}\) grayscale image.

\section*{Data Types}
single | double | int8 | int16 | int32 | uint8 | uint16 | uint32

\section*{transformType - Transform type}
'translation' | 'rigid' | 'similarity' | 'affine'
Transform type is the geometric transformation to be applied to the moving image, specified as one of the text strings listed in this table.
\begin{tabular}{l|l}
\hline Transform Type & Description \\
\hline 'translation' & \((x, y)\) translation. \\
\hline 'rigid' & \begin{tabular}{l} 
Rigid transformation consisting of translation and \\
rotation.
\end{tabular} \\
\hline 'similarity ' & \begin{tabular}{l} 
Nonreflective similarity transformation consisting \\
of translation, rotation, and scale.
\end{tabular} \\
\hline 'affine' & \begin{tabular}{l} 
Affine transformation consisting of translation, \\
rotation, scale, and shear.
\end{tabular} \\
\hline
\end{tabular}

\section*{optimizer - Optimization configuration}

\section*{optimizer object}

Optimizer configuration describes the method for optimizing the similarity metric, specified as an optimizer object returned by the imregconfig function: registration.optimizer.RegularStepGradientDescent or registration.optimizer.OnePlusOneEvolutionary.

\section*{metric - Metric configuration}
metric object
Metric configuration describes the image similarity metric to be optimized during registration, specified as a metric object returned by the imregconfig function: registration.metric.MeanSquares or registration.metric.MattesMutualInformation.

\section*{Name-Value Pair Arguments}

Specify 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

\section*{imregister}

\section*{Output Arguments}

Tips
specify several name and value pair arguments in any order as Name1, Value1, . . . , NameN, Valuen.

Example: 'Display0ptimization', 1 enables the verbose optimization mode.

\section*{DisplayOptimization - Verbose optimization flag false (default) | true}

Verbose optimization flag controls whether optimization information is displayed in the command window during the registration process, specified as the comma-separated pair consisting of 'DisplayOptimization' and either true or false.

\section*{Data Types}
logical

\section*{PyramidLevels - Number of pyramid levels}

3 (default) | positive integer
Number of pyramid levels that imregister uses during the registration process, specified as the comma-separated pair consisting of 'PyramidLevels' and a positive integer.

Example: 'PyramidLevels', 4 sets the number of pyramid levels to 4.

\section*{Data Types}
double

\section*{movingRegistered - Transformed moving image}
matrix
Transformed moving image, returned as a matrix. Any fill pixels introduced that do not correspond to locations in the original image are 0 .
- Create optimizer and metric with the imregconfig function before calling imregister.
- Your registration results can improve if you adjust the optimizer or metric settings. For example, if you increase the number of
iterations in the optimizer, reduce the optimizer step size, or change the number of samples in a stochastic metric, the registration improves to a point, at the expense of performance.
- If the spatial scaling of your images differs by more than \(10 \%\), you should resize them with imresize before registering them.
- Use imshowpair or imfuse to visualize the results of registration.
- Use imregister to register several images in an automated workflow.

\section*{Definitions Monomodal}

Images captured on the same device. Monomodal images have similar brightness ranges.

\section*{Multimodal}

Images captured on different devices. Multimodal images usually have different brightness ranges.

\section*{Examples Register 2-D Images from Same Capture Device}

Read the reference image and create an unregistered copy.
```

fixed = imread('pout.tif');
moving = imrotate(fixed, 5, 'bilinear', 'crop');

```

View the misaligned images.
```

imshowpair(fixed, moving,'Scaling','joint');

```

\section*{imregister}


Create a configuration suitable for registering images from the same sensor.
```

[optimizer, metric] = imregconfig('monomodal')
optimizer =
registration.optimizer.RegularStepGradientDescent
Properties:
GradientMagnitudeTolerance: 1.000000e-04
MinimumStepLength: 1.000000e-05
MaximumStepLength: 6.250000e-02
MaximumIterations: 100
RelaxationFactor: 5.000000e-01
metric =

```
registration.metric.MeanSquares

This class has no properties.

Now modify the optimizer configuration to get more precision.
optimizer.MaximumIterations = 300; optimizer.MinimumStepLength = 5e-4;

Perform the registration.
movingRegistered = imregister(moving,fixed,'rigid',optimizer,metric);
View registered images.
figure
imshowpair(fixed, movingRegistered,'Scaling','joint');


\section*{imregister}
\begin{tabular}{ll} 
See Also & \begin{tabular}{l} 
imregconfig | imshowpair | imfuse | \\
imtransformregistration.metric.MattesMutual Information \\
| registration.metric.MeanSquares | \\
registration.optimizer.RegularStepGradientDescent | \\
registration.optimizer.OnePlusOneEvolutionary |
\end{tabular} \\
\begin{tabular}{ll} 
Related \\
Examples & - "Registering Multimodal MRI Images"
\end{tabular} \\
Concepts & - "Intensity-Based Automatic Image Registration"
\end{tabular}
\begin{tabular}{|c|c|}
\hline Purpose & Resize image \\
\hline \multirow[t]{4}{*}{Syntax} & \(B=\) imresize(A, scale) \\
\hline & \(B=\) imresize(A, [numrows numcols]) \\
\hline & [Y newmap] = imresize(X, map, scale) \\
\hline & \([. .]=\). imresize(..., method)
\([. .]=\). imresize(..., parameter, value \\
\hline
\end{tabular}

Description
\(B=\) imresize (A, scale) returns image \(B\) that is scale times the size of \(A\). The input image \(A\) can be a grayscale, RGB, or binary image. If scale is between 0 and 1.0, \(B\) is smaller than \(A\). If scale is greater than 1.0, \(B\) is larger than \(A\).
\(B=\) imresize (A, [numrows numcols]) returns image \(B\) that has the number of rows and columns specified by [numrows numcols]. Either numrows or numcols may be NaN, in which case imresize computes the number of rows or columns automatically to preserve the image aspect ratio.
[ \(Y\) newmap] = imresize(X, map, scale) resizes the indexed image \(X\). scale can either be a numeric scale factor or a vector that specifies the size of the output image ([numrows numcols]). By default, imresize returns a new, optimized colormap (newmap) with the resized image. To return a colormap that is the same as the original colormap, use the 'Colormap ' parameter (see below).
[...] = imresize(..., method) resizes the indexed image. method can be (1) a text string that specifies a general interpolation method, (2) a text string that specifies an interpolation kernel, or (3) a two-element cell array that specifies an interpolation kernel.

\section*{imresize}
(1) Text String Specifying Interpolation Method
\begin{tabular}{ll}
\hline Method Name & Description \\
'nearest' & \begin{tabular}{l} 
Nearest-neighbor interpolation; the \\
output pixel is assigned the value of \\
the pixel that the point falls within. \\
No other pixels are considered.
\end{tabular} \\
'bilinear' & \begin{tabular}{l} 
Bilinear interpolation; the output pixel \\
value is a weighted average of pixels \\
in the nearest 2-by-2 neighborhood
\end{tabular} \\
'bicubic' & \begin{tabular}{l} 
Bicubic interpolation (the default); \\
the output pixel value is a weighted \\
average of pixels in the nearest 4-by-4 \\
neighborhood
\end{tabular} \\
\hline
\end{tabular}
(2) Text String Specifying Interpolation Kernel
\begin{tabular}{ll}
\hline Kernel Name & Description \\
\hline 'box' & Box-shaped kernel \\
'triangle' & \begin{tabular}{l} 
Triangular kernel (equivalent to \\
\\
\\
'bilinear')
\end{tabular} \\
'cubic' & \begin{tabular}{l} 
Cubic kernel (equivalent to \\
\\
'bicubic' ) \\
'lanczos2'
\end{tabular} \\
\hline
\end{tabular}
(3) Two-element Cell Array Specifying Interpolation Kernel
\begin{tabular}{l|l}
\hline Form & Description \\
\hline\(\{f, w\}\) & \(f\) is a function handle for a custom \\
interpolation kernel and \(w\) is the \\
custom kernel's width. \(f(x)\) must be \\
& \begin{tabular}{l} 
zero outside the interval \(-w / 2<=x\) \\
\(<w / 2\). Your function handle \(f\) may \\
be called with a scalar or a vector \\
input.
\end{tabular} \\
\hline
\end{tabular}
[...] = imresize(..., parameter, value, ...) you can control various aspects of the resizing operation by specifying parameter/value pairs with any of the previous syntaxes. The following table lists these parameters.
\begin{tabular}{ll}
\hline Parameter & Value \\
'Antialiasing' \(\quad\)\begin{tabular}{l} 
A Boolean value that specifies whether to \\
perform antialiasing when shrinking an image. \\
The default value depends on the interpolation \\
method. If the method is nearest-neighbor \\
('nearest '), the default is false; for all other \\
interpolation methods, the default is true.
\end{tabular} \\
'Colormap' & \begin{tabular}{l} 
A text string that specifies whether imresize \\
returns an optimized colormap or the original \\
colormap (Indexed images only). If set to \\
'original', the output colormap (newmap) \\
is the same as the input colormap (map). If
\end{tabular} \\
& \begin{tabular}{l} 
set to 'optimized ', imresize returns a new \\
optimized colormap. The default value is
\end{tabular} \\
'optimized'.
\end{tabular}

\section*{imresize}
\begin{tabular}{ll}
\hline Parameter & Value \\
\hline 'Method' & \begin{tabular}{l} 
As described above \\
'OutputSize' \\
A two-element vector, [numrows numcols], \\
that specifies the size of the output image. If \\
you specify NaN for one of the values, imresize \\
computes the value of the dimension to preserve \\
the aspect ratio of the original image.
\end{tabular} \\
'Scale' & \begin{tabular}{l} 
A scalar or two-element vector that specifies \\
the resize scale factors. If you specify a scalar, \\
imresize uses the value as the scale factor \\
for each dimension. If you specify a vector, \\
imresize uses the individual values as the scale \\
factors for the row and column dimensions, \\
respectively.
\end{tabular} \\
\hline
\end{tabular}

Tips

Class Support

\section*{Examples}

The function imresize changed in version 5.4 (R2007a). Previous versions of the Image Processing Toolbox used a somewhat different algorithm by default. If you need the same results produced by the previous implementation, use the function imresize_old.

For bicubic interpolation, the output image may have some values slightly outside the range of pixel values in the input image. This may also occur for user-specified interpolation kernels.

The input image can be numeric or logical and it must be nonsparse. The output image is of the same class as the input image. An input image that is an indexed image can be uint8, uint16, or double.

Shrink by factor of two using the defaults of bicubic interpolation and antialiasing.
```

I = imread('rice.png');
J = imresize(I, 0.5);
figure, imshow(I), figure, imshow(J)

```

Shrink by factor of two using nearest-neighbor interpolation. (This is the fastest method, but it has the lowest quality.)

J2 = imresize(I, 0.5, 'nearest');
Resize an indexed image
[X, map] = imread('trees.tif');
[Y, newmap] = imresize(X, map, 0.5); imshow(Y, newmap)

Resize an RGB image to have 64 rows. The number of columns is computed automatically.

RGB = imread('peppers.png');
RGB2 = imresize(RGB, [64 NaN]);
See Also
imrotate | imtransform | tformarray | interp2

Purpose Region-of-interest (ROI) base class
Because the imroi class is abstract, creating an instance of the imroi class is not allowed.

\section*{Methods}
imroi supports the following methods. Type methods imroi to see a complete list.

\section*{addNewPositionCallback - Add new-position callback to ROI object}
id = addNewPositionCallback(h,fcn) adds the function handle fcn to the list of new-position callback functions of the ROI object \(h\). Whenever the ROI object changes its position each function in the list is called with the syntax:
```

fcn(pos)

```
where pos is of the form returned by the object's getPosition method.
The return value, id, is used only with removeNewPositionCallback.

\section*{createMask - Create mask within image}

BW = createMask( \(h\) ) returns a mask, or binary image, that is the same size as the input image with 1 s inside the ROI object h and 0 s everywhere else. The input image must be contained within the same axes as the ROI.

BW = createMask(h,h_im) returns a mask the same size as the image h _im with 1 s inside the ROI object h and 0 s outside. This syntax is required when the axes that contain the ROI hold more than one image.

\section*{delete - Delete ROI object}
delete(h) deletes the ROI object h

\section*{getColor - Get color used to draw ROI object.}
color = getColor(h) gets the color used to draw the ROI object h. The three-element vector color specifies an RGB triplet.

\section*{getPosition - Return current position of ROI object}
pos \(=\) getPosition( \(h\) ) returns current position of the ROI object \(h\).

\section*{getPositionConstraintFen - Return function handle to current position constraint function}
\(\mathrm{fcn}=\) getPositionConstraintFcn(h) returns a function handle fcn to the current position constraint function of the ROI object \(h\).

\section*{removeNewPositionCallback - Remove new-position callback from ROI object}
removeNewPositionCallback( h ,id) removes the corresponding function from the new-position callback list of the ROI object \(h\). id is the identifier returned by the addNewPositionCallback method.

\section*{resume - Resume execution of MATLAB command line}
resume ( h ) resumes execution of the MATLAB command line. When called after a call to wait, resume causes wait to return an accepted position. The resume method is useful when you need to exit wait from a callback function.
setColor - Set color used to draw ROI object.
setColor (h, new_color) sets the color used to draw the ROI object h. new_color can be a three-element vector specifying an RGB triplet, or a text string specifying the long or short name of a predefined color, such as 'white' or 'w'. See ColorSpec for a list of predefined colors.
setConstrainedPosition - Set ROI object to new position setConstrainedPosition(h, candidate_position) sets the ROI object \(h\) to a new position. The candidate position is subject to the position constraint function. candidate_position is of the form expected by the setPosition method.
setPositionConstraintFcn - Set position constraint function of ROI object
setPositionConstraintFcn(h,fen) sets the position constraint function of the ROI object \(h\) to be the specified function handle, fcn. Whenever the object is moved because of a mouse drag, the constraint function is called using the syntax:
```

constrained_position = fcn(new_position)

```
where new_position is of the form returned by the getPosition method. You can use the makeConstrainToRectFcn to create this function.
wait - Block MATLAB command line until ROI creation is finished accepted_pos = wait (h) blocks execution of the MATLAB command line until you finish positioning the ROI object \(h\). You indicate completion by double-clicking on the ROI object. The returned position, accepted_pos, is of the form returned by the object's getPosition method.

\section*{See Also}
makeConstrainToRectFcn

\section*{Purpose Rotate image}

Syntax \(\quad B=\) imrotate (A, angle)
\(B=\) imrotate(A, angle,method)
\(B\) = imrotate(A,angle, method,bbox)

\section*{Description}
\(B=\) imrotate (A, angle) rotates image \(A\) by angle degrees in a counterclockwise direction around its center point. To rotate the image clockwise, specify a negative value for angle. imrotate makes the output image B large enough to contain the entire rotated image. imrotate uses nearest neighbor interpolation, setting the values of pixels in \(B\) that are outside the rotated image to 0 (zero).
\(B=\) imrotate (A, angle, method) rotates image A, using the interpolation method specified by method. method is a text string that can have one of these values. The default value is enclosed in braces (\{\}).
\begin{tabular}{l|l}
\hline Value & Description \\
\hline \{'nearest' \} & Nearest-neighbor interpolation \\
\hline 'bilinear' & Bilinear interpolation \\
\hline 'bicubic' & Bicubic interpolation \\
\cline { 2 - 3 } \begin{tabular}{l} 
Note Bicubic interpolation can produce pixel \\
values outside the original range.
\end{tabular} \\
\hline
\end{tabular}
\(B\) = imrotate(A, angle, method, bbox) rotates image \(A\), where bbox specifies the size of the returned image. bbox is a text string that can have one of the following values. The default value is enclosed in braces (\{\}).

\section*{imrotate}
\begin{tabular}{l|l}
\hline Value & Description \\
\hline 'crop' & \begin{tabular}{l} 
Make output image B the same size as the input \\
image A, cropping the rotated image to fit
\end{tabular} \\
\hline\(\{\) 'loose' \} & \begin{tabular}{l} 
Make output image B large enough to contain the \\
entire rotated image. B is generally larger than \(A\).
\end{tabular} \\
\hline
\end{tabular}

\section*{Class Support}

\section*{Performance Note}

Examples

The input image can be numeric or logical. The output image is of the same class as the input image.

This function may take advantage of hardware optimization for data types uint8, uint16, and single to run faster.

Read a solar spectra image, stored in FITS format, and rotate the image to bring it into horizontal alignment. A rotation of -1 degree is all that is required.
```

I = fitsread('solarspectra.fts');
I = mat2gray(I);
J = imrotate(I,-1,'bilinear','crop');
figure, imshow(I)
figure, imshow(J)

```


Original Image


Rotuted Image

See Also imcrop | imresize | imtransform | tformarray

\section*{Purpose Save Image Tool}

\section*{Syntax imsave}
imsave(h)
[filename, user_canceled] = imsave( )

\section*{Description}
imsave creates a Save Image tool in a separate figure that is associated with the image in the current figure, called the target image. The Save Image tool displays an interactive file chooser dialog box (shown below) in which you can specify a path and filename. When you click Save, the Save Image tool writes the target image to a file using the image file format you select in the Files of Type menu. imsave uses imwrite to save the image, using default options.


If you specify a filename that already exists, imsave displays a warning message. Select Yes to use the filename or No to return to the dialog to select another filename. If you select Yes, the Save Image tool attempts to overwrite the target file.

Note The Save Image tool is modal; it blocks the MATLAB command line until you respond.

> imsave \((h)\) creates a Save Image tool associated with the image specified by the handle \(h\). \(h\) can be an image, axes, uipanel, or figure handle. If \(h\) is an axes or figure handle, imsave uses the first image returned by findobj(h, 'Type' , 'image').
> [filename, user_canceled] = imsave( ) returns the full path to the file selected in filename. If you press the Cancel button, imsave setsuser_canceled to true (1); otherwise, false (0).

\section*{Remarks}

In contrast to the Save as option in the figure File menu, the Save Image tool saves only the image displayed in the figure. The Save as option in the figure window File menu saves the entire figure window, not just the image.
```

Examples imshow peppers.png
imsave

```

See Also imformats | imgetfile | imputfile | imwrite

\section*{Purpose}

Syntax
Description

API
Functions

Scroll panel for interactive image navigation
hpanel = imscrollpanel(hparent, himage)
hpanel = imscrollpanel(hparent, himage) creates a scroll panel containing the target image (the image to be navigated). himage is a handle to the target image. hparent is a handle to the figure or uipanel that will contain the new scroll panel. The function returns hpanel, a handle to the scroll panel, which is a uipanel object.

A scroll panel makes an image scrollable. If the size or magnification makes an image too large to display in a figure on the screen, the scroll panel displays a portion of the image at \(100 \%\) magnification (one screen pixel represents one image pixel). The scroll panel adds horizontal and vertical scroll bars to enable navigation around the image.
imscrollpanel changes the object hierarchy of the target image. Instead of the familiar figure->axes->image object hierarchy, imscrollpanel inserts several uipanel and uicontrol objects between the figure and the axes object.

A scroll panel contains a structure of function handles, called an API. You can use the functions in this API to manipulate the scroll panel. To retrieve this structure, use the iptgetapi function, as in the following example.
api \(=\) iptgetapi(hpanel)
This table lists the scroll panel API functions, in the order they appear in the structure.

\section*{imscrollpanel}
\begin{tabular}{l|l}
\hline Function & Description \\
\hline setMagnification & \begin{tabular}{l} 
Sets the magnification of the target image in \\
units of screen pixels per image pixel. \\
mag = api.setMagnification(new_mag) \\
where new_mag is a scalar magnification factor.
\end{tabular} \\
\hline getMagnification & \begin{tabular}{l} 
Returns the current magnification factor of the \\
target image in units of screen pixels per image \\
pixel.
\end{tabular} \\
\begin{tabular}{ll} 
mag = api.getMagnification() \\
Multiply mag by 100 to convert to percentage. For \\
example if mag=2, the magnification is 200\%.
\end{tabular} \\
\hline setMagnificationAndCenter & \begin{tabular}{l} 
Changes the magnification and makes the point \\
cx, cy in the target image appear in the center of \\
the scroll panel. This operation is equivalent to a \\
simultaneous zoom and recenter.
\end{tabular} \\
\hline api.setMagnificationAndCenter(mag, cx, cy)
\end{tabular}, \begin{tabular}{l} 
Returns the magnification factor that would \\
make the target image just fit in the scroll panel. \\
mag = api.findFitMag()
\end{tabular}
\begin{tabular}{l|l}
\hline Function & Description \\
\hline getVisibleLocation & \begin{tabular}{l} 
Returns the location of the currently visible \\
portion of the target image. \\
loc = api.getVisibleLocation() \\
where loc is a vector [xmin ymin].
\end{tabular} \\
\hline getVisibleImageRect & Returns the current visible portion of the image. \\
r= api.getVisibleImageRect() \\
where r is a rectangle [xmin ymin width \\
height]. \\
\hline AddNewMagnificationCallback & \begin{tabular}{l} 
Adds the function handle fcn to the list of \\
new-magnification callback functions. \\
id = api.addNewMagnificationCallback(fcn)
\end{tabular} \\
& \begin{tabular}{l} 
Whenever the scroll panel magnification changes, \\
each function in the list is called with the syntax: \\
fcn(mag) \\
where mag is a scalar magnification factor.
\end{tabular} \\
\hline removeNewMagnificationCallback & \begin{tabular}{l} 
The return value, id, is used only with \\
removeNewMagnificationCallback.
\end{tabular} \\
\begin{tabular}{l} 
Removes the corresponding function from the \\
new-magnification callback list. \\
api.removeNewMagnificationCallback(id)
\end{tabular} \\
where id is the identifier returned by \\
addNewMagnificationCallback.
\end{tabular}

\section*{imscrollpanel}
\begin{tabular}{l|l}
\hline Function & Description \\
\hline addNewLocationCallback & \begin{tabular}{l} 
Adds the function handle fcn to the list of \\
new-location callback functions. \\
id = api.addNewLocationCallback(fcn) \\
Whenever the scroll panel location changes, each \\
function in the list is called with the syntax: \\
fcn(loc)
\end{tabular} \\
\hline removeNewLocationCallback & \begin{tabular}{l} 
where loc is [xmin ymin]. \\
The return value, id, is used only with \\
removeNewLocationCallback.
\end{tabular} \\
\hline \begin{tabular}{l} 
Removes the corresponding function from the \\
new-location callback list.
\end{tabular} \\
\hline replaceImage & \begin{tabular}{l} 
api.removeNewLocationCallback(id) \\
where id is the identifier returned by \\
addNewLocationCallback.
\end{tabular} \\
\hline \begin{tabular}{l} 
api.replaceImage(..., PARAM1, VAL1, PARAM2, \\
VAL2, ...) replaces the image displayed in the \\
scroll panel.
\end{tabular} \\
\hline \begin{tabular}{l} 
api.replaceImage(I) \\
api.replaceImage(BW) \\
api.replaceImage(RGB) \\
api.replaceImage(I,MAP) \\
api.replaceImage(filename)
\end{tabular} \\
\hline By default, the new image data is displayed \\
centered, at 100\% magnification. The image \\
handle is unchanged.
\end{tabular}
\begin{tabular}{l|l}
\hline Function & Description \\
\hline & \begin{tabular}{l} 
The parameters you can specify include many \\
of the parameters supported by imshow, \\
including 'Colormap ', 'DisplayRange ', and \\
'InitialMagnification '. In addition, you \\
can use the 'PreserveView ' parameter to \\
preserve the current magnification and centering \\
of the image during replacement. Specify the \\
logical scalar True to preserve current centering \\
and magnification. Parameter names can be \\
abbreviated, and case does not matter.
\end{tabular} \\
\hline
\end{tabular}

\section*{Note \\ Examples}

Scrollbar navigation as provided by imscrollpanel is incompatible with the default MATLAB figure navigation buttons (pan, zoom in, zoom out). The corresponding menu items and toolbar buttons should be removed in a custom GUI that includes a scrollable uipanel created by imscrollpanel.

When you run imscrollpanel, it appears to take over the entire figure because, by default, an hpanel object has 'Units' set to 'normalized' and 'Position' set to [ \(\left.\begin{array}{llll}0 & 0 & 1 & 1\end{array}\right]\). If you want to see other children of hparent while using your new scroll panel, you must manually set the 'Position' property of hpanel.

Create a scroll panel with a Magnification Box and an Overview tool.
1 Create a scroll panel.
```

hFig = figure('Toolbar','none',...
'Menubar','none');
hIm = imshow('saturn.png');
hSP = imscrollpanel(hFig,hIm);
set(hSP,'Units','normalized',...
'Position',[0 .1 1 .9])

```

2 Add a Magnification Box and an Overview tool.

\section*{imscrollpanel}
```

hMagBox = immagbox(hFig,hIm);
pos = get(hMagBox,'Position');
set(hMagBox,'Position',[0 0 pos(3) pos(4)])
imoverview(hIm)

```

3 Get the scroll panel API to programmatically control the view.
```

api = iptgetapi(hSP);

```

4 Get the current magnification and position.
```

mag = api.getMagnification();

```
\(r=\) api.getVisibleImageRect();

5 View the top left corner of the image.
api.setVisibleLocation(0.5,0.5)

6 Change the magnification to the value that just fits.
api.setMagnification(api.findFitMag())

7 Zoom in to \(1600 \%\) on the dark spot.
api.setMagnificationAndCenter(16,306,800)
```

See Also immagbox | imoverview | imoverviewpanel | imtool | iptgetapi
How To . "Adding Navigation Aids to a GUI"

```

\section*{Purpose}

Display image

\section*{Note}
- The syntax imshow(x,y,...) has been removed. Use the imshow(...,'XData', \(x\), 'YData',\(y\) ) syntax instead.
- The syntax imshow(I,N) has been removed. Your grayscale image will be displayed using 256 shades of gray.
- The syntax imshow(...,'truesize') has been removed. Use the imshow(...,'InitialMagnification', 100) syntax instead.
- The syntax imshow(..., 'notruesize') has been removed. Use the imshow(...,'InitialMagnification','fit') syntax instead.

\section*{Syntax imshow(I)}
imshow(I,[low high])
imshow(RGB)
imshow (BW)
imshow(X,map)
imshow(filename)
himage = imshow(...)
imshow(..., param1, val1, param2, val2,...)

\section*{Description}
imshow(I) displays the grayscale image \(I\).
imshow(I,[low high]) displays the grayscale image I, specifying the display range for I in [low high]. The value low (and any value less than low) displays as black; the value high (and any value greater than high) displays as white. Values in between are displayed as intermediate shades of gray, using the default number of gray levels. If you use an empty matrix ([]) for [low high], imshow uses [min(I (:)) \(\max (\mathrm{I}(:))]\); that is, the minimum value in I is displayed as black, and the maximum value is displayed as white.
imshow (RGB) displays the truecolor image RGB.

\section*{imshow}
imshow (BW) displays the binary image BW. imshow displays pixels with the value 0 (zero) as black and pixels with the value 1 as white.
imshow ( \(X\), map) displays the indexed image \(X\) with the colormap map. A color map matrix may have any number of rows, but it must have exactly 3 columns. Each row is interpreted as a color, with the first element specifying the intensity of red light, the second green, and the third blue. Color intensity can be specified on the interval 0.0 to 1.0 .
imshow(filename) displays the image stored in the graphics file filename. The file must contain an image that can be read by imread or dicomread. imshow calls imread or dicomread to read the image from the file, but does not store the image data in the MATLAB workspace. If the file contains multiple images, imshow displays the first image in the file. The file must be in the current directory or on the MATLAB path.
himage \(=\) imshow(...) returns the handle to the image object created by imshow.
imshow(..., param1, val1, param2, val2,...) displays the image, specifying parameters and corresponding values that control various aspects of the image display. The following table lists all imshow parameters in alphabetical order. Parameter names can be abbreviated, and case does not matter.
\begin{tabular}{l|l}
\hline Parameter & Value \\
\hline 'Border' & \begin{tabular}{l} 
Text string that controls whether imshow includes a border \\
around the image displayed in the figure window. Valid \\
strings are 'tight ' and 'loose'. \\
Note: There can still be a border if the image is very small, \\
or if there are other objects besides the image and its axes \\
in the figure. \\
By default, the border is set to the value returned by \\
iptgetpref( 'ImshowBorder').
\end{tabular} \\
\hline 'Colormap' & \begin{tabular}{l} 
2-D, real, \(m\)-by-3 matrix specifying a colormap. imshow \\
uses this to set the figure's colormap property. Use this \\
parameter to view grayscale images in false color. If
\end{tabular} \\
\hline
\end{tabular}
\begin{tabular}{l|l}
\hline \multicolumn{1}{l}{ Parameter } & Value \\
\hline & \begin{tabular}{l} 
you specify an empty colormap ([ ]), imshow ignores this \\
parameter.
\end{tabular} \\
\hline 'DisplayRange' & \begin{tabular}{l} 
Two-element vector [LOW HIGH] that controls the display \\
range of a grayscale image. See the imshow(I, [low high]) \\
syntax for more details about how to set this parameter.
\end{tabular} \\
\hline & \begin{tabular}{l} 
Note Including the parameter name is optional, \\
except when the image is specified by a filename. \\
The syntax imshow(I, [LOW HIGH]) is equivalent to \\
imshow(I, 'DisplayRange', [Low HIGH]). However,
\end{tabular} \\
the 'DisplayRange' parameter must be specified \\
when calling imshow with a filename, for example \\
imshow(filename, 'DisplayRange' [LOW HIGH]).
\end{tabular}

\section*{imshow}
\begin{tabular}{l|l}
\hline Parameter & Value \\
\hline & \begin{tabular}{l} 
Note: If you specify the axes position (using subplot or \\
axes), imshow ignores any initial magnification you might \\
have specified and defaults to the 'fit' behavior. \\
When used with the 'Reduce ' parameter, only 'fit' is \\
allowed as an initial magnification.
\end{tabular} \\
\hline 'Parent' & \begin{tabular}{l} 
Handle of an axes that specifies the parent of the image \\
object that will be created by imshow.
\end{tabular} \\
\hline 'Reduce' & \begin{tabular}{l} 
Logical value that specifies whether imshow subsamples the \\
image in filename. The 'Reduce ' parameter is only valid \\
for TIFF images and you must specify a file name. Use this \\
parameter to display overviews of very large images.
\end{tabular} \\
\hline 'XData' & \begin{tabular}{l} 
Two-element vector that establishes a nondefault spatial \\
coordinate system by specifying the image XData. The value \\
can have more than two elements, but only the first and last \\
elements are actually used.
\end{tabular} \\
\hline 'YData' & \begin{tabular}{l} 
Two-element vector that establishes a nondefault spatial \\
coordinate system by specifying the image YData. The value \\
can have more than two elements, but only the first and last \\
elements are actually used.
\end{tabular} \\
\hline
\end{tabular}

Note If you are building a GUI where you want to control the figure and axes properties, be sure to use the imshow(..., 'Parent', ax) syntax.

A truecolor image can be uint8, uint16, single, or double. An indexed image can be logical, uint8, single, or double. A grayscale image can be logical, uint8, int16, uint16, single, or double. A binary image must be of class logical.

For grayscale images of class single or double, the default display range is [ 0 1]. If your image's data range is much larger or smaller than the default display range, you might need to experiment with setting the display range to see features in the image that would not be visible using the default display range. For all grayscale images having integer types, the default display range is [intmin(class(I)) intmax (class(I))].

If your image is int8, int16, uint32, int32 or single, the CData in the resulting image object will be double. For all other classes, the CData matches the input image class.

\section*{Related Toolbox Preferences}

Tips

You can use the iptsetpref function to set several toolbox preferences that modify the behavior of imshow.
- 'ImshowBorder' controls whether imshow displays the image with a border around it.
- 'ImshowAxesVisible' controls whether imshow displays the image with the axes box and tick labels.
- 'ImshowInitialMagnification' controls the initial magnification for image display, unless you override it in a particular call by specifying imshow(...,'InitialMagnification',initial_mag).

For more information about these preferences, see iptprefs.
imshow is the toolbox's fundamental image display function, optimizing figure, axes, and image object property settings for image display. imtool provides all the image display capabilities of imshow but also provides access to several other tools for navigating and exploring images, such as the Pixel Region tool, Image Information tool, and the Adjust Contrast tool. imtool presents an integrated environment for displaying images and performing some common image processing tasks.

The imshow function is not supported when MATLAB is started with the -nojvm option.

\section*{imshow}

You can access imshow through the Plot Selector workspace tool, which is represented by this icon: \(\$\) select data to plot In your workspace, select the data you want to display. The Plot Selector icon changes to look like this: Mplot \((x, y)\). Scroll down to Image Processing Toolbox Plots. Select imshow(I).

\section*{Examples \\ Display an image from a file.}
imshow('board.tif')
Display an indexed image.
```

[X,map] = imread('trees.tif');

```
imshow(X,map)

Display a grayscale image.
```

I = imread('cameraman.tif');
imshow(I)

```

Display the same grayscale image, adjusting the display range.
```

h = imshow(I,[0 80]);

```

\section*{See Also}
imread | imtool | iptprefs | subimage | truesize | warp | image | imagesc

\section*{Purpose Compare differences between images}

Syntax imshowpair \((A, B)\)
imshowpair (A, B, method)
imshowpair(__, Name, Value)

Description

\section*{Input Arguments}
imshowpair (A, B) displays the differences between images \(A\) and \(B\). If \(A\) and \(B\) are different sizes, the smaller dimensions are padded with zeros on the bottom and right edges so that the two image are the same size in the display.
imshowpair(A, B, method) uses the visualization method specified by method.
imshowpair \(\qquad\) , Name, Value) specifies additional options with one or more Name, Value pair arguments, using any of the previous syntaxes.

\section*{A,B - Input images \\ grayscale images | truecolor images | binary images}

Input images to be combined into a composite image, specified as any combination of grayscale, truecolor, or binary images.

\section*{Data Types}
single | double | int8 | int16 | int32 | int64 | uint16 | uint32 | uint64
| logical

\section*{method - Visualization method}
'falsecolor' (default) | 'blend' | 'diff' | 'montage'
Visualization method for creating the composite image, specified as one of the text strings in the following table.

\section*{imshowpair}
\begin{tabular}{l|l}
\hline Method & Description \\
\hline 'falsecolor' & \begin{tabular}{l} 
Creates a composite RGB image showing \\
A and B overlaid in different color bands. \\
Gray regions in the composite image show \\
where the two images have the same \\
intensities. Magenta and green regions \\
show where the intensities are different. \\
This is the default method.
\end{tabular} \\
\hline 'blend' & Overlays A and B using alpha blending. \\
\hline 'diff' & Creates a difference image from A and B. \\
\hline 'montage' & \begin{tabular}{l} 
Places A and B next to each other in the \\
same image.
\end{tabular} \\
\hline
\end{tabular}

Example: imshowpair(A, B, 'montage') displays A and B next to each other.

\section*{Name-Value Pair Arguments}

Specify 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 and value pair arguments in any order as Name1, Value1, . . . , NameN, ValueN.

Example: 'Scaling', 'joint' scales the intensity values of A and B together as a single data set.

\section*{Scaling - Image data scaling option}
'independent' (default) | 'joint' | 'none'
Image data scaling option that controls the intensity scaling of the pixels representing the input images in the output image, specified as the comma-separated pair consisting of 'Scaling' and one of the text strings in the following table.
\(\left.\begin{array}{ll}\text { 'independent' } & \begin{array}{l}\text { Scales the intensity values of A and B } \\ \text { independently from each other. }\end{array} \\ \text { 'joint' } & \begin{array}{l}\text { Scales the intensity values in the images } \\ \text { jointly as if they were together in the }\end{array} \\ \text { same image. This option is useful when } \\ \text { you want to visualize registrations of } \\ \text { monomodal images, where one image } \\ \text { contains fill values that are outside the } \\ \text { dynamic range of the other image. }\end{array}\right\}\)

\section*{ColorChannels - Output color channel for each input image} [R G B] | 'red-cyan' | 'green-magenta' (default)

Output color channel for each input image, specified as the comma-separated pair consisting of 'ColorChannels ' and one of the text strings from the following table. 'ColorChannels' can only be used with the 'falsecolor' visualization method.
\begin{tabular}{|c|c|}
\hline [ R G B] & A three element vector that specifies which image to assign to the red, green, and blue channels. The R, G, and B values must be 1 (for the first input image), 2 (for the second input image), and 0 (for neither image). \\
\hline red-cyan' & A shortcut for the vector [ \(\left.\begin{array}{lll}1 & 2 & 2\end{array}\right]\), which is suitable for red/cyan stereo anaglyphs. \\
\hline green-magenta' & A shortcut for the vector [12 2], which is a high contrast option, ideal for people with many kinds of color blindness. \\
\hline
\end{tabular}

\section*{imshowpair}

\section*{Examples}

\section*{Display Two Images That Differ by Rotation and Offset}

Display a pair of grayscale images with two different visualization methods, 'diff' and 'blend'.

Load an image into the workspace. Create a copy with a rotation and offset applied.

A = imread('cameraman.tif');
\(B=\) imrotate(A,5,'bicubic','crop');
Display the difference of A and B.
imshowpair(A, B, 'diff');


Display a blended overlay A and B.
figure;
imshowpair(A, B,'blend','Scaling','joint');


\section*{Display Two Images with Different Brightness Ranges}

Load an image into the workspace. Create a copy and apply rotation, offset, and a brightness adjustment.

A = dicomread('CT-MONO2-16-ankle.dcm');
B = double(imrotate(A, 10,'bicubic','crop'));
B = B * 0.2;
Display the images with the default, 'falsecolor', method and apply brightness scaling independently to each image.
```

figure;
imshowpair(A, B,'Scaling','independent');

```

\section*{imshowpair}


See Also
```

imfuse | imregister | imshow | imtransform

```

\section*{Purpose}

Subtract one image from another or subtract constant from image
Syntax
Z = imsubtract( \(\mathrm{X}, \mathrm{Y}\) )
\(Z=\) imsubtract \((X, Y)\) subtracts each element in array \(Y\) from the corresponding element in array \(X\) and returns the difference in the corresponding element of the output array Z. \(X\) and \(Y\) are real, nonsparse numeric arrays of the same size and class, or \(Y\) is a double scalar. The array returned, \(Z\), has the same size and class as \(X\) unless \(X\) is logical, in which case \(Z\) is double.

If X is an integer array, elements of the output that exceed the range of the integer type are truncated, and fractional values are rounded.

Note On Intel architecture processors, imsubtract can take advantage of the Intel Integrated Performance Primitives (Intel IPP) library, thus accelerating its execution time. The (Intel IPP) library is activated only if array \(X\) is of class uint8, int16, or single.

\section*{Examples}

Subtract two uint8 arrays. Note that negative results are rounded to 0 .
```

X = uint8([ 255 10 75; 44 225 100]);
Y = uint8([ 50 50 50; 50 50 50 ]);
Z = imsubtract(X,Y)
Z =
205 0 25
0 175 50

```

Estimate and subtract the background of an image:
```

I = imread('rice.png');
background = imopen(I,strel('disk',15));
Ip = imsubtract(I,background);
imshow(Ip,[])

```

\section*{imsubtract}

Subtract a constant value from an image:
```

I = imread('rice.png');
Iq = imsubtract(I,50);
figure, imshow(I), figure, imshow(Iq)

```

See Also
imabsdiff | imadd | imcomplement | imdivide | imlincomb | immultiply | ippl
Purpose Image Tool
Syntax

imtool
imtool(I)
imtool(I,[low high])
imtool(RGB)
imtool(BW)
imtool(X,map)
imtool(filename)
hfigure = imtool(...)
imtool close all
imtool(..., param1,val1,param2,val2,...)

\section*{Description}
imtool opens a new Image Tool in an empty state. Use the File menu options Open or Import from Workspace to choose an image for display.
imtool(I) displays the grayscale image I.
imtool(I,[low high]) displays the grayscale image I, specifying the display range for I in the vector [low high]. The value low (and any value less than low) is displayed as black, the value high (and any value greater than high) is displayed as white. Values in between are displayed as intermediate shades of gray. imtool uses the default number of gray levels. If you use an empty matrix ([]) for [low high], imtool uses \([\min (\mathrm{I}(:)) \quad \max (\mathrm{I}(:))]\); the minimum value in I is displayed as black, and the maximum value is displayed as white.
imtool (RGB) displays the truecolor image RGB.
imtool (BW) displays the binary image BW. Pixel values of 0 display as black; pixel values of 1 display as white.
imtool ( X, map) displays the indexed image X with colormap map.
imtool(filename) displays the image contained in the graphics file filename. The file must contain an image that can be read by imread or dicomread or a reduced resolution dataset (R-Set) created by rsetwrite. If the file contains multiple images, the first one is
displayed. The file must be in the current directory or on the MATLAB path.
hfigure \(=\) imtool (...) returns hfigure, a handle to the figure created by imtool. close (Hfigure) closes the Image Tool.
imtool close all closes all image tools.
imtool(..., param1, val1, param2, val2,...) displays the image, specifying parameters and corresponding values that control various aspects of the image display. The following table lists all imshow parameters. Parameter names can be abbreviated, and case does not matter.
\begin{tabular}{l|l}
\hline Parameter & Value \\
\hline 'Colormap' & \begin{tabular}{l} 
2-D, real, \(m\)-by-3 matrix specifying the colormap to use for \\
the figure's colormap property. Use this parameter to view \\
grayscale images in false color. If you specify an empty \\
colormap ([ ]), imtool ignores this parameter.
\end{tabular} \\
\hline 'DisplayRange ' & \begin{tabular}{l} 
Two-element vector [LOW HIGH] that controls the display \\
range of a grayscale image. See the imtool(I, [low high]) \\
syntax for more details about how to set this parameter.
\end{tabular} \\
\hline \begin{tabular}{l} 
Note Including the parameter name is optional, \\
except when the image is specified by a filename. \\
The syntax imtool(I, [LOW HIGH]) is equivalent to \\
imtool(I, 'DisplayRange ', [LOW HIGH]). However, \\
the 'DisplayRange' parameter must be specified \\
when calling imtool with a filename, as in the syntax \\
imtool(filename, 'DisplayRange' , [LOW HIGH]).
\end{tabular} \\
\hline 'InitialMagnification' & \begin{tabular}{l} 
One of two text strings: ' adaptive ' or 'fit' or a numeric \\
scalar value that specifies the initial magnification used \\
to display the image.
\end{tabular} \\
\hline
\end{tabular}
\begin{tabular}{l|l}
\hline Parameter & Value \\
& \begin{tabular}{l} 
When set to ' adaptive ', the entire image is visible on \\
initial display. If the image is too large to display on \\
the screen, imtool displays the image at the largest \\
magnification that fits on the screen. \\
When set to ' fit ', imtool scales the entire image to fit in \\
the window. \\
When set to a numeric value, the value specifies the \\
magnification as a percentage. For example, if you specify \\
100, the image is displayed at 100\% magnification (one \\
screen pixel for each image pixel).
\end{tabular} \\
& \begin{tabular}{l} 
Note When the image aspect ratio is such that less than \\
one pixel would be displayed in either dimension at the \\
requested magnification, imtool issues a warning and \\
displays the image at 100\%.
\end{tabular} \\
\hline
\end{tabular} \begin{tabular}{l} 
By default, the initial magnification \\
parameter is set to the value returned by \\
iptgetpref( 'ImtoolInitialMagnification ' ).
\end{tabular}

\section*{Class \\ Support}

A truecolor image can be uint8, uint16, single, or double. An indexed image can be logical, uint8, single, or double. A grayscale image can be uint8, uint16, int16, single, or double. A binary image must be logical. A binary image is of class logical.

For all grayscale images having integer types, the default display range is [intmin(class(I)) intmax(class(I))].

For grayscale images of class single or double, the default display range is [0 1]. If the data range of a single or double image is much larger or smaller than the default display range, you might need to
experiment with setting the display range to see features in the image that would not be visible using the default display range.

\section*{Large \\ Data Support}

To view very large TIFF or NITF images that will not fit into memory, you can use rsetwrite to create a reduced resolution dataset (R-Set) viewable in imtool. R-Sets can also improve performance of imtool for large images that fit in memory.

The following tools can be used with an R-Set: Overview, Zoom, Pan, Image Information, and Distance. Other tools, however, will not work with an R-Set. You cannot use the Pixel Region, Adjust Contrast, Crop Image, and Window/Level tools. Please note that the Pixel Information tool displays only the \(x\) and \(y\) coordinates of a pixel and not the associated intensity, index, or [R G B] values.

You can use the Image Processing Preferences dialog box to set toolbox preferences that modify the behavior of imtool. To access the dialog, select File > Preferences in the MATLAB desktop or Image Tool menu. Also, you can set preferences programmatically with iptsetpref. The imtool preferences include:
- 'ImtoolInitialMagnification' controls the initial magnification for image display. To override this toolbox preference, specify the 'InitialMagnification' parameter when you call imtool, as follows:
imtool(...,'InitialMagnification', initial_mag).
- 'ImtoolStartWithOverview' controls whether the Overview tool opens automatically when you open an image using the Image Tool. Possible values:
true- Overview tool opens when you open an image.
\{false\}-Overview tool does not open when you open an image. This is the default behavior.

For more information about these preferences, see iptprefs.
Tips \(\left.\begin{array}{l}\text { imshow is the toolbox's fundamental image display function, optimizing } \\ \text { figure, axes, and image object property settings for image display. } \\ \text { imtool provides all the image display capabilities of imshow but also } \\ \text { provides access to several other tools for navigating and exploring } \\ \text { images, such as the Pixel Region tool, Image Information tool, and the } \\ \text { Adjust Contrast tool. imtool presents an integrated environment for } \\ \text { displaying images and performing some common image processing } \\ \text { tasks. } \\ \text { You can access imtool through the Plot Selector workspace tool, which } \\ \text { is represented by this icon: Select data to plot } \\ \text { workspace, select the data you want to display. The Plot Selector icon } \\ \text { changes to look like this: }\end{array}\right\}\) plot(x,y)
Image Processing Toolbox Plots. Select imtool(I). Scroll down to

\section*{imtophat}

\section*{Purpose Top-hat filtering}
```

Syntax IM2 = imtophat(IM,SE)
IM2 = imtophat(IM,NHOOD)

```

Description IM2 = imtophat(IM, SE) performs morphological top-hat filtering on the grayscale or binary input image IM. Top-hat filtering computes the morphological opening of the image (using imopen) and then subtracts the result from the original image. imtophat uses the structuring element SE, where SE is returned by strel. SE must be a single structuring element object, not an array containing multiple structuring element objects.

IM2 = imtophat(IM,NHOOD) where NHOOD is an array of 0 s and 1 s that specifies the size and shape of the structuring element, is the same as imptophat(IM, strel(NHOOD)).

\section*{Class Support}

Examples You can use top-hat filtering to correct uneven illumination when the background is dark. This example uses top-hat filtering with a disk-shaped structuring element to remove the uneven background illumination from an image.

1 Read an image into the MATLAB workspace.
```

I = imread('rice.png');
imshow(I)

```


2 Create the structuring element and perform top-hat filtering of the image.
```

se = strel('disk',12);
J = imtophat(I,se);
figure, imshow(J)

```


3 Use imadjust to improve the visibility of the result.
K = imadjust(J);
figure, imshow(K)

\section*{imtophat}


See Also
imbothat | strel

\author{
Purpose \\ \section*{Syntax} \\ Description
}

Apply 2-D spatial transformation to image

Tips
\(B=i m t r a n s f o r m(A, t f o r m)\)
B = imtransform(A,tform,interp)
[B,xdata,ydata] = imtransform(...)
[B,xdata,ydata] = imtransform(...,Name, Value)
\(B=\) imtransform(A,tform) transforms the image A according to the 2-D spatial transformation defined by tform. If ndims (A) > 2, such as for an RGB image, then imtransform applies the same 2-D transformation to all 2-D planes along the higher dimensions. to use. output image \(B\) in the output X-Y space. By default, imtransform calculates xdata and ydata automatically so that B contains the calculation by specifying values for the 'XData' and 'YData' arguments. spatial transformation specified by one or more Name, Value pair arguments.
- Image Registration. The imtransform function automatically

B = imtransform(A,tform,interp) specifies the form of interpolation
[ \(B\),xdata, ydata] = imtransform(...) returns the location of the entire transformed image A. However, you can override this automatic
[B,xdata,ydata] = imtransform(...,Name, Value) transforms the image with additional options for controlling various aspects of the shifts the origin of your output image to make as much of the transformed image visible as possible. If you use imtransform to do image registration, the syntax \(B=\) imtransform ( \(A\), tform) can produce unexpected results. To control the spatial location of the output image, set 'XData' and 'YData' explicitly.
- Pure Translation. Calling the imtransform function with a purely translational transformation, results in an output image that is exactly like the input image unless you specify 'XData' and 'YData' values in your call to imtransform. For example, if you want the
output to be the same size as the input revealing the translation relative to the input image, call imtransform as shown in the following syntax:
```

B = imtransform(A,T,'XData',[1 size(A,2)],...
'YData',[1 size(A,1)])

```

For more information about this topic, see "Translate Image Using maketform and imtransform" in the User's Guide, especially the section "Understanding the Coordinates of the Transformed Image".
- Transformation Speed. When you do not specify the output-space location for B using 'XData' and 'YData', imtransform estimates the location automatically using the function findbounds. You can use findbounds as a quick forward-mapping option for some commonly used transformations, such as affine or projective. For transformations that do not have a forward mapping, such as the polynomial ones computed by cp2tform, findbounds can take much longer. If you can specify 'XData' and 'YData' directly for such transformations, imtransform may run noticeably faster.
- Clipping. The automatic estimate of 'XData' and 'YData' using findbounds sometimes clips the output image. To avoid clipping, set 'XData' and 'YData' directly.
- Arbitrary Dimensional Transformations. Use a 2-D transformation for tform when using imtransform. For arbitrary-dimensional array transformations, see tformarray.

\section*{Input \\ Arguments}

\section*{A}

An image of any nonsparse numeric class (real or complex) or of class logical.

\section*{tform}

A spatial transformation structure returned by maketform or cp2tform. imtransform assumes spatial-coordinate conventions for the transformation tform. Specifically, the first dimension of
the transformation is the horizontal or \(x\)-coordinate, and the second dimension is the vertical or \(y\)-coordinate. This convention is the reverse of the array subscripting convention in MATLAB.

\section*{interp}

A string that specifies the form of interpolation to use. interp can be one of the following strings: 'bicubic', 'bilinear', or 'nearest' (nearest-neighbor). Alternatively, interp can be a resampler structure returned by makeresampler. This option allows more control over how imtransform performs resampling.

Default: 'bilinear'

\section*{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 within single quotes (' ') and is not case sensitive. You can specify several name and value pair arguments in any order as Name1, Value1, ..., NameN, ValueN.

\section*{UData}

A two-element, real vector that, when combined with 'VData', specifies the spatial location of image \(A\) in the 2-D input space U-V. The two elements of 'UData' give the \(u\)-coordinates (horizontal) of the first and last columns of A, respectively.

Default: [1 size(A,2)]

\section*{VData}

A two-element, real vector that, when combined with 'UData', specifies the spatial location of image A in the 2-D input space U-V. The two elements of 'VData' give the \(v\)-coordinates (vertical) of the first and last rows of \(A\), respectively.

Default: [1 \(\operatorname{size}(\mathrm{A}, 1)]\)

\section*{XData}

A two-element, real vector that, when combined with 'YData', specifies the spatial location of the output image \(B\) in the \(2-D\) output space \(X-Y\). The two elements of 'XData' give the \(x\)-coordinates (horizontal) of the first and last columns of B, respectively.

Default: If you do not specify 'XData' and 'YData', imtransform estimates values that contain the entire transformed output image. To determine these values, imtransform uses the findbounds function.

\section*{YData}

A two-element real vector that, when combined with 'XData', specifies the spatial location of the output image B in the \(2-\mathrm{D}\) output space \(\mathrm{X}-\mathrm{Y}\). The two elements of 'YData' give the \(y\)-coordinates (vertical) of the first and last rows of B, respectively.

Default: If you do not specify 'XData' and 'YData', imtransform estimates values that contain the entire transformed output image. To determine these values, imtransform uses the findbounds function.

\section*{XYScale}

A one- or two-element real vector. The first element of 'XYScale' specifies the width of each output pixel in X-Y space. The second element (if present) specifies the height of each output pixel. If 'XYScale' has only one element, then the same value specifies both width and height.

Default: If you do not specify 'XYScale' but you do specify 'Size', then imtransform calculates 'XYScale' from 'Size', 'XData', and 'YData'. If you do not provide 'XYScale' or 'Size', then imtransform uses the scale of the input pixels for 'XYScale', except in cases where an excessively large output image would result.

\begin{abstract}
Note In cases where preserving the scale of the input image would result in an excessively large output image, the imtransform function automatically increases the 'XYScale'. To ensure that the output pixel scale matches the input pixel scale, specify the 'XYScale' parameter. For example, call imtransform as shown in the following syntax:
```

B = imtransform(A,T,'XYScale',1)

```
\end{abstract}

\section*{Size}

A two-element vector of nonnegative integers that specifies the number of rows and columns of the output image B. For higher dimensions, imtransform takes the size of B directly from the size of A. Thus, size \((B, k)\) equals size \((A, k)\) for \(k>2\).

Default: If you do not specify 'Size', imtransform derives this value from 'XData', 'YData', and 'XYScale'.

\section*{FillValues}

An array containing one or several fill values. The imtransform function uses fill values for output pixels when the corresponding transformed location in the input image is completely outside the input image boundaries. If A is 2-D, 'FillValues ' requires a scalar. However, if A's dimension is greater than two, then you can specify 'FillValues ' as an array whose size satisfies the following constraint: size(fill_values, \(k\) ) must equal either size ( \(\mathrm{A}, \mathrm{k}+2\) ) or 1 .

For example, if A is a uint8 RGB image that is 200-by-200-by-3, then possibilities for 'FillValues' include the following values.
\begin{tabular}{l|l}
\hline Value & Fill \\
\hline 0 & Fill with black \\
\hline\([0 ; 0 ; 0]\) & Fill with black \\
\hline
\end{tabular}
\begin{tabular}{l|l}
\hline Value & Fill \\
\hline 255 & Fill with white \\
\hline\([255 ; 255 ; 255]\) & Fill with white \\
\hline\([0 ; 0 ; 255]\) & Fill with blue \\
\hline\([255 ; 255 ; 0]\) & Fill with yellow \\
\hline
\end{tabular}

If \(A\) is 4 -D with size 200 -by-200-by- 3 -by- 10 , then you can specify
'FillValues' as a scalar, 1-by-10, 3-by-1, or 3-by-10.

\section*{Output \\ Arguments}

\section*{B}

Output image of any nonsparse numeric class (real or complex) or of class logical.

\section*{xdata}

Two-element vector that specifies the \(x\)-coordinates of the first and last columns of \(B\).

Note Sometimes the output values xdata and ydata do not exactly equal the input 'XData' and 'YData' arguments. The values differ either because of the need for an integer number of rows and columns, or because you specify values for 'XData', 'YData', 'XYScale', and 'Size' that are not entirely consistent. In either case, the first element of xdata and ydata always equals the first element of 'XData' and 'YData', respectively. Only the second elements of xdata and ydata can be different.

\section*{ydata}

Two-element vector that specifies the \(y\)-coordinates of the first and last rows of B.

Examples

Simple Transformation. Apply a horizontal shear to an intensity image:
```

I = imread('cameraman.tif');
tform = maketform('affine',[1 0 0; .5 1 0; 0 0 1]);
J = imtransform(I,tform);
imshow(I), figure, imshow(J)

```


\section*{Horizontal Shear}

Projective Transformation. Map a square to a quadrilateral with a projective transformation:
\% Set up an input coordinate system so that the input image \% fills the unit square with vertices (0 0),(10),(11),(01). I = imread('cameraman.tif'); udata \(=[01] ;\) vdata \(=[01]\);
\% Transform to a quadrilateral with vertices (-4 2),(-8 3), \(\%(-3-5),\left(\begin{array}{ll}6\end{array}\right)\).
tform \(=\) maketform('projective',[ 0 0; 1 \(0 ; 1\) 1; 0 1],... [-4 2; -8 -3; -3 -5; 6 3]);
\% Fill with gray and use bicubic interpolation.
\% Make the output size the same as the input size.
[B,xdata,ydata] = imtransform(I, tform, 'bicubic', ...
                            'udata', udata,...
                                'vdata', vdata,...
                                'size', size(I),...
                                'fill', 128);
subplot(1,2,1), imshow(I,'XData',udata,'YData',vdata), ...
    axis on
subplot(1,2,2), imshow(B,'XData',xdata,'YData',ydata), ...
    axis on


\section*{Projective Transformation}

Image Registration. Register an aerial photo to an orthophoto:
\% Read in the aerial photo. unregistered = imread('westconcordaerial.png'); figure, imshow(unregistered)


\section*{Aerial Photo}
\% Read in the orthophoto. figure, imshow('westconcordorthophoto.png')


\section*{Orthophoto}
\% Load control points that were previously picked. load westconcordpoints
```

% Create a transformation structure for a projective
% transformation.
t_concord = cp2tform(input_points,base_points,'projective');
% Get the width and height of the orthophoto and perform
% the transformation.
info = imfinfo('westconcordorthophoto.png');
registered = imtransform(unregistered,t_concord,...
'XData',[1 info.Width], 'YData',[1 info.Height]);
figure, imshow(registered)

```


\section*{Transformed Image}
```

See Also
checkerboard | cp2tform | imresize | imrotate | maketform | makeresampler | tformarray

```

\section*{Tutorials \\ Tutorials}
- "Translate Image Using maketform and imtransform"
- Exploring Slices from a 3-Dimensional MRI Data Set
- Padding and Shearing an Image Simultaneously

Purpose Display image in image tool

Note imview has been removed. Use imtool instead.

Purpose Convert indexed image to grayscale image
Syntax \(\quad\) I \(=\) ind2gray ( \(X\), map )
Description
\(\mathrm{I}=\) ind2gray ( X , map) converts the image X with colormap map to a grayscale image I. ind2gray removes the hue and saturation information from the input image while retaining the luminance.

Note A grayscale image is also called a gray-scale, gray scale, or gray-level image.

Class Support

Examples
\(X\) can be of class uint8, uint16, single, or double. map is double. I is of the same class as \(X\).
load trees
I = ind2gray(X,map);
imshow(X,map)
figure,imshow(I)

ind2gray converts the colormap to NTSC coordinates using rgb2ntsc, and sets the hue and saturation components ( \(I\) and \(Q\) ) to zero, creating a
gray colormap. ind2gray then replaces the indices in the image \(X\) with the corresponding grayscale intensity values in the gray colormap.

\author{
See Also \\ gray2ind | imshow | imtool | mat2gray | rgb2gray | rgb2ntsc
}

\section*{ind2rgb}

Purpose Convert indexed image to RGB image

\section*{Syntax \(\quad R G B=\operatorname{ind} 2 r g b(X\), map \()\)}

Description \(\quad R G B=\) ind2rgb ( \(X\), map) converts the matrix \(X\) and corresponding colormap map to RGB (truecolor) format.

Class
Support
\(X\) can be of class uint8, uint16, or double. RGB is an m-by-n-by- 3 array of class double.

See Also ind2gray | rgb2ind

\section*{Purpose Read metadata from Interfile file}

Syntax info = interfileinfo(filename)
Description info = interfileinfo(filename) returns a structure whose fields contain information about an image in a Interfile file. filename is a string that specifies the name of the file. The file must be in the current directory or in a directory on the MATLAB path.
The Interfile file format was developed for the exchange of nuclear medicine data. In Interfile 3.3, metadata is stored in a header file, separate from the image data. The two files have the same name with different file extensions. The header file has the file extension .hdr and the image file has the file extension .img.

\section*{Examples Read metadata from an Interfile file.}
```

info = interfileinfo('MyFile.hdr');

```

For more information about this file format, visit the Interfile Archive, maintained by the Department of Medical Physics and Bioengineering, University College, London, UK.

See Also interfileread

\section*{interfileread}

\section*{Purpose Read images in Interfile format}
```

Syntax A = interfileread(filename)
A = interfileread(filename, window)

```

Description \(\quad A=\) interfileread (filename) reads the images in the first energy window of filename into \(A\), where \(A\) is an M-by-N array for a single image and an M-by-N-by-P array for multiple images. The file must be in the current directory or in a directory on the MATLAB path.

A = interfileread(filename, window) reads the images in the energy window specified by window of filename into \(A\).

The images in the energy window must be of the same size.
Examples Read image data from an Interfile file.
img = interfileread('MyFile.hdr');
For more information about this file format, visit the Interfile Archive, maintained by the Department of Medical Physics and Bioengineering, University College, London, UK.

\section*{See also interfileinfo}

\section*{Purpose Convert integer values using lookup table}

\section*{Syntax \\ B = intlut(A, LUT)}

Description
\(B=\) intlut (A, LUT) converts values in array \(A\) based on lookup table LUT and returns these new values in array B.

For example, if A is a vector whose \(k\) th element is equal to alpha, then \(B(k)\) is equal to the LUT value corresponding to alpha, i.e., LUT (alpha+1).

Class Support
 LUT \(=\) repmat(uint8([0 150 200 255]),1,64); \(B=\) intlut (A, LUT)

See Also
ind2gray | rgb2ind

Purpose

\author{
Syntax
}

Description

Notes

Check for presence of Intel Integrated Performance Primitives (Intel IPP) library

TF = ippl
[TF B] = ippl

The Intel Integrated Performance Primitives (Intel IPP) library provides a collection of basic functions used in signal and image processing. The Intel IPP library takes advantage of the parallelism of the Single-Instruction, Multiple-Data (SIMD) instructions that make up the core of the MMX technology and Streaming SIMD Extensions. These instructions are available only on the Intel architecture processors. The Intel IPP library is used by some of the Image Processing Toolbox functions to accelerate their execution time.

TF = ippl returns true (1) if the Intel IPP library is available and false (0) otherwise.
[TF B] = ippl returns an additional column cell array B. The array B contains a string describing the Intel IPP library module.
When the Intel IPP library is available, some of the Image Processing Toolbox arithmetic functions (imabsdiff, imdivide, and immultiply) and the imfilter function take advantage of it. Toolbox functions that use these functions also benefit.

The Intel IPP library is used only for some data types and only under specific conditions. See the help sections of the functions listed above for detailed information on when the Intel IPP library is activated.

You can enable or disable the Intel IPP library by using the Image Processing Preferences dialog box, part of the MATLAB Preferences dialog box. You can open this dialog box by selecting Preferences from the MATLAB Desktop File menu and then choosing Image Processing.
You can also enable or disable the Intel IPP library at the command line. To disable the Intel IPP library, use this command:
iptsetpref('UseIPPL', false)

To enable IPPL, use this command:
iptsetpref('UseIPPL', true)
Note that enabling or disabling the Intel IPP library has the effect of clearing all loaded MEX-files.

See Also imabsdiff | imdivide | imfilter | immultiply | iptprefs
\begin{tabular}{ll} 
Purpose & Add function handle to callback list \\
Syntax & ID = iptaddcallback ( h , callback, func_handle)
\end{tabular} Description \begin{tabular}{l} 
ID = iptaddcallback ( h , callback, func_handle) adds the function \\
handle func_handle to the list of functions to be called when the \\
callback specified by callback executes. callback is a string specifying \\
the name of a callback property of the Handle Graphics object specified \\
by the handle h. \\
iptaddcallback returns a unique callback identifier, ID, that can be \\
used with iptremovecallback to remove the function from the callback \\
list. \\
iptaddcallback can be useful when you need to notify more than one \\
tool about the same callback event for a single object.
\end{tabular}

\section*{Purpose Check validity of connectivity argument}
```

Syntax

```
```

iptcheckconn(conn, func_name, var_name, arg_pos)

```
```

iptcheckconn(conn, func_name, var_name, arg_pos)

```
Description
iptcheckconn(conn, func_name, var_name, arg_pos) checks whether conn is a valid connectivity argument. If it is invalid, the function issues a formatted error message.
A connectivity argument can be one of the following scalar values: 1, 4, \(6,8,18\), or 26 . A connectivity argument can also be a 3 -by- 3 -by- ... -by- 3 array of 0 's and 1 s . The central element of a connectivity array must be nonzero and the array must be symmetric about its center.
func_name is a string that specifies the name used in the formatted error message to identify the function checking the connectivity argument.
var_name is a string that specifies the name used in the formatted error message to identify the argument being checked.
arg_pos is a positive integer that indicates the position of the argument being checked in the function argument list. iptcheckconn includes this information in the formatted error message.

\section*{Class Support}

\section*{Examples \\ Create a 4 -by- 4 array and pass it as the connectivity argument.}
conn must be of class double or logical and must be real and nonsparse.
```

iptcheckconn(eye(4), 'func_name','var_name',2)

```

\section*{iptcheckhandle}

Purpose Check validity of handle
Syntax iptcheckhandle(H, valid_types, func_name, var_name, arg_pos)
Description

\section*{Examples}

To trigger the error message, create a figure that does not contain an axes object and then check for a valid axes handle.
```

fig = figure; % create figure without an axes
iptcheckhandle(fig,{'axes'},'my_function','my_variable',2)

```

The following shows the format of the error message and indicates which parts you can customize using iptcheckhandle arguments.

iptcheckinput | iptcheckmap | iptchecknargin | iptcheckstrs | iptnum2ordinal

\section*{iptcheckinput}
\begin{tabular}{ll} 
Purpose & \begin{tabular}{l} 
Check validity of array \\
Syntax \\
iptcheckinput (A, classes, attributes, func_name, var_name, \\
arg_pos)
\end{tabular} \\
\begin{tabular}{l} 
iptcheckinput (A, classes, attributes, func_name, var_name, \\
arg_pos) checks the validity of the array A and issues a formatted error \\
message if it is invalid.
\end{tabular} \\
classes is a cell array of strings specifying the set of classes to \\
which A is expected to belong. For example, if you specify classes as \\
\{'logical' 'cell'\}, A is required to be either a logical array or a cell \\
array. The string 'numeric' is interpreted as an abbreviation for the \\
classes uint8, uint16, uint32, int8, int16, int32, single, and double.
\end{tabular}

\section*{iptcheckinput}

\section*{Examples}

To trigger this error message, create a three-dimensional array and then check for the attribute ' 2 d '.
```

A = [ 1 2 3; 4 5 6 ];
B = [ 7 8 9; 10 11 12];
C = cat(3,A,B);
iptcheckinput(C,{'numeric'},{'2d'},'func_name','var_name', 2)

```

The following shows the format of the error message and indicates which parts you can customize using iptcheckinput arguments.


Function FUNC_NAME expected its second input, var_name, to be two-dimensional.


\footnotetext{
See Also
iptcheckhandle | iptcheckmap | iptchecknargin | iptcheckstrs | iptnum2ordinal
}

\section*{iptcheckmap}

\section*{Purpose Check validity of colormap}
```

Syntax iptcheckmap(map, func_name, var_name, arg_pos)

```

Description
iptcheckmap(map, func_name, var_name, arg_pos) checks the validity of the MATLAB colormap and issues a formatted error message if it is invalid.
func_name is a string that specifies the name used in the formatted error message to identify the function checking the colormap.
var_name is a string that specifies the name used in the formatted error message to identify the argument being checked.
arg_pos is a positive integer that indicates the position of the argument being checked in the function argument list. iptcheckmap includes this information in the formatted error message.
```

Examples bad_map = ones(10);
iptcheckmap(bad_map,'func_name','var_name',2)

```

The following shows the format of the error message and indicates which parts you can customize using iptcheckmap arguments.


See Also iptcheckhandle | iptcheckinput | iptchecknargin | iptcheckstrs
\(\left.\begin{array}{ll}\text { Purpose } & \text { Check number of input arguments } \\
\text { Syntax } & \begin{array}{l}\text { iptchecknargin(low, high, num_inputs, func_name) }\end{array} \\
\text { Description } & \begin{array}{l}\text { iptchecknargin(low, high, num_inputs, func_name) checks } \\
\text { whether num_inputs is in the range indicated by low and high. If not, } \\
\text { iptchecknargin issues a formatted error message. } \\
\text { low should be a scalar nonnegative integer. }\end{array} \\
\text { high should be a scalar nonnegative integer or Inf. } \\
\text { func_name is a string that specifies the name used in the formatted } \\
\text { error message to identify the function checking the handle. }\end{array}\right\}\)\begin{tabular}{l} 
Create a function and use iptchecknargin to check that the number of \\
arguments passed to the function is within the expected range. \\
function test_function(varargin) \\
iptchecknargin(1,3, nargin, mfilename);
\end{tabular}

Purpose Check validity of option string
```

Syntax
out = iptcheckstrs(in, valid_strs, func_name, var_name,
arg_pos)

```
out = iptcheckstrs(in, valid_strs, func_name, var_name, arg_pos) checks the validity of the option string in. It returns the matching string in valid_strs in out. iptcheckstrs looks for a case-insensitive, nonambiguous match between in and the strings in valid_strs.
valid_strs is a cell array containing strings.
func_name is a string that specifies the name used in the formatted error message to identify the function checking the strings.
var_name is a string that specifies the name used in the formatted error message to identify the argument being checked.
arg_pos is a positive integer that indicates the position of the argument being checked in the function argument list. iptcheckstrs converts this value to an ordinal number and includes this information in the formatted error message.

\section*{Examples}

To trigger this error message, define a cell array of some text strings and pass in another string that isn't in the cell array.
```

iptcheckstrs('option3',{'option1','option2'},...
'func_name','var_name',2)

```

The following shows the format of the error message and indicates which parts you can customize using iptcheckhandle arguments.


\author{
See Also
}
iptcheckhandle | iptcheckinput | iptcheckmap | iptchecknargin | iptnum2ordinal

\section*{iptdemos}

Purpose Index of Image Processing Toolbox examples

\section*{Syntax iptdemos}

Description iptdemos displays the HTML page that lists all the Image Processing examples. iptdemos displays the page in the MATLAB Help browser.
Purpose Get Application Programmer Interface (API) for handle
Syntax API = iptgetapi(h)
Description API = iptgetapi(h) returns the API structure associated with handle\(h\) if there is one. Otherwise, iptgetapi returns an empty array.
For more information about handle APIs, see the help for immagbox, impositionrect, or imscrollpanel.
Examples hFig = figure('Toolbar','none',... 'Menubar','none');

hIm = imshow('tape.png');

hSP = imscrollpanel(hFig,hIm);

api = iptgetapi(hSP);

api.setMagnification(2) \% 2X = 200\%
See Also immagbox | imrect | imscrollpanel

\section*{iptGetPointerBehavior}

Purpose Retrieve pointer behavior from HG object
```

Syntax
pointerBehavior = iptGetPointerBehavior(h)

```

Description
pointerBehavior = iptGetPointerBehavior(h) returns the pointer behavior structure associated with the Handle Graphics object h. A pointer behavior structure contains function handles that interact with a figure's pointer manager (see iptPointerManager) to control what happens when the figure's mouse pointer moves over and then exits the object. See iptSetPointerBehavior for details.

If \(h\) does not contain a pointer behavior structure, iptGetPointerBehavior returns [].

\section*{See Also}
iptPointerManager | iptSetPointerBehavior

\section*{Purpose Get values of Image Processing Toolbox preferences}
```

Syntax
prefs = iptgetpref
value = iptgetpref(prefname)

```

Description prefs = iptgetpref returns a structure containing all the Image Processing Toolbox preferences with their current values. Each field in the structure has the name of an Image Processing Toolbox preference.
value \(=\) iptgetpref(prefname) returns the value of the Image Processing Toolbox preference specified by the string prefname. See iptprefs for a complete list of valid preference names or access the Image Processing preferences dialog box from the File menu in the MATLAB desktop. Preference names are not case sensitive and can be abbreviated.
```

Examples value = iptgetpref('ImshowAxesVisible')
value =
off

```

See Also imshow | iptprefs | iptsetpref

\section*{ipticondir}
Purpose Directories containing IPT and MATLAB icons
Syntax [D1, D2] = ipticondir
Description [D1, D2] = ipticondir returns the names of the directories containing the Image Processing Toolbox icons (D1) and the MATLAB icons (D2).
Examples [iptdir, MATLABdir] = ipticondir dir(iptdir)
See Also ..... imtool

Purpose Convert positive integer to ordinal string
Syntax string = iptnum2ordinal(number)
Description string = iptnum2ordinal (number) converts the positive integer number to the ordinal text string string.

Examples The following example returns the string 'fourth '.
str = iptnum2ordinal(4)
The following example returns the string ' 23 rd'.
str \(=\) iptnum2ordinal(23)

\section*{iptPointerManager}
\begin{tabular}{ll} 
Purpose & Create pointer manager in figure \\
Syntax & \begin{tabular}{l} 
iptPointerManager(hFigure) \\
iptPointerManager(hFigure, 'disable') \\
iptPointerManager(hFigure, 'enable')
\end{tabular}
\end{tabular}
iptPointerManager(hFigure) creates a pointer manager in the specified figure. The pointer manager controls pointer behavior for any Handle Graphics objects in the figure that contain pointer behavior structures. Use iptSetPointerBehavior to associate a pointer behavior structure with a particular object to define specific actions that occur when the mouse pointer moves over and then leaves the object. See iptSetPointerBehavior for more information.
iptPointerManager(hFigure, 'disable') disables the figure's pointer manager.
iptPointerManager(hFigure, 'enable') enables and updates the figure's pointer manager.

Note If the figure already contains a pointer manager, iptPointerManager(hFigure) does not create a new one. It has the same effect as iptPointerManager(hFigure, 'enable').

Tips
iptPointerManager considers not just the object the pointer is over, but all objects in the figure. iptPointerManager searches the HG hierarchy to find the first object that contains a pointer behavior structure. The iptPointerManager then executes that object's pointer behavior function. For example, you could set the pointer to be a fleur and associate that pointer with the axes. Then, when you slide the pointer into the figure window, it will initially be the default pointer, then change to a fleur when you cross into the axes, and remain a fleur when you slide over the objects parented to the axes.

\section*{iptPointerManager}
```

Examples Plot a line. Create a pointer manager in the figure. Then, associate a pointer behavior structure with the line object in the figure that changes the mouse pointer into a fleur whenever the pointer is over it.

```
```

h = plot(1:10);

```
h = plot(1:10);
iptPointerManager(gcf);
iptPointerManager(gcf);
enterFcn = @(hFigure, currentPoint)...
enterFcn = @(hFigure, currentPoint)...
    set(hFigure, 'Pointer', 'fleur');
    set(hFigure, 'Pointer', 'fleur');
iptSetPointerBehavior(h, enterFcn);
iptSetPointerBehavior(h, enterFcn);
See Also iptGetPointerBehavior | iptSetPointerBehavior
```

Purpose Display Image Processing Preferences dialog box

## Syntax iptprefs

Description iptprefs opens the Image Processing Preferences dialog box, part of the MATLAB Preferences dialog box. You can also open this dialog box by selecting Preferences from the MATLAB Desktop File menu, and then choosing Image Processing.

The Image Processing Preferences dialog box contains display preferences for imtool and imshow and an option for enabling the Intel Integrated Performance Primitives (Intel IPP) library. Also, you can set all preferences at the command line with the iptsetpref function. To see how the options in the dialog box correspond to the commands, view the following picture.


## Image Processing Preferences Dialog Box

The following table details the available preferences and their syntaxes. Note that preference names are case insensitive and you can abbreviate them. The default value appears enclosed in braces (\{\}).

## iptprefs

## Available Image Processing Preferences

| Preference Name | Description |
| :---: | :---: |
| 'ImtoolStartWithOverview' | Controls whether the Overview tool opens automatically when you open an image using the Image Tool (imtool). Possible values: <br> true- Overview tool opens when you open an image. <br> \{false\}- Overview tool does not open when you open an image. This is the default behavior. |
| 'ImtoolInitialMagnification' | Controls the initial magnification of the image displayed by imtool. Possible values: <br> \{'adaptive' \} - Display the entire image. If the image is too large to display on the screen at $100 \%$ magnification, display the image at the largest magnification that fits on the screen. This is the default. <br> Any numeric value - Specify the magnification as a percentage. A magnification of $100 \%$ means that there should be one screen pixel for every image pixel. <br> ' fit ' - Scale the image so that it fits into the window in its entirety. <br> You can override this preference by specifying the 'InitialMagnification' parameter when you call imtool. |

## Available Image Processing Preferences (Continued)

| Preference Name | Description |
| :---: | :---: |
| 'ImshowAxesVisible' | Controls whether imshow displays images with the axes box and tick labels. Possible values: <br> ' on ' - Include axes box and tick labels. <br> \{'off'\} — Do not include axes box and tick labels. |
| 'ImshowBorder' | Controls whether imshow includes a border around the image in the figure window. Possible values: <br> \{'loose' \} - Include a border between the image and the edges of the figure window, thus leaving room for axes labels, titles, etc. 'tight ' - Adjust the figure size so that the image entirely fills the figure. |
|  | Note There still can be a border if the image is very small, or if there are other objects besides the image and its axes in the figure. |
|  | You can override this preference by specifying the 'Border' parameter when you call imshow. |

## iptprefs

## Available Image Processing Preferences (Continued)

| Preference Name | Description |
| :--- | :--- |
| 'ImshowInitialMagnification' | Controls the initial magnification of the <br> image displayed by imshow. Possible values: <br> Any numeric value - imshow interprets <br> numeric values as a percentage. The default <br> value is 100. A magnification of 100\% <br> means that there should be one screen pixel <br> for every image pixel. <br> 'fit - Scale the image so that it fits into <br> the window in its entirety. |
|  | You can override this preference by <br> specifying the ' Initialmagnification' <br> parameter when you call imshow, or by <br> calling the truesize function manually <br> after displaying the image. |
| 'UseIPPL' | Controls whether some toolbox functions <br> use the Intel IPP library or not. Possible <br> values: |
|  | \{true - Enable use of the Intel IPP library. |
| false - Disable use of the Intel IPP library. |  |
|  | Note: Setting this preference value clears <br> all loaded MEX-files. |

[^4]
## Purpose Delete function handle from callback list

## Syntax iptremovecallback(h,callback, ID)

Description
iptremovecallback ( h , callback, ID) deletes a callback from the list of callbacks created by imaddcallback for the object with handle $h$ and the associated callback string callback. ID is the identifier of the callback to be deleted. This ID is returned by iptaddcallback when you add the function handle to the callback list.

Examples Register three callbacks and try them interactively.
h = figure;
f1 = @(varargin) disp('Callback 1');
f2 = @(varargin) disp('Callback 2');
f3 = @(varargin) disp('Callback 3');
id1 = iptaddcallback(h, 'WindowButtonMotionFcn', f1);
id2 = iptaddcallback(h, 'WindowButtonMotionFcn', f2);
id3 = iptaddcallback(h, 'WindowButtonMotionFcn', f3);
Remove one of the callbacks and then move the mouse over the figure again. Whenever MATLAB detects mouse motion over the figure, function handles f1 and f3 are called in that order.
iptremovecallback(h, 'WindowButtonMotionFcn', id2);
See Also iptaddcallback

## iptSetPointerBehavior

| Purpose | Store pointer behavior structure in Handle Graphics object |
| :--- | :--- |
| Syntax | iptSetPointerBehavior $(h$, pointerBehavior $)$ <br> iptSetPointerBehavior $(h,[])$ <br> iptSetPointerBehavior $(h$, enterFcn $)$ |

Description
iptSetPointerBehavior(h, pointerBehavior) stores the specified pointer behavior structure in the specified Handle Graphics object, h. If $h$ is an array of objects, iptSetPointerBehavior stores the same structure in each object.

When used with a figure's pointer manager (see iptPointerManager), a pointer behavior structure controls what happens when the figure's mouse pointer moves over and then exits an object in the figure. For details about this structure, see "Pointer Behavior Structure" on page 3-614.
iptSetPointerBehavior(h, []) clears the pointer behavior from the Handle Graphics object or objects.
iptSetPointerBehavior(h, enterFcn) creates a pointer behavior structure, setting the enterFcn field to the function handle specified, and setting the traverseFcn and exitFcn fields to []. See "Pointer Behavior Structure" on page 3-614 for details about these fields. This syntax is provided as a convenience because, for most common uses, only the enterFcn is necessary.

## Pointer Behavior Structure

A pointer behavior structure contains three fields: enterFcn, traverseFcn, and exitFcn. You set the value of these fields to function handles and use the iptSetPointerBehavior function to associate this structure with an HG object in a figure. If the figure has a pointer manager installed, the pointer manager calls these functions when the following events occur. If you set a field to [ ], no action is taken.

| Function Handle | When Called |
| :--- | :--- |
| enterFcn | Called when the mouse pointer moves over <br> the object. |
| traverseFcn | Called once when the mouse pointer moves <br> over the object, and called again each time <br> the mouse moves within the object. |
| exitFcn | Called when the mouse pointer leaves the <br> object. |

When the pointer manager calls the functions you create, it passes two arguments: a handle to the figure and the current position of the pointer.

## Examples Example 1

Change the mouse pointer to a fleur whenever it is over a specific object and restore the original pointer when the mouse pointer moves off the object. The example creates a patch object and associates a pointer behavior structure with the object. Because this scenario requires only an enterFcn, the example uses the iptSetPointerBehavior ( $n$, enterFcn) syntax. The example then creates a pointer manager in the figure. Note that the pointer manager takes care of restoring the original figure pointer.

```
hPatch = patch([. 25 .75 .75 . 25 .25],...
    [.25 .25 .75 .75 .25], 'r');
xlim([0 1]);
ylim([0 1]);
enterFcn = @(figHandle, currentPoint)...
    set(figHandle, 'Pointer', 'fleur');
iptSetPointerBehavior(hPatch, enterFcn);
iptPointerManager(gcf);
```


## iptSetPointerBehavior

## Example 2

Change the appearance of the mouse pointer, depending on where it is within the object. This example sets up the pointer behavior structure, setting the enterFcn and exitFcn fields to [], and setting traverseFen to a function named overMe that handles the position-specific behavior. overMe is an example function (in \toolbox \images $\backslash i m d e m o s$ ) that varies the mouse pointer depending on the location of the mouse within the object. For more information, edit overMe.

```
hPatch = patch([.25 .75 .75 .25 .25],...
    [.25 .25 .75 .75 .25], 'r');
```

$x \lim \left(\left[\begin{array}{ll}0 & 1\end{array}\right]\right)$
ylim([0 1])

```
pointerBehavior.enterFcn = [];
pointerBehavior.exitFcn = [];
pointerBehavior.traverseFcn = @overMe;
iptSetPointerBehavior(hPatch, pointerBehavior);
iptPointerManager(gcf);
```


## Example 3

Change the figure's title when the mouse pointer is over the object. In this scenario, enterFcn and exitFcn are used to achieve the desired side effect, and traverseFcn is [].

```
hPatch = patch([.25 .75 .75 .25 .25],...
    [.25 .25 .75 .75 .25], 'r');
xlim([0 1])
ylim([0 1])
pointerBehavior.enterFcn = ...
    @(figHandle, currentPoint)...
            set(figHandle, 'Name', 'Over patch');
pointerBehavior.exitFcn = ...
    @(figHandle, currentPoint) set(figHandle, 'Name', '');
pointerBehavior.traverseFcn = [];
```

iptSetPointerBehavior(hPatch, pointerBehavior); iptPointerManager(gcf)

See Also iptGetPointerBehavior | iptPointerManager

## iptsetpref

Purpose Set Image Processing Toolbox preferences or display valid values
Syntax iptsetpref(prefname) ..... iptsetpref(prefname, value)
Description iptsetpref(prefname) displays the valid values for the ImageProcessing Toolbox preference specified by prefname.iptsetpref(prefname, value) sets the Image Processing Toolboxpreference specified by the string prefname to the value specified byvalue. The setting persists until you change it. You can also usethe Image Processing Preferences dialog box to set the preferences.To access the dialog, select Preferences from the File menu in theMATLAB desktop. For more information about available preferences,see iptprefs.
Examples iptsetpref('ImshowBorder','tight')
See Also imshow | imtool | iptgetpref | iptprefs

## iptwindowalign

## Purpose

Align figure windows

## Syntax

Description moving_fig_edge)
iptwindowalign(fixed_fig, fixed_fig_edge, moving_fig,
iptwindowalign(fixed_fig, fixed_fig_edge, moving_fig, moving_fig_edge) moves the figure moving_fig to align it with the figure fixed_fig. moving_fig and fixed_fig are handles to figure objects.
fixed_fig_edge and moving_fig_edge describe the alignment of the figures in relation to their edges and can take any of the following values: 'left', 'right', 'hcenter', 'top', 'bottom', or 'vcenter'. 'hcenter' means center horizontally and 'vcenter' means center vertically. The following figure shows these alignments.


## iptwindowalign

## Notes

The two specified locations must be consistent in terms of their direction. For example, you cannot specify 'left' for fixed_fig_edge and 'bottom' for moving_fig_edge.
iptwindowalign constrains the position adjustment of moving_fig to keep it entirely visible on the screen.
iptwindowalign has no effect if either figure window is docked.
Examples
To illustrate some possible figure window alignments, first create two figures: fig1 and fig2. Initially, fig2 overlays fig1 on the screen.
fig1 = figure;
fig2 = figure;

Use iptwindowalign to move fig2 so its left edge is aligned with the right edge of fig1.

```
iptwindowalign(fig1,'right',fig2,'left');
```



Now move fig2 so its top edge is aligned with the bottom edge of fig1.

```
iptwindowalign(fig1, 'bottom', fig2, 'top');
```



Now move fig2 so the two figures are centered horizontally. iptwindowalign(fig1, 'hcenter', fig2, 'hcenter');

## iptwindowalign



Purpose
Inverse Radon transform
Syntax

```
I = iradon(R, theta)
I = iradon(P, theta, interp, filter, frequency_scaling,
    output_size)
[I,H] = iradon(...)
```

Description
$I=$ iradon( $R$, theta) reconstructs the image $I$ from projection data in the two-dimensional array R. The columns of $R$ are parallel beam projection data. iradon assumes that the center of rotation is the center point of the projections, which is defined as ceil(size ( $\mathrm{R}, 1$ )/2).
theta describes the angles (in degrees) at which the projections were taken. It can be either a vector containing the angles or a scalar specifying $D$ _theta, the incremental angle between projections. If theta is a vector, it must contain angles with equal spacing between them. If theta is a scalar specifying $D$ _theta, the projections were taken at angles theta $=m * D \_$theta, where $m=0,1,2, \ldots$, size $(R, 2)-1$. If the input is the empty matrix ([]), D_theta defaults to $180 / \operatorname{size}(R, 2)$.
iradon uses the filtered back-projection algorithm to perform the inverse Radon transform. The filter is designed directly in the frequency domain and then multiplied by the FFT of the projections. The projections are zero-padded to a power of 2 before filtering to prevent spatial domain aliasing and to speed up the FFT.
I = iradon(P, theta, interp, filter, frequency_scaling, output_size) specifies parameters to use in the inverse Radon transform. You can specify any combination of the last four arguments. iradon uses default values for any of these arguments that you omit.
interp specifies the type of interpolation to use in the back projection. The available options are listed in order of increasing accuracy and computational complexity.

| Value | Description |
| :--- | :--- |
| 'nearest' | Nearest-neighbor interpolation |
| 'linear' | Linear interpolation (the default) |


| Value | Description |
| :--- | :--- |
| 'spline ' | Spline interpolation |
| 'pchip' | Shape-preserving piecewise cubic interpolation |
| 'cubic' $^{\text {'v5cubic' }}$ | Same as 'pchip' |
| Cubic interpolation from MATLAB 5. This method <br> does not extrapolate, and it issues a warning and <br> uses 'spline ' if X is not equally spaced. |  |

filter specifies the filter to use for frequency domain filtering. filter can be any of the strings that specify standard filters.

| Value | Description |
| :--- | :--- |
| 'Ram-Lak' | Cropped Ram-Lak or ramp filter. This is the <br> default. The frequency response of this filter is I <br> f I. Because this filter is sensitive to noise in the <br> projections, one of the filters listed below might be <br> preferable. These filters multiply the Ram-Lak filter <br> by a window that deemphasizes high frequencies. |
| 'Shepp-Logan' | Multiplies the Ram-Lak filter by a sinc function |
| 'Cosine' | Multiplies the Ram-Lak filter by a cosine function |
| 'Hamming' | Multiplies the Ram-Lak filter by a Hamming <br> window |
| 'Hann' | Multiplies the Ram-Lak filter by a Hann window |
| 'None' | No filtering. When you specify this value, iradon <br> returns unfiltered backprojection data. |

frequency_scaling is a scalar in the range $(0,1]$ that modifies the filter by rescaling its frequency axis. The default is 1 . If frequency_scaling is less than 1 , the filter is compressed to fit into the frequency range [ 0, frequency_scaling], in normalized frequencies; all frequencies above frequency_scaling are set to 0 .
output_size is a scalar that specifies the number of rows and columns in the reconstructed image. If output_size is not specified, the size is determined from the length of the projections.
output_size = 2*floor(size(R,1)/(2*sqrt(2)))

If you specify output_size, iradon reconstructs a smaller or larger portion of the image but does not change the scaling of the data. If the projections were calculated with the radon function, the reconstructed image might not be the same size as the original image.
$[\mathrm{I}, \mathrm{H}]=$ iradon(...) returns the frequency response of the filter in the vector H .

Class Support

Examples

R can be double or single. All other numeric input arguments must be of class double. I has the same class as R. H is double.

Compare filtered and unfiltered backprojection.

```
P = phantom(128);
R = radon(P,0:179);
I1 = iradon(R,0:179);
I2 = iradon(R,0:179,'linear','none');
subplot(1,3,1), imshow(P), title('Original')
subplot(1,3,2), imshow(I1), title('Filtered backprojection')
subplot(1,3,3), imshow(I2,[]), title('Unfiltered backprojection')
```



## iradon

Compute the backprojection of a single projection vector. The iradon syntax does not allow you to do this directly, because if theta is a scalar it is treated as an increment. You can accomplish the task by passing in two copies of the projection vector and then dividing the result by 2 .

```
P = phantom(128);
R = radon(P,0:179);
r45 = R(:,46);
I = iradon([r45 r45], [45 45])/2;
imshow(I, [])
title('Backprojection from the 45-degree projection')
```


## Algorithms

References

See Also
iradon uses the filtered back projection algorithm to perform the inverse Radon transform. The filter is designed directly in the frequency domain and then multiplied by the FFT of the projections. The projections are zero-padded to a power of 2 before filtering to prevent spatial domain aliasing and to speed up the FFT.
[1] Kak, A. C., and M. Slaney, Principles of Computerized Tomographic Imaging, New York, NY, IEEE Press, 1988.
fan2para | fanbeam | ifanbeam | para2fan | phantom | radon
Purpose True for binary image
Syntax flag = isbw(A)
isbw has been removed.
Description flag $=$ isbw(A) returns 1 if $A$ is a binary image and 0 otherwise.The input image $A$ is considered to be a binary image if it is a nonsparselogical array.
Class The input image A can be any MATLAB array. Support
See Also ..... isind | isgray | isrgb

Purpose True for flat structuring element

## Syntax $\quad$ TF $=$ isflat $(S E)$

Description TF = isflat(SE) returns true (1) if the structuring element SE is flat; otherwise it returns false (0). If SE is an array of STREL objects, then TF is the same size as SE.

Class
SE is a STREL object. TF is a double-precision value.
Support
See Also strel
Purpose True for grayscale image
Syntax flag = isgray(A)
isgray has been removed.
Description flag = isgray (A) returns 1 if $A$ is a grayscale intensity image and 0 otherwise.
isgray uses these criteria to decide whether $A$ is an intensity image:

- If A is of class double, all values must be in the range [0,1], and the number of dimensions of $A$ must be 2 .
- If A is of class uint16 or uint8, the number of dimensions of A must be 2 .

Note A four-dimensional array that contains multiple grayscale images returns 0 , not 1 .

The input image A can be of class logical, uint8, uint16, or double.

See Also isbw | isind | isrgb

Purpose True for valid ICC color profile

## Syntax $\quad$ TF $=\operatorname{isicc}(P)$

Description TF $=\operatorname{isicc}(P)$ returns True if structure $P$ is a valid ICC color profile; otherwise False.
isicc checks if $P$ has a complete set of the tags required for an ICC profile. P must contain a Header field, which in turn must contain a Version field and a DeviceClass field. These fields, and others, are used to determine the set of required tags according to the ICC Profile Specification, either Version 2 (ICC.1:2001-04) or Version 4 (ICC.1:2001-12), which are available at www.color.org. The set of required tags is given in Section 6.3 in either version.

## Examples

Read in an ICC profile and isicc returns True.

```
P = iccread('sRGB.icm');
```

TF = isicc( P )
TF =

1
This example creates a MATLAB structure and uses isicc to test if it's a valid ICC profile. isicc returns False.
S.name = 'Any Student';
S.score = 83;
S.grade $=$ ' $B+$ '

TF = isicc(S)
TF =

See Also applycform | iccread | iccwrite | makecform

## Purpose True for indexed image

## Syntax flag $=$ isind $(A)$

isind has been removed.

## Description <br> flag $=$ isind $(A)$ returns 1 if $A$ is an indexed image and 0 otherwise. <br> isind uses these criteria to determine if $A$ is an indexed image: <br> - If A is of class double, all values in A must be integers greater than or equal to 1 , and the number of dimensions of $A$ must be 2 . <br> - If A is of class uint8 or uint16, the number of dimensions of A must be 2 .

Note A four-dimensional array that contains multiple indexed images returns 0 , not 1 .

## Class A can be of class logical, uint8, uint16, or double.

```
isbw | isgray | isrgb
```

Purpose
Check if file is National Imagery Transmission Format (NITF) file
Syntax [tf, NITF_version] = isnitf(filename)
Description
[tf, NITF_version] = isnitf(filename) returns True (1) if the file specified by filename is a National Imagery Transmission Format (NITF) file, otherwise False (0). If the file is a NITF file, isnitf returns a text string identifying the NITF version in NITF_version, such as '2.1'. If the file is not a NITF file, NITF_version contains the text string 'UNK'.

See Also nitfinfo|nitfread

Purpose True for RGB image
Syntax flag $=\operatorname{isrgb}(A)$
isrgb has been removed.

## Description

flag $=$ isrgb ( $A$ ) returns 1 if $A$ is an RGB truecolor image and 0 otherwise.
isrgb uses these criteria to determine whether A is an RGB image:

- If A is of class double, all values must be in the range [0,1], and A must be m-by-n-by-3.
- If A is of class uint16 or uint8, A must be m-by-n-by-3.

Note A four-dimensional array that contains multiple RGB images returns 0 , not 1 .

## Class A can be of class logical, uint8, uint16, or double. <br> Support

See Also isbw | isgray | isind

## Purpose Check if file is R-Set

```
Syntax [tf, supported] = isrset(filename)
```

Description [tf, supported] = isrset(filename) sets tf to true if the file filename is a reduced resolution dataset (R-Set) created by rsetwrite and false if it is not. The value of supported is true if the R -Set file is compatible with the $R$-Set tools (such as imtool) in the version of the Image Processing Toolbox you are using. If supported is false, the R-Set file was probably created by a newer version of rsetwrite than the one in the version of the Image Processing Toolbox you are using.

## See Also <br> rsetwrite

## lab2double

## Purpose Convert $L^{*} a^{*} b^{*}$ data to double

Syntax labd = lab2double(lab)
Description labd = lab2double(lab) converts an M-by-3 or M-by-N-by-3 array of $L^{*} a^{*} b^{*}$ color values to class double. The output array labd has the same size as lab.

The Image Processing Toolbox software follows the convention that double-precision $L^{*} a^{*} b^{*}$ arrays contain 1976 CIE $L^{*} a^{*} b^{*}$ values. $L^{*} a^{*} b^{*}$ arrays that are uint8 or uint 16 follow the convention in the ICC profile specification (ICC.1:2001-4, www.color.org) for representing $L^{*} a^{*} b^{*}$ values as unsigned 8 -bit or 16 -bit integers. The ICC encoding convention is illustrated by these tables.

| Value (L*) | uint8 Value | uint16 Value |
| :--- | :--- | :--- |
| 0.0 | 0 | 0 |
| 100.0 | 255 | 65280 |
| $100.0+$ <br> $(25500 / 65280)$ | None | 65535 |


| Value (a* or $\mathbf{b}^{*}$ ) | uint8 Value | uint16 Value |
| :--- | :--- | :--- |
| -128.0 | 0 | 0 |
| 0.0 | 128 | 32768 |
| 127.0 | 255 | 65280 |
| $127.0+(255 / 256)$ | None | 65535 |

## Class

lab is a uint8, uint16, or double array that must be real and nonsparse. labd is double.

Examples Convert full intensity neutral color (white) from uint8 to double.
lab2double(uint8([255 128 128]))

```
ans =
    100 0 0
```

See Also applycform | lab2uint8 | lab2uint16 | makecform | whitepoint | xyz2double | xyz2uint16

## lab2uint 16

## Purpose Convert $L^{*} a^{*} b^{*}$ data to uint16

Syntax lab16 = lab2uint16(lab)
Description lab16 = lab2uint16(lab) converts an M-by-3 or M-by-N-by-3 array of $L^{*} a^{*} b^{*}$ color values to uint16. lab16 has the same size as lab.

The Image Processing Toolbox software follows the convention that double-precision $L^{*} a^{*} b^{*}$ arrays contain 1976 CIE $L^{*} a^{*} b^{*}$ values. $L^{*} a^{*} b^{*}$ arrays that are uint8 or uint16 follow the convention in the ICC profile specification (ICC.1:2001-4, www.color.org) for representing $L^{*} a^{*} b *$ values as unsigned 8 -bit or 16 -bit integers. The ICC encoding convention is illustrated by these tables.

| Value (L*) | uint8 Value | uint16 Value |
| :--- | :--- | :--- |
| 0.0 | 0 | 0 |
| 100.0 | 255 | 65280 |
| $100.0+(25500 / 65280)$ | None | 65535 |


| Value (a* or $\mathbf{b}^{*}$ ) | uint8 Value | uint16 Value |
| :--- | :--- | :--- |
| -128.0 | 0 | 0 |
| 0.0 | 128 | 32768 |
| 127.0 | 255 | 65280 |
| $127.0+(255 / 256)$ | None | 65535 |

## Class <br> Support

lab can be a uint8, uint16, or double array that must be real and nonsparse. lab16 is of class uint16.

Examples Convert full intensity neutral color (white) from double to uint16.

```
lab2uint16(100 0 0)
ans =
```


## See Also

applycform | lab2double | lab2uint8 | makecform | whitepoint | xyz2double | xyz2uint16

## lab2uint8

## Purpose Convert $L^{*} a^{*} b^{*}$ data to uint8

Syntax lab8 = lab2uint8(lab)
Description lab8 = lab2uint8(lab) converts an M-by-3 or M-by-N-by-3 array of $L^{*} a^{*} b^{*}$ color values to uint8. lab8 has the same size as lab.
The Image Processing Toolbox software follows the convention that double-precision $L^{*} a^{*} b^{*}$ arrays contain 1976 CIE $L^{*} a^{*} b^{*}$ values. $L^{*} a^{*} b^{*}$ arrays that are uint8 or uint16 follow the convention in the ICC profile specification (ICC.1:2001-4, www.color.org) for representing $L^{*} a^{*} b^{*}$ values as unsigned 8 -bit or 16 -bit integers. The ICC encoding convention is illustrated by these tables.

| Value (L*) | uint8 Value | uint16 Value |
| :--- | :--- | :--- |
| 0.0 | 0 | 0 |
| 100.0 | 255 | 65280 |
| $100.0+$ <br> $(25500 / 65280)$ | None | 65535 |


| Value (a* or $\mathbf{b}^{*}$ ) | uint8 Value | uint16 Value |
| :--- | :--- | :--- |
| -128.0 | 0 | 0 |
| 0.0 | 128 | 32768 |
| 127.0 | 255 | 65280 |
| $127.0+(255 / 256)$ | None | 65535 |

## Class <br> Support

lab is a uint8, uint16, or double array that must be real and nonsparse. lab8 is uint8.

Examples Convert full intensity neutral color (white) from double to uint8.
lab2uint8([100 0 0 $]$ )
ans =

## lab2uint8

See Also applycform | lab2double | lab2uint16 | makecform | whitepoint | xyz2double | xyz2uint16

## label2rgb

Purpose
Convert label matrix into RGB image
Syntax
RGB = label2rgb(L)
RGB $=$ label2rgb(L, map)
RGB = label2rgb(L, map, zerocolor)
RGB = label2rgb(L, map, zerocolor, order)

## Description

RGB = label2rgb( L ) converts a label matrix, $L$, such as those returned by labelmatrix, bwlabel, bwlabeln, or watershed, into an RGB color image for the purpose of visualizing the labeled regions. The label2rgb function determines the color to assign to each object based on the number of objects in the label matrix and range of colors in the colormap. The label2rgb function picks colors from the entire range.

RGB = label2rgb(L, map) defines the colormap map to be used in the RGB image. map can have any of the following values:

- $n$-by- 3 colormap matrix
- String containing the name of a MATLAB colormap function, such as 'jet' or 'gray' (See colormap for a list of supported colormaps.)
- Function handle of a colormap function, such as @jet or @gray

If you do not specify map, the default value is ' jet'.
RGB = label2rgb(L, map, zerocolor) defines the RGB color of the elements labeled 0 (zero) in the input label matrix L. As the value of zerocolor, specify an RGB triple or one of the strings listed in this table.

| Value | Color |
| :--- | :--- |
| $'^{\prime} b^{\prime}$ | Blue |
| $'^{\prime} c^{\prime}$ | Cyan |
| $'^{\prime} g^{\prime}$ | Green |
| $' k '$ | Black |
| $'^{\prime} m^{\prime}$ | Magenta |


| Value | Color |
| :--- | :--- |
| $' r '$ | Red |
| ' $w$ ' | White |
| ' $y$ ' | Yellow |

If you do not specify zerocolor, the default value for zero-labeled elements is [ $\left.\begin{array}{lll}1 & 1 & 1\end{array}\right]$ (white).

RGB = label2rgb(L, map, zerocolor, order) controls how label2rgb assigns colormap colors to regions in the label matrix. If order is 'noshuffle' (the default), label2rgb assigns colormap colors to label matrix regions in numerical order. If order is 'shuffle', label2rgb assigns colormap colors pseudorandomly.
label2rgb supports the generation of efficient, production-quality C/C++ code from MATLAB. For best results, when using the standard syntax:

RGB = label2rgb(L, map, zerocolor, order)

- Submit at least two input arguments: the label matrix, L, and the colormap matrix, map.
- map must be an $n$-by-3, double, colormap matrix. You cannot use a string containing the name of a MATLAB colormap function or a function handle of a colormap function.
- If you set the boundary color zerocolor to the same color as one of the regions, label2rgb will not issue a warning.
- If you supply a value for order, it must be 'noshuffle'.

To see a complete list of toolbox functions that support code generation, see "Supported Functions".

Class
The input label matrix $L$ can have any numeric class. It must contain Support finite, nonnegative integers. The output of label2rgb is of class uint8.

## label2rgb

Examples Use label2rgb to customize display of labelmatrix.

```
I = imread('rice.png');
figure, imshow(I)
```



## Original

BW = im2bw(I, graythresh(I));
CC = bwconncomp(BW);
L = labelmatrix(CC);
RGB = label2rgb(L);
figure, imshow(RGB)



## RGB2

## See Also

bwconncomp | bwlabel | colormap | ismember | labelmatrix | watershed

## labelmatrix

Purpose Create label matrix from bwconncomp structure

## Syntax L = labelmatrix(CC)

Description
$L=$ labelmatrix(CC) creates a label matrix from the connected components structure CC returned by bwconncomp. The size of $L$ is CC. ImageSize. The elements of $L$ are integer values greater than or equal to 0 . The pixels labeled 0 are the background. The pixels labeled 1 make up one object; the pixels labeled 2 make up a second object; and so on. The class of L depends on CC. NumObjects, as shown in the following table.

| Class | Range |
| :--- | :--- |
| 'uint8' | CC. Num0bjects $\leq 255$ |
| 'uint16' | $256 \leq$ CC. NumObjects $\leq 65535$ |
| 'uint32' | $65536 \leq$ CC. NumObjects $\leq 2^{32}-1$ |
| 'double' | CC. NumObjects $\geq 2^{32}$ |

labelmatrix is more memory efficient than bwlabel and bwlabeln because it returns its label matrix in the smallest numeric class necessary for the number of objects.

Class Support

## Examples

$C C$ is a structure returned by bwconncomp. The label matrix $L$ is uint8, uint16, uint32, or double.

Calculate the connected components and display results:

```
BW = imread('text.png');
CC = bwconncomp(BW);
L = labelmatrix(CC);
L2 = bwlabel(BW);
whos L L2
```

The output for whos appears as follows:

| Name | Size | Bytes Class | Attributes |
| :---: | :---: | ---: | :--- |
| L | $256 \times 256$ | 65536 uint8 |  |
| L2 | $256 \times 256$ | 524288 double |  |

The output for imshow appears as follows:

## The term watershed refers to a ridge that ...



See Also
bwconncomp | bwlabel | bwlabeln | label2rgb | regionprops

Purpose Create color transformation structure
Syntax

```
C = makecform(type)
C = makecform(type, 'WhitePoint', WP)
C = makecform(type, 'AdaptedWhitePoint', WP)
C = makecform('srgb2cmyk', 'RenderingIntent', intent)
C = makecform('cmyk2srgb', 'RenderingIntent', intent)
C = makecform('adapt', 'WhiteStart', WPS, 'WhiteEnd', WPE,
    'AdaptModel', modelname)
C = makecform('icc', src_profile, dest_profile)
C = makecform('icc', src_profile, dest_profile,
    'SourceRenderingIntent', src_intent, 'DestRenderingIntent',
    dest_intent)
C = makecform('clut', profile, LUTtype)
C = makecform('mattrc', MatTrc, 'Direction', direction)
C = makecform('mattrc', profile, 'Direction', direction)
C = makecform('mattrc', profile, 'Direction', direction,
    'RenderingIntent', intent)
C = makecform('graytrc', profile, 'Direction', direction)
C = makecform('graytrc', profile, 'Direction', direction,
    'RenderingIntent', intent)
C = makecform('named', profile, space)
```


## Description

C = makecform(type) creates the color transformation structure $C$ that defines the color space conversion specified by type. To perform the transformation, pass the color transformation structure as an argument to the applycform function.

The type argument specifies one of the conversions listed in the following table. makecform supports conversions between members of the family of device-independent color spaces defined by the CIE, Commission Internationale de l'Éclairage (International Commission on Illumination). In addition, makecform also supports conversions to and from the $s R G B$ and $C M Y K$ color spaces. For a list of the abbreviations used by the Image Processing Toolbox software for each color space, see the Remarks section of this reference page.

| Type | Description |
| :---: | :---: |
| 'cmyk2srgb' | Convert from the CMYK color space to the $s R G B$ color space. |
| 'lab2lch' | Convert from the $L^{*} a^{*} b^{*}$ to the $L^{*}$ ch color space. |
| 'lab2srgb' | Convert from the $L^{*} a^{*} b^{*}$ to the $s R G B$ color space. |
| 'lab2xyz' | Convert from the $L^{*} a^{*} b^{*}$ to the $X Y Z$ color space. |
| 'lch2lab' | Convert from the $L^{*} c h$ to the $L^{*} a^{*} b^{*}$ color space. |
| 'srgb2cmyk' | Convert from the $s R G B$ to the CMYK color space. |
| 'srgb2lab' | Convert from the $s R G B$ to the $L^{*} a^{*} b^{*}$ color space. |
| 'srgb2xyz' | Convert from the $s R G B$ to the $X Y Z$ color space. |
| 'upvpl2xyz' | Convert from the $u^{\prime} v^{\prime} L$ to the $X Y Z$ color space. |
| 'uvl2xyz' | Convert from the $u v L$ to the $X Y Z$ color space. |
| 'xyl2xyz' | Convert from the $x y Y$ to the $X Y Z$ color space. |
| 'xyz2lab' | Convert from the $X Y Z$ to the $L^{*} a^{*} b^{*}$ color space. |
| 'xyz2srgb' | Convert from the $X Y Z$ to the $s R G B$ color space. |
| 'xyz2upvpl' | Convert from the $X Y Z$ to the $u^{\prime} v^{\prime} L$ color space. |
| 'xyz2uvl' | Convert from the $X Y Z$ to the $u v L$ color space. |
| 'xyz2xyl' | Convert from the $X Y Z$ to the $x y Y$ color space. |

C = makecform(type, 'WhitePoint', WP) specifies the value of the reference white point. type can be either 'xyz2lab' or 'lab2xyz'. WP is a 1 -by- 3 vector of $X Y Z$ values scaled so that $Y=1$. The default is whitepoint('ICC'). Use the whitepoint function to create the WP vector.

C = makecform(type, 'AdaptedWhitePoint', WP) specifies the adapted white point. type can be either 'srgb2lab', 'lab2srgb', 'srgb2xyz', or 'xyz2srgb'. As above, WP is a row vector of XYZ values scaled so that $Y=1$. If not specified, the default adapted white point is whitepoint ('ICC'). To get answers consistent with some published $s R G B$ equations, specify whitepoint ('D65') for the adapted white point.
C = makecform('srgb2cmyk', 'RenderingIntent', intent) and $\mathrm{C}=$ makecform('cmyk2srgb', 'RenderingIntent', intent) specify the rendering intent for transforms of type srgb2cmyk and cmyk2srgb. These transforms convert data between $s R G B$ IEC61966-2.1 and "Specifications for Web Offset Publications" (SWOP) CMYK. intent must be one of these strings: 'AbsoluteColorimetric', 'Perceptual', 'RelativeColorimetric', or 'Saturation'. For more information, see the table Rendering Intent on page 3-651.

C = makecform('adapt', 'WhiteStart', WPS, 'WhiteEnd', WPE, 'AdaptModel', modelname) creates a linear chromatic-adaptation transform. WPS and WPE are row vectors of XYZ values, scaled so that $Y=1$, specifying the starting and ending white points. modelname is either 'vonKries' or 'Bradford' and specifies the type of chromatic-adaptation model to be employed. If 'AdaptModel' is not specified, it defaults to 'Bradford'.
C = makecform('icc', src_profile, dest_profile) creates a color transform based on two ICC profiles. src_profile and dest_profile are ICC profile structures returned by iccread.
C = makecform('icc', src_profile, dest_profile, 'SourceRenderingIntent', src_intent, 'DestRenderingIntent', dest_intent) creates a color transform based on two ICC color profiles,
src_profile and dest_profile, specifying rendering intent arguments for the source, src_intent, and the destination, dest_intent, profiles.
Rendering intents specify the style of reproduction that should be used when these profiles are combined. For most devices, the range of reproducible colors is much smaller than the range of colors represented by the PCS. Rendering intents define gamut mapping techniques. Possible values for these rendering intents are listed below. Each rendering intent has distinct aesthetic and color-accuracy trade-offs.

## Rendering Intent

| Value | Description |
| :--- | :--- |
| 'AbsoluteColorimetric' | Maps all out-of-gamut colors to the nearest gamut <br> surface while maintaining the relationship of all <br> in-gamut colors. This absolute rendering contains <br> color data that is relative to a perfectly reflecting <br> diffuser. |
| 'Perceptual' (default) | Employs vendor-specific gamut mapping techniques <br> for optimizing the range of producible colors of <br> a given device. The objective is to provide the <br> most aesthetically pleasing result even though the <br> relationship of the in-gamut colors might not be <br> maintained. This media-relative rendering contains <br> color data that is relative to the device's white point. |

Rendering Intent (Continued)

| Value | Description |
| :--- | :--- |
| 'RelativeColorimetric' | Maps all out-of-gamut colors to the nearest gamut <br> surface while maintaining the relationship of all <br> in-gamut colors. This media-relative rendering <br> contains color data that is relative to the device's <br> white point. |
| 'Saturation' | Employs vendor-specific gamut mapping techniques <br> for maximizing the saturation of device colors. This <br> rendering is generally used for simple business <br> graphics such as bar graphs and pie charts. This <br> media-relative rendering contains color data that is <br> relative to the device's white point. |

C = makecform('clut', profile, LUTtype) creates the color transformation structure C based on a color lookup table (CLUT) contained in an ICC color profile. profile is an ICC profile structure returned by iccread. LUTtype specifies which clut in the profile structure is to be used. Each LUTtype listed in the table below contains the components of an 8-bit or 16 -bit LUTtag that performs a transformation between device colors and PCS colors using a particular rendering. For more information about 'clut' transformations, see Section 6.5 .7 of the International Color Consortium specification ICC.1:2001-04 (Version 2) or Section 6.5.9 of ICC.1:2001-12 (Version 4), available at www.color.org.

| LUT Type | Description |
| :--- | :--- |
| 'AToBO' <br> (default) | Device to PCS: perceptual rendering intent |
| 'AToB1' | Device to PCS: media-relative colorimetric <br> rendering intent |
| 'AToB2' | Device to PCS: saturation rendering intent |
| 'AToB3' | Device to PCS: ICC-absolute rendering intent |


| LUT Type | Description |
| :--- | :--- |
| 'BToAO' | PCS to device: perceptual rendering intent |
| 'BToA1' | PCS to device: media-relative colorimetric rendering <br> intent |
| 'BToA2' | PCS to device: saturation rendering intent |
| 'BToA3' | PCS to device: ICC-absolute rendering intent |
| 'Gamut ' | Determines which PCS colors are out of gamut for <br> a given device |
| 'PreviewO' | PCS colors to the PCS colors available for soft <br> proofing using the perceptual rendering |
| 'Preview1' | PCS colors available for soft proofing using the <br> media-relative colorimetric rendering. |
| 'Preview2' | PCS colors to the PCS colors available for soft <br> proofing using the saturation rendering. |

C = makecform('mattrc', MatTrc, 'Direction', direction) creates the color transformation structure C based on a Matrix/Tone Reproduction Curve (MatTRC) model, containing an $R G B$-to-XYZ matrix and $R G B$ Tone Reproduction Curves. MatTRC is typically the 'MatTRC' field of an ICC profile structure returned by iccread, based on tags contained in an ICC color profile. direction can be either 'forward' or 'inverse' and specifies whether the MatTRC is to be applied in the forward ( $R G B$ to $X Y Z$ ) or inverse ( $X Y Z$ to $R G B$ ) direction. For more information, see section 6.3.1.2 of the International Color Consortium specification ICC.1:2001-04 or ICC.1:2001-12, available at www.color.org.

C = makecform('mattrc', profile, 'Direction', direction) creates a color transform based on the MatTRC field of the given ICC profile structure profile. direction is either 'forward' or 'inverse' and specifies whether the MatTRC is applied in the forward ( $R G B$ to $X Y Z$ ) or inverse ( $X Y Z$ to $R G B$ ) direction.

C = makecform('mattrc', profile, 'Direction', direction, 'RenderingIntent', intent) is similar, but adds the option of specifying the rendering intent. intent must be either 'RelativeColorimetric' (the default) or 'AbsoluteColorimetric'. When 'AbsoluteColorimetric' is specified, the colorimetry is referenced to a perfect diffuser, rather than to the Media White Point of the profile.

C = makecform('graytrc', profile, 'Direction', direction) creates the color transformation structure $C$ that specifies a monochrome transform based on a single-channel Tone Reproduction Curve (GrayTRC) contained in an ICC color profile. direction can be either 'forward ' or 'inverse' and specifies whether the grayTRC transform is to be applied in the forward (device to PCS) or inverse (PCS to device) direction. ("Device" here refers to the grayscale signal communicating with the monochrome device. "PCS" is the Profile Connection Space of the ICC profile and can be either $X Y Z$ or $L^{*} a^{*} b^{*}$, depending on the 'ConnectionSpace' field in profile.Header.)

C = makecform('graytrc', profile, 'Direction', direction, 'RenderingIntent', intent) is similar but adds the option of specifying the rendering intent. intent must be either 'RelativeColorimetric' (the default) or 'AbsoluteColorimetric'. When 'AbsoluteColorimetric' is specified, the colorimetry is referenced to a perfect diffuser, rather than to the Media White Point of the profile.

C = makecform('named', profile, space) creates the color transformation structure $C$ that specifies the transformation from color names to color-space coordinates. profile must be a profile structure for a Named Color profile (with a NamedColor2 field). space is either 'PCS' or 'Device'. The 'PCS' option is always available and will return $L^{*} a^{*} b^{*}$ or $X Y Z$ coordinates, depending on the 'ConnectionSpace ' field in profile.Header, in 'double' format. The 'Device' option, when active, returns device coordinates, the dimension depending on the 'ColorSpace' field in profile. Header, also in 'double' format.

## Tips

The Image Processing Toolbox software uses the following abbreviations to represent color spaces.

| Abbreviation | Description |
| :---: | :---: |
| xyz | 1931 CIE XYZ tristimulus values ( $2^{\circ}$ observer) |
| xyl | 1931 CIE $x y Y$ chromaticity values ( $2^{\circ}$ observer), where x and y refer to the $x y$-coordinates of the associated CIE chromaticity diagram, and 1 refers to $Y$ (luminance). |
| uvl | 1960 CIE $u v Y$ values, where $u$ and $v$ refer to the $u v$-coordinates, and 1 refers to $Y$ (luminance). |
| upvpl | 1976 CIE $u^{\prime} v^{\prime} Y$ values, where up and vp refer to the $u^{\prime} v^{\prime}$-coordinates and $l$ refers to $Y$ (luminance). |
| lab | 1976 CIE $L * a^{*} b^{*}$ values |
|  | Note 1 or L refers to $L^{*}$ (CIE 1976 psychometric lightness) rather than luminance ( $Y$ ). |
| lch | Polar transformation of CIE $L^{*} a^{*} b^{*}$ values, where $\mathrm{c}=$ chroma and $\mathrm{h}=$ hue |
| cmyk | Standard values used by printers |
| srgb | Standard computer monitor RGB values, (IEC 61966-2-1) |

## Examples Convert RGB image to $L^{*} a^{*} b^{*}$, assuming input image is $s R G B$.

```
rgb = imread('peppers.png');
cform = makecform('srgb2lab');
lab = applycform(rgb,cform);
```

Convert from a non-standard RGB color profile to the device-independent $X Y Z$ profile connection space. Note that the ICC input profile must includes a MatTRC value.

InputProfile = iccread('myRGB.icc');
C = makecform('mattrc',InputProfile.MatTRC, ...
'direction', 'forward');
See Also $\begin{gathered}\text { applycform | iccread | iccwrite | isicc | lab2double | lab2uint8 } \\ \text { | lab2uint16 | whitepoint | xyz2double | xyz2uint16 }\end{gathered}$
How To . "Converting Color Data Between Color Spaces"

| Purpose | Create rectangularly bounded drag constraint function |
| :---: | :---: |
| Syntax | $\mathrm{fcn}=$ makeConstrainToRectFcn(type, xlim, ylim) |
| Description | fcn = makeConstrainToRectFcn(type, xlim, ylim) creates a position constraint function for draggable tools of a given type, where type is one of the following strings: 'imellipse', 'imfreehand', 'imline', 'impoint', 'impoly', or 'imrect'. The rectangular boundaries of the position constraint function are described by the vectors xlim and ylim where xlim $=[x m i n ~ x m a x]$ and ylim $=[y m i n$ ymax]. |
| Examples | Constrain drag of impoint within axes limits. ```figure, plot(1:10); h = impoint(gca,2,6); api = iptgetapi(h); fcn = makeConstrainToRectFcn('impoint',get(gca,'XLim'),... get(gca,'YLim')); api.setPositionConstraintFcn(fcn);``` |
| See Also | ```imdistline \| imellipse | imfreehand | imline | impoint | impoly | imrect``` |

## makehdr

Purpose Create high dynamic range image

```
Syntax HDR = makehdr(files)
HDR = makehdr(files, param1, val1,...)
```

HDR $=$ makehdr(files) creates the single-precision, high dynamic range image from the set of spatially registered low dynamic range images listed in the files cell array. makehdr uses the middle exposure between the brightest and darkest images as the base exposure for the high dynamic range calculations. (This value does not need to appear in any particular file.)

Note When you call makehdr with this syntax, the low dynamic range image files must contain exif exposure metadata.

HDR = makehdr(files, param1, val1,...) creates a high dynamic range image from the low dynamic range images in files, specifying parameters and corresponding values that control various aspects of the image creation. Parameter names can be abbreviated and case does not matter.

Note Only one of the BaseFile, ExposureValues, and RelativeExposure parameters may be used at a time.

| Parameter | Description |
| :--- | :--- |
| 'BaseFile' | Character array containing the name of the file <br> to use as the base exposure. |
| 'ExposureValues' | Vector of exposure values, with one element for <br> each low dynamic range image in the cell array <br> files. An increase in one exposure value (EV) <br> corresponds to a doubling of exposure, while a <br> decrease in one EV corresponds to a halving of <br> exposure. Any positive value is allowed. This <br> parameter overrides EXIF exposure metadata. |
| 'RelativeExposure | Vector of relative exposure values, with one <br> element for each low dynamic range image in <br> the cell array files. An image with a relative <br> exposure (RE) of 0.5 has half as much exposure <br> as an image with an RE of 1. An RE value of 3 <br> has three times the exposure of an image with <br> an RE of 1. This parameter overrides EXIF <br> exposure metadata. |
| 'MinimumLimit' | Numeric scalar value in the range [0 255] that <br> specifies the minimum correctly exposed value. <br> For each low dynamic range image, pixels with <br> smaller values are considered underexposed and <br> will not contribute to the final high dynamic <br> range image. |
| 'MaximumLimit' | Numeric scalar value in the range [0 255] that <br> specifies the maximum correctly exposed value. <br> For each low dynamic range image, pixels with <br> larger values are considered overexposed and <br> will not contribute to the final high dynamic <br> range image. |

## Examples

Make a high dynamic range image from a series of six low dynamic range images that share the same f/stop number and have different exposure times. Use tonemap to visualize the HDR image.

```
files = {'office_1.jpg', 'office_2.jpg', 'office_3.jpg', ...
    'office_4.jpg', 'office_5.jpg', 'office_6.jpg'};
expTimes = [0.03可3, 0.1000, 0.33\overline{3}3, 0.6250, 1.30000, 4.0000];
hdr = makehdr(files, 'RelativeExposure', expTimes ./ expTimes(1));
rgb = tonemap(hdr);
figure; imshow(rgb)
```


## References

[1] Reinhard, et al. "High Dynamic Range Imaging." 2006. Ch. 4.
See Also hdrread I tonemap
Purpose Create lookup table for use with bwlookup
Syntax ..... lut = makelut(fun, n)
Description lut $=$ makelut (fun, $n$ ) returns a lookup table for use with bwlookup.fun is a function that accepts an $n$-by- $n$ matrix of 1 's and 0 's as inputand return a scalar. n can be either 2 or 3 . makelut creates lut bypassing all possible 2 -by- 2 or 3-by- 3 neighborhoods to fun, one at a time,and constructing either a 16 -element vector (for 2 -by- 2 neighborhoods)or a 512 -element vector (for 3 -by- 3 neighborhoods). The vector consistsof the output from fun for each possible neighborhood. fun must be afunction handle.

## Parameterizing Functions, in the MATLAB Mathematics

 documentation, explains how to provide additional parameters to the function fun.
## Class <br> lut is returned as a vector of class double.

Examples Construct a lookup table for 2-by-2 neighborhoods. In this example, the function passed to makelut returns TRUE if the number of 1's in the neighborhood is 2 or greater, and returns FALSE otherwise.

```
f = @(x) (sum(x(:)) >= 2);
lut = makelut(f,2)
lut =
    0
    0
    0
    1
    0
    1
    1
    1
    O
    1
```


## See Also bwlookup

How To . "Anonymous Functions"

- "Parameterizing Functions"


## Purpose

Create resampling structure

## Syntax

Description

R = makeresampler(interpolant, padmethod)
$R=$ makeresampler(interpolant, padmethod) creates a separable resampler structure for use with tformarray and imtransform.

The interpolant argument specifies the interpolating kernel that the separable resampler uses. In its simplest form, interpolant can have any of the following strings as a value.

| Interpolant | Description |
| :--- | :--- |
| 'cubic' | Cubic interpolation |
| 'linear' | Linear interpolation |
| 'nearest' | Nearest-neighbor interpolation |

If you are using a custom interpolating kernel, you can specify interpolant as a cell array in either of these forms:

| \{half_width, <br> positive_half\} | half_width is a positive scalar designating <br> the half width of a symmetric interpolating <br> kernel. positive_half is a vector of values <br> regularly sampling the kernel on the closed <br> interval [0 positive_half]. |
| :--- | :--- |
| \{half_width, <br> interp_fcn $\}$ | interp_fon is a function handle that returns <br> interpolating kernel values, given an array of <br> input values in the interval <br> [0 positive_half]. |

To specify the interpolation method independently along each dimension, you can combine both types of interpolant specifications. The number of elements in the cell array must equal the number of transform dimensions. For example, if you specify this value for interpolant

```
{'nearest', 'linear', {2 KERNEL_TABLE}}
```

the resampler uses nearest-neighbor interpolation along the first transform dimension, linear interpolation along the second dimension, and a custom table-based interpolation along the third.

The padmethod argument controls how the resampler interpolates or assigns values to output elements that map close to or outside the edge of the input array. The following table lists all the possible values of padmethod.

| Pad Method | Description |
| :--- | :--- |
| 'bound' | Assigns values from the fill value array to points <br> that map outside the array and repeats border <br> elements of the array for points that map inside the <br> array (same as 'replicate'). When interpolant <br> is 'nearest', this pad method produces the same <br> results as 'fill'. 'bound' is like 'fill', but <br> avoids mixing fill values and input image values. |
| 'circular' | Pads array with circular repetition of elements <br> within the dimension. Same as padarray. |
| 'fill' | Generates an output array with smooth-looking <br> edges (except when using nearest-neighbor <br> interpolation). For output points that map near the <br> edge of the input array (either inside or outside), <br> it combines input image and fill values. When <br> interpolant is 'nearest', this pad method <br> produces the same results as 'bound '. |
| 'replicate' | Pads array by repeating border elements of array. <br> Same as padarray. |
| 'symmetric' | Pads array with mirror reflections of itself. Same <br> as padarray. |

In the case of 'fill', 'replicate', 'circular', or 'symmetric', the resampling performed by tformarray or imtransform occurs in two logical steps:

1 Pad the array A infinitely to fill the entire input transform space.
2 Evaluate the convolution of the padded A with the resampling kernel at the output points specified by the geometric map.

Each nontransform dimension is handled separately. The padding is virtual, (accomplished by remapping array subscripts) for performance and memory efficiency. If you implement a custom resampler, you can implement these behaviors.

Custom The syntaxes described above construct a resampler structure that uses Resamplers the separable resampler function that ships with the Image Processing Toolbox software. It is also possible to create a resampler structure that uses a user-written resampler by using this syntax:

R = makeresampler(PropertyName,PropertyValue, ...)
The makeresampler function supports the following properties.

| Property | Description |
| :--- | :--- |
| 'Type' | Can have the value 'separable' or 'custom' and must always be <br> supplied. If 'Type' is 'separable', the only other properties that can <br> be specified are 'Interpolant' and 'PadMethod', and the result is <br> equivalent to using the makeresampler (interpolant, padmethod) <br> syntax. If 'Type' is 'custom', you must specify the 'NDims ' and <br> 'ResampleFcn' properties and, optionally, the 'CustomData' property. |
| 'PadMethod' | See the padmethod argument for more information. |
| 'Interpolant' | See the interpolant argument for more information. |
| 'NDims' | Positive integer indicating the dimensionality the custom resampler <br> can handle. Use a value of Inf to indicate that the custom resampler <br> can handle any dimension. If 'Type' is 'custom', NDims is required. |

## makeresampler

| Property | Description |
| :---: | :---: |
| 'ResampleFcn' | Handle to a function that performs the resampling. The function is called with the following interface. <br> $B=r e s a m p l e \_f c n\left(A, M, T D I M S \_A, T D I M S \_B, F S I Z E \_A, F S I Z E \_B, F, R\right)$ <br> See the help for tformarray for information about the inputs A, TDIMS_A, TDIMS_B, and F. The argument $M$ is an array that maps the transform subscript space of $B$ to the transform subscript space of $A$. If $A$ has $N$ transform dimensions ( $N=$ length(TDIMS_A)) and $B$ has $P$ transform dimensions ( $P=$ length (TDIMS_B) ), then ndims $(M)=P+$ 1 , if $N>1$ and $P$ if $N==1$, and $\operatorname{size}(M, P+1)=N$. <br> The first $P$ dimensions of $M$ correspond to the output transform space, permuted according to the order in which the output transform dimensions are listed in TDIMS_B. (In general TDIMS_A and TDIMS_B need not be sorted in ascending order, although such a limitation might be imposed by specific resamplers.) Thus, the first $P$ elements of size (M) determine the sizes of the transform dimensions of B. The input transform coordinates to which each point is mapped are arrayed across the final dimension of $M$, following the order given in TDIMS_A. $M$ must be double. FSIZE_A and FSIZE_B are the full sizes of $A$ and $B$, padded with 1's as necessary to be consistent with TDIMS_A, TDIMS_B, and size(A). |
| 'CustomData' | User-defined. |

## Examples

Stretch an image in the $y$-direction using a separable resampler that applies cubic interpolation in the $y$-direction and nearest-neighbor interpolation in the $x$-direction. (This is equivalent to, but faster than, applying bicubic interpolation.)

```
A = imread('moon.tif');
resamp = makeresampler({'nearest','cubic'},'fill');
stretch = maketform('affine',[1 0; 0 1.3; 0 0]);
B = imtransform(A,stretch,resamp);
```

See Also imtransform | tformarray

Purpose
Create spatial transformation structure (TFORM)
Syntax

```
T = maketform(transformtype,...)
T = maketform('affine',A)
T = maketform('affine',U,X)
T = maketform('projective',A)
T = maketform('projective',U,X)
T = maketform('custom', NDIMS_IN, NDIMS_OUT, FORWARD_FCN,
    INVERSE_FCN, TDATA)
T = maketform('box',tsize,LOW,HIGH)
T = maketform('box',INBOUNDS, OUTBOUNDS)
T = maketform('composite',T1,T2,...,TL)
T = maketform('composite', [T1 T2 ... TL])
```


## Description

$\mathrm{T}=$ maketform(transformtype,.. ) creates a multidimensional spatial transformation structure (called a TFORM struct) that can be used with the tformfwd, tforminv, fliptform, imtransform, or tformarray functions.
transformtype can be any of the following spatial transformation types. maketform supports a special syntax for each transformation type. See the following sections for information about these syntax.

| Transform <br> Type | Description |
| :--- | :--- |
| 'affine' | Affine transformation in 2-D or N-D |
| 'projective' | Projective transformation in 2-D or N-D |
| 'custom' | User-defined transformation that can be N-D to M-D |
| 'box' | Independent affine transformation (scale and shift) in <br> each dimension |
| 'composite' | Composition of an arbitrary number of more basic <br> transformations |

## Transform

 Types
## Affine

$\mathrm{T}=$ maketform('affine', A$)$ builds a TFORM struct T for an N -dimensional affine transformation. A is a nonsingular real $(\mathrm{N}+1)$-by- $(\mathrm{N}+1)$ or $(\mathrm{N}+1)$-by- N matrix. If A is $(\mathrm{N}+1)$-by- $(\mathrm{N}+1)$, the last column of A must be [zeros ( $N, 1$ );1]. Otherwise, A is augmented automatically, such that its last column is [zeros( $N, 1$ );1]. The matrix A defines a forward transformation such that tformfwd $(\mathrm{U}, \mathrm{T})$, where $U$ is a 1 -by- $N$ vector, returns a 1 -by- $N$ vector $X$, such that $X$ $=U * A(1: N, 1: N)+A(N+1,1: N)$. T has both forward and inverse transformations.

T = maketform('affine', $\mathrm{U}, \mathrm{X}$ ) builds a TFORM struct T for a two-dimensional affine transformation that maps each row of $U$ to the corresponding row of $X$. The $U$ and $X$ arguments are each 3 -by- 2 and define the corners of input and output triangles. The corners cannot be collinear.

## Projective

T = maketform('projective', A) builds a TFORM struct for an N -dimensional projective transformation. A is a nonsingular real $(N+1)$-by- $(N+1)$ matrix. $A(N+1, N+1)$ cannot be 0 . The matrix $A$ defines a forward transformation such that tformfwd $(U, T)$, where $U$ is a 1-by-N vector, returns a 1 -by- $N$ vector $X$, such that $X=W(1: N) / W(N+1)$, where $W=\left[\begin{array}{ll}U & 1\end{array}\right]$ * $A$. The transformation structure $T$ has both forward and inverse transformations.

T = maketform('projective', $\mathrm{U}, \mathrm{X}$ ) builds a TFORM struct T for a two-dimensional projective transformation that maps each row of $U$ to the corresponding row of $X$. The $U$ and $X$ arguments are each 4 -by- 2 and define the corners of input and output quadrilaterals. No three corners can be collinear.

Note An affine or projective transformation can also be expressed like this, for a 3-by-2 A:

```
[X Y]' = A' * [U V 1] '
```

Or, like this, for a 3-by-3 A:

```
[X Y 1]' = A' * [U V 1]'
```


## Custom

T = maketform('custom', NDIMS_IN, NDIMS_OUT, FORWARD_FCN, INVERSE_FCN, TDATA) builds a custom TFORM struct T based on user-provided function handles and parameters. NDIMS_IN and NDIMS_OUT are the numbers of input and output dimensions. FORWARD_FCN and INVERSE_FCN are function handles to forward and inverse functions. Those functions must support the following syntax:

$$
\begin{array}{ll}
\text { Forward function: } & X=\text { FORWARD_FCN }(U, T) \\
\text { Inverse function: } & U=\text { INVERSE_FCN }(X, T)
\end{array}
$$

where $U$ is a $P$-by-NDIMS_IN matrix whose rows are points in the transformation's input space, and X is a P-by-NDIMS_OUT matrix whose rows are points in the transformation's output space. The TDATA argument can be any MATLAB array and is typically used to store parameters of the custom transformation. It is accessible to FORWARD_FCN and INVERSE_FCN via the tdata field of T. Either FORWARD_FCN or INVERSE_FCN can be empty, although at least INVERSE_FCN must be defined to use T with tformarray or imtransform.

## Box

T = maketform('box',tsize, LOW, HIGH) or T = maketform('box', INBOUNDS, OUTBOUNDS) builds an N -dimensional affine TFORM struct T . The tsize argument is an

N-element vector of positive integers. LOW and HIGH are also N-element vectors. The transformation maps an input box defined by the opposite corners ones ( $1, \mathrm{~N}$ ) and tsize or, alternatively, by corners $\operatorname{INBOUNDS}(1,:)$ and $\operatorname{INBOUND}(2,:)$ to an output box defined by the opposite corners LOW and HIGH or OUTBOUNDS ( $1,:$ ) and OUTBOUNDS ( $2,:$ ). LOW(K) and HIGH(K) must be different unless tsize (K) is 1, in which case the affine scale factor along the Kth dimension is assumed to be 1.0. Similarly, $\operatorname{INBOUNDS}(1, K)$ and $\operatorname{INBOUNDS}(2, K)$ must be different unless OUTBOUNDS $(1, K)$ and $\operatorname{OUTBOUNDS}(2, K)$ are the same, and vice versa. The 'box' TFORM is typically used to register the row and column subscripts of an image or array to some world coordinate system.

## Composite

T = maketform('composite', T1, T2, ..., TL) or
T = maketform('composite', [T1 T2 ... TL]) builds a TFORM struct $T$ whose forward and inverse functions are the functional compositions of the forward and inverse functions of T1, T2, ..., TL.

Note that the inputs T1, T2, ..., TL are ordered just as they would be when using the standard notation for function composition: $\mathrm{T}=\mathrm{T} 1 \circ \mathrm{~T} 2 \circ \ldots \circ \mathrm{TL}$ and note also that composition is associative, but not commutative. This means that in order to apply $T$ to the input $U$, one must apply $T L$ first and $T 1$ last. Thus if $L=3$, for example, then tformfwd $(U, T)$ is the same as tformfwd(tformfwd(tformfwd(U,T3), T2), T1). The components T1 through TL must be compatible in terms of the numbers of input and output dimensions. T has a defined forward transform function only if all the component transforms have defined forward transform functions. T has a defined inverse transform function only if all the component functions have defined inverse transform functions.

## Examples Make and apply an affine transformation.

```
T = maketform('affine',[.5 0 0; . 5 2 0; 0 0 1]);
tformfwd([10 20],T)
I = imread('cameraman.tif');
I2 = imtransform(I,T);
```

imshow(I), figure, imshow(I2)
See Also tformfwd | tforminv | fliptform | imtransform | tformarray

Convert matrix to grayscale image
I = mat2gray(A, [amin amax])
I = mat2gray(A)

Purpose
Syntax

Description

Class Support

Examples

I = mat2gray (A, [amin amax]) converts the matrix A to the intensity image I. The returned matrix I contains values in the range 0.0 (black) to 1.0 (full intensity or white). amin and amax are the values in A that correspond to 0.0 and 1.0 in I.

I = mat2gray (A) sets the values of amin and amax to the minimum and maximum values in $A$.

The input array A can be logical or numeric. The output image I is double.

I = imread('rice.png');
$J=$ filter2(fspecial('sobel'),I);
K = mat2gray(J);
imshow(I), figure, imshow(K)

Purpose Average or mean of matrix elements
Syntax $B=\operatorname{mean2}(A)$
Description $B=$ mean2 $(A)$ computes the mean of the values in $A$.
Class
Support
The input image $A$ can be numeric or logical. The output image $B$ is a scalar of class double.
Algorithms mean2 computes the mean of an array $A$ using mean(A(:)).
See Also ..... std2 | mean | std

## Purpose

2-D median filtering

Note The syntax medfilt2(A,[M N],(Mb Nb],...) has been removed.

Syntax<br>Description

$B=$ medfilt2(A, [m n])
$B=$ medfilt2(A)
B = medfilt2(A, 'indexed', ...)
B = medfilt2(..., padopt)

Median filtering is a nonlinear operation often used in image processing to reduce "salt and pepper" noise. A median filter is more effective than convolution when the goal is to simultaneously reduce noise and preserve edges.
$B=$ medfilt2(A, $[m n])$ performs median filtering of the matrix $A$ in two dimensions. Each output pixel contains the median value in the $m$-by-n neighborhood around the corresponding pixel in the input image. medfilt2 pads the image with 0 s on the edges, so the median values for the points within [ $\mathrm{m} n$ ]/2 of the edges might appear distorted.
$B=$ medfilt2(A) performs median filtering of the matrix $A$ using the default 3-by-3 neighborhood.
$B=$ medfilt2(A, 'indexed', ...) processes A as an indexed image, padding with 0 s if the class of $A$ is uint8, or 1 s if the class of $A$ is double.
$B=$ medfilt2(..., padopt) controls how the matrix boundaries are padded. padopt may be 'zeros' (the default), 'symmetric', or 'indexed'. If padopt is 'symmetric ', A is symmetrically extended at the boundaries. If padopt is 'indexed', $A$ is padded with ones if it is double; otherwise it is padded with zeros.

Class The input image A can be of class logical or numeric (unless the Support
'indexed ' syntax is used, in which case $A$ cannot be of class uint16). The output image $B$ is of the same class as $A$.

Note For information about performance considerations, see ordfilt2.

Tips

## Examples

If the input image $A$ is of an integer class, all the output values are returned as integers. If the number of pixels in the neighborhood (i.e., $m * n$ ) is even, some of the median values might not be integers. In these cases, the fractional parts are discarded. Logical input is treated similarly.

For example, suppose you call medfilt2 using 2-by-2 neighborhoods, and the input image is a uint8 array that includes this neighborhood.

15
48
medfilt2 returns an output value of 4 for this neighborhood, although the true median is 4.5.

Add salt and pepper noise to an image and then restore the image using medfilt2.

```
I = imread('eight.tif');
J = imnoise(I,'salt & pepper',0.02);
K = medfilt2(J);
imshow(J), figure, imshow(K)
```



Algorithms medfilt2 uses ordfilt2 to perform the filtering.
References $\quad$ [1] Lim, Jae S., Two-Dimensional Signal and Image Processing,
See Also filter2 | ordfilt2 | wiener2

Purpose Display multiple image frames as rectangular montage

```
Syntax montage(filenames)
montage(I)
montage(X, map)
montage(..., param1, value1, param2, value2, ...)
h = montage(...)
```


## Description

montage(filenames) displays a montage of the images specified in filenames. filenames is an N -by-1 or 1-by-N cell array of filenames. If the files are not in the current directory or in a directory on the MATLAB path, you must specify the full pathname. See the imread command for more information. If one or more of the image files contains an indexed image, montage uses the colormap from the first indexed image file. montage arranges the frames so that they roughly form a square.
montage (I) displays all the frames of a multiframe image array I in a single image object. I can be a sequence of binary, grayscale, or truecolor images. A binary or grayscale image sequence must be an M-by-N-by-1-by-K array. A truecolor image sequence must be an M-by-N-by-3-by-K array.
montage ( $X$, map) displays all the frames of the indexed image array $X$, using the colormap map for all frames. X is an M -by-N-by-1-by-K array.
montage(..., param1, value1, param2, value2, ...) returns a customized display of an image montage, depending on the values of the optional parameter/value pairs. See "Parameters" on page 3-678 for a list of available parameters.
$\mathrm{h}=$ montage (...) returns the handle to the image object.

## Parameters

The following table lists the parameters available, alphabetically by name. Parameter names can be abbreviated, and case does not matter.

| Parameter | Value |
| :---: | :---: |
| 'DisplayRange ' | A 1-by-2 vector, [LOW HIGH] that controls the display range of each image in a grayscale sequence. The value LOW (and any value less than LOW) displays as black; the value HIGH (and any value greater than HIGH) displays as white. If you specify an empty matrix ([]), montage uses the minimum and maximum values of the images to be displayed in the montage as specified by 'Indices'. For example, if 'Indices' is $1: K$ and the <br> 'DisplayRange' is set to [], the minimum value in I (min(I(:)) is displayed as black, and the maximum value $(\max (\mathrm{I}(:))$ is displayed as white. <br> Default: Range of the data type of I. |
| 'Indices ' | A numeric array specifying which frames to display in the montage. For example, to create a montage of the first four frames in I, enter montage(I, 'Indices', 1:4) ;. You can use this parameter to specify individual frames or skip frames. For example, the value 1:2:20 displays every other frame. Default: $1: K$, where $K$ is the total number of frames to display. |
| 'Size' | A 2 -element vector, [NROWS NCOLS], specifying the number of rows and number of columns in the montage. You can use NaNs in the size vector to indicate that montage should calculate size in a particular dimension in a way that includes all the images in the montage. For example, if 'Size' is [ 2 NaN ], the montage will have 2 rows, and the number of columns will be computed automatically to include all of the images in the montage. The images are displayed horizontally across columns. <br> Default: Calculated so the images in the montage roughly form a square.montage considers the aspect ratio when calculating the number of images to display horizontally and vertically. |

A grayscale image array can be logical, uint8, uint16, int16, single, or double. An indexed image can be logical, uint8, uint16, single, or double. The colormap must be double. A truecolor image can be
uint8, uint16, single, or double. The output is a handle to the image object produced by montage.

## Examples

Create a montage from a series of files. By default, montage arranges the images into a square.

```
fileFolder = fullfile(matlabroot,'toolbox','images','imdemos');
dirOutput = dir(fullfile(fileFolder,'AT3_1m4_*.tif'));
fileNames = {dirOutput.name}'
montage(fileNames);
```

Display the same set of images in two rows and five columns.

```
montage(fileNames, 'Size', [2 5]);
```

This example shows you how to customize the number of images in the montage and the contrast in the montage.

```
load mri
montage(D,map)
```



Create a new montage of the first 9 images.
figure
montage(D, map, 'Indices', 1:9);

Maximize the contrast of D without using the colormap.
figure
montage(D, 'DisplayRange', []);
immovie | imshow

## multithresh

Purpose Multilevel image thresholds using Otsu 's method

Syntax

Description

## Input <br> Arguments

```
thresh = multithresh(A)
thresh = multithresh(A,N)
[thresh,metric] = multithresh( __ )
```

thresh $=$ multithresh $(A)$ returns the single threshold value thresh computed for image A using Otsu's method.

- thresh is an input argument to imquantize that converts A into a binary image.
thresh $=$ multithresh $(A, N)$ returns thresh containing $N$ threshold values using Otsu's method.
- thresh is a 1 xN vector which can be used to convert image $A$ into an image with $N+1$ discrete levels using imquantize.
[thresh,metric] = multithresh( __ ) returns metric, a measure of the effectiveness of the computed thresholds. metric is in the range [ $\left.0 \begin{array}{ll}0 & 1\end{array}\right]$ and a higher value indicates greater effectiveness of the thresholds in separating the input image into $N+1$ classes based on Otsu's objective criterion.


## A - Input image

## image

Input image, specified as a non-sparse numeric matrix of any dimension. multithresh finds the thresholds based on the aggregate histogram of the entire matrix. An RGB image is considered a 3-D numeric array and the thresholds are computed for the combined data from all three color planes.
multithresh uses the range of the input $A[\min (A(:)) \quad \max (A(:))]$ as the limits for computing the histogram which is used in subsequent computations. Any NaNs are ignored in computation. Any Infs and - Infs are counted in the first and last bin of the histogram, respectively.

For degenerate inputs where the number of unique values in $A$ is less than or equal to N, there is no viable solution using Otsu's method. For such inputs, thresh contains all the unique values from $A$ and possibly some extra values that are chosen arbitrarily.

## Data Types

single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32
| uint64

## $\mathbf{N}$ - Number of threshold values <br> 1 (default) | scalar

Number of threshold values, specified as a scalar value. For $N>2$, multithresh uses search-based optimization of Otsu's criterion to find the thresholds. The search-based optimization guarantees only locally optimal results. Since the chance of converging to local optimum increases with N , it is preferable to use smaller values of N , typically N < 10. The maximum allowed value for N is 20 .

## Data Types

single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32 | uint64

## Output Arguments

## thresh - Set of values used to quantize an image 1 xN vector

Set of values used to quantize an image, returned as a 1 xN vector, whose data type is the same as image $A$.

## metric - Measure of the effectiveness of the thresholds scalar

Measure of the effectiveness of the thresholds, returned as a scalar value. Higher values indicates greater effectiveness of the thresholds in separating the input image into $\mathrm{N}+1$ classes based on Otsu's objective criterion. For degenerate inputs where the number of unique values in A is less than or equal to $N$, metric equals 0 .

## Data Types

double

## multithresh

## Examples Image Threshold

Compute multiple thresholds for an image using multithresh and apply those thresholds to the image using imquantize to get segment labels.

I = imread('circlesBrightDark.png');

Computing two thresholds quantizes the image into three discrete levels.

```
thresh = multithresh(I,2);
seg_I = imquantize(I,thresh); % Apply the thresholds to obtain segmented
RGB = label2rgb(seg_I); % convert to color image
figure;
imshowpair(I,RGB,'montage'); % display images side-by-side
axis off;
title('Original Image RGB Segmented Image'
```

Original Image


## Two Schemes for RGB Image Quantization

Quantize the truecolor RGB image to eight levels using multilevel thresholding function multithresh. Compare results between thresholding the entire RGB image versus plane-by-plane thresholding.

Read in a truecolor RGB image.

## multithresh

```
I = imread('peppers.png');
imshow(I); axis off;
title('RGB Image');
```

RGB Image


Generate thresholds for seven levels from the entire RGB image; then repeat process for each plane in the RGB image

```
threshRGB = multithresh(I,7) % 7 thresholds from entire RGB image
threshPlanes = zeros(3,7); % initialize
% Compute thresholds for each R, G, and B plane
for i = 1:3
    threshPlane(i,:) = multithresh(I(:,:,i),7);
end
threshPlane
threshRGB =
    24
threshPlane =
\begin{tabular}{rrrrrrr}
40 & 69 & 92 & 125 & 159 & 195 & 231 \\
27 & 49 & 74 & 100 & 128 & 164 & 209 \\
18 & 38 & 60 & 86 & 127 & 165 & 222
\end{tabular}
```

Process the entire image with the set of threshold values computed from the entire image. Similarly, process each RGB plane separately using the threshold vector computed from the given plane. Add black (0) and white (255) to value vector which assigns values to the output image.

```
value = [0 threshRGB(2:end) 255];
% Quantize entire image using one threshold vector
quantRGB = imquantize(I, threshRGB, value);
quantPlane = zeros( size(I) );
% Quantize each RGB plane using threshold vector generated for that p
for i = 1:3
    value = [0 threshPlane(i,2:end) 255] % output value to assign
    quantPlane(:,:,i) = imquantize(I(:,:,i), threshPlane(i,:), value)
end
```


## multithresh

quantPlane $=$ uint8( quantPlane $)$; \% convert from double to uint8

Display both posterized images and note the visual differences in the two thresholding schemes.

Full RGB Image Quantization


The following code snippet computes the number of unique RGB pixel vectors in each output image. Note that the plane-by-plane thresholding scheme yields about $23 \%$ more colors than the full RGB image scheme.

```
% Convert images to mx3 matrices
dim = size( quantRGB );
quantRGBmx3 = reshape(quantRGB, prod(dim(1:2)), 3);
quantPlanemx3 = reshape(quantPlane, prod(dim(1:2)), 3);
% Extract only unique 3 element RGB pixel vectors from each matrix
colorsRGB = unique( quantRGBmx3, 'rows');
colorsPlane = unique( quantPlanemx3, 'rows');
disp(['Number of unique colors in RGB image: ' int2str(ler
disp(['Number of unique colors in Plane-by-Plane image : ' int2str(ler
Number of unique colors in RGB image : 188
Number of unique colors in Plane-by-Plane image : 231
```


## Behavior of Output Argument metric

Compute various thresholds for different values of $N$ and on different images as a way of showing the variation of metric.

```
I = imread('circlesBrightDark.png');
```

\% find all unique grayscale values in image
uniqLevels = unique(I(:));
disp(['Number of unique levels = ' int2str( length(uniqLevels) )]);
Number of unique levels $=148$

Compute a series of thresholds at monotonically increasing values of N

```
% Compute the thresholds
Nvals = [1 2 4 8];
for i = 1:length(Nvals)
    [thresh, metric] = multithresh(I, Nvals(i) );
    disp(['N = ' int2str(Nvals(i)) ' | metric = ' num2str(metric)])
end
N = 1 | metric = 0.54767
```

```
N = 2 metric = 0.98715
N=4 | metric = 0.99648
N=8 | metric = 0.99902
```

Apply the $N=8$ set of thresholds to obtain a 9 level segmented image via imquantize.

```
seg_Neq8 = imquantize(I,thresh);
uniqLevels = unique( seg_Neq8(:) ) % Verify that image has only 9 level
uniqLevels =
    1
    2
    3
    4
    5
    6
    7
    8
    9
```

seg_Neq8 is input to multithresh and $N$ is set to equal to 8 which is 1 less than the number of levels in this segmented image.
[thresh, metric] = multithresh(seg_Neq8,8)
thresh =

Columns 1 through 7
1.8784
2.7882
3.6667
4.5451
5.4549
6.3333
7.2118

Column 8
8.1216

```
metric =
```

1

Note what happens when $N$ is increased by 1 and now equals the number of levels in the image.

```
[thresh, metric] = multithresh(seg_Neq8,9)
Warning: No solution exists because the number of unique levels in im
too few to find 9 thresholds. Returning an arbitrarily chosen solutior
> In multithresh at 171
```

thresh =
$\begin{array}{lllllllll}1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9\end{array}$
metric =
0

Here the input was degenerate because the number of levels in the image was too few for the number of requested thresholds. Hence metric is 0 .

## References

[1] Otsu, N., "A Threshold Selection Method from Gray-Level Histograms," IEEE Transactions on Systems, Man, and Cybernetics, Vol. 9, No. 1, 1979, pp. 62-66.

## See Also

graythresh | imquantize | im2bw | rgb2ind

Purpose Read metadata from National Imagery Transmission Format (NITF) file

```
Syntax metadata = nitfinfo(filename)
```

Description
metadata $=$ nitfinfo(filename) returns a structure whose fields contain file-level metadata about the images, annotations, and graphics in a National Imagery Transmission Format (NITF) file. NITF is an mage format used by the U.S. government and military for transmitting documents. A NITF file can contain multiple images and include text and graphic layers. filename is a character array that specifies the name of the NITF file, which must be in the current directory, in a directory on the MATLAB path, or contain the full path to the file.
nitfinfo supports version 2.0 and 2.1 NITF files, at all Joint Interoperability Test Command (JITC) compliance levels, as well as the NATO Secondary Image Format (NSIF) 1.0. nitfinfo does not support NITF 1.1 files.

[^5]| Purpose | Read image from NITF file |
| :--- | :--- |
| Syntax | $X=$ nitfread(filename) |
|  | $X=$ nitfread(filename, idx) |
|  | $X=$ nitfread(...,'PixelRegion',$\{$ rows, cols $\})$ |

## Description

$X=$ nitfread(filename) reads the first image from the National Imagery Transmission Format (NITF) file specified by the character array filename. The filename array must be in the current directory or in a directory on the MATLAB path, or it must contain the full path to the file.

X = nitfread(filename,idx) reads the image with index number idx from a NITF file that contains multiple images.

X = nitfread(...,'PixelRegion', \{rows, cols\}) reads a region of pixels from a NITF image. rows and cols are two or three element vectors, where the first value is the starting location, and the last value is the ending location. In the three value syntax, the second value is the increment.

This function supports version 2.0 and 2.1 NITF files, as well as NSIF 1.0. Compressed images, image submasks, and NITF 1.1 files are not supported.

## See Also <br> isnitf | nitfinfo

## nlfilter

Purpose General sliding-neighborhood operations
Syntax $\quad B=\operatorname{nlfilter}(A,[m n]$, fun)
$B=$ nlfilter (A, 'indexed',...)
Description $B=$ nlfilter (A, [m n], fun) applies the function fun to each $m$-by- $n$ sliding block of the grayscale image A. fun is a function that accepts an $m$-by-n matrix as input and returns a scalar result.
$c=\operatorname{fun}(x)$
fun must be a function handle.
Parameterizing Functions, in the MATLAB Mathematics documentation, explains how to provide additional parameters to the function fun.
$c$ is the output value for the center pixel in the m-by-n block $x$. nlfilter calls fun for each pixel in A. nlfilter zero-pads the m-by-n block at the edges, if necessary.

B = nlfilter(A, 'indexed',...) processes A as an indexed image, padding with 1's if A is of class single or double and 0's if A is of class logical, uint8, or uint16.

## Class <br> Support

Tips

Examples This example produces the same result as calling medfilt2 with a 3-by-3 neighborhood.

```
A = imread('cameraman.tif');
A = im2double(A);
```

fun $=@(x)$ median(x(:));
$B=n l f i l t e r(A,[33], f u n) ;$
imshow(A), figure, imshow(B)
See Also blockproc | colfilt | function_handle
How To - "Anonymous Functions"

- "Parameterizing Functions"


## Purpose Normalized 2-D cross-correlation

```
Syntax C = normxcorr2(template, A)
C = normxcorr2(template, A)
```

Description

Class Support

Tips

## Algorithms

C = normxcorr2(template, A) computes the normalized cross-correlation of the matrices template and A. The matrix A must be larger than the matrix template for the normalization to be meaningful. The values of template cannot all be the same. The resulting matrix C contains the correlation coefficients, which can range in value from -1.0 to 1.0.

The input matrices can be numeric. The output matrix C is double.

Normalized cross-correlation is an undefined operation in regions where A has zero variance over the full extent of the template. In these regions, we assign correlation coefficients of zero to the output $C$.
normxcorr2 uses the following general procedure [1], [2]:
1 Calculate cross-correlation in the spatial or the frequency domain, depending on size of images.

2 Calculate local sums by precomputing running sums. [1]
3 Use local sums to normalize the cross-correlation to get correlation coefficients.

The implementation closely follows following formula from [1]:

$$
\gamma(u, v)=\frac{\sum_{x, y}\left[f(x, y)-\bar{f}_{u, v}\right][t(x-u, y-v)-\bar{t}]}{\left\{\sum_{x, y}\left[f(x, y)-\bar{f}_{u, v}\right]^{2} \sum_{x, y}[t(x-u, y-v)-\bar{t}]^{2}\right\}^{0.5}}
$$

where

- $f$ is the image.
- $\bar{t}$ is the mean of the template
- $\bar{f}_{u, v}$ is the mean of $f(x, y)$ in the region under the template.


## Examples

References

## See Also

template $=.2^{*}$ ones(11); \% Make light gray plus on dark gray background template $(6,3: 9)=.6 ;$
template $(3: 9,6)=.6 ;$
BW = template $>0.5 ; \quad$ \% Make white plus on black background
figure, imshow(BW), figure, imshow(template)
\% Make new image that offsets the template
offsetTemplate = .2*ones(21);
offset $=$ [3 5]; \% Shift by 3 rows, 5 columns
offsetTemplate( (1:size(template,1))+offset(1),... (1:size(template, 2)) +offset(2) ) = template;
figure, imshow(offsetTemplate)
\% Cross-correlate BW and offsetTemplate to recover offset
cc = normxcorr2(BW,offsetTemplate);
[max_cc, imax] = max(abs(cc(:)));
[ypeak, xpeak] = ind2sub(size(cc),imax(1));
corr_offset $=$ [ (ypeak-size(template,1)) (xpeak-size(template,2)) ];
isequal(corr_offset,offset) \% 1 means offset was recovered
[1] Lewis, J. P., "Fast Normalized Cross-Correlation," Industrial Light \& Magic
[2] Haralick, Robert M., and Linda G. Shapiro, Computer and Robot Vision, Volume II, Addison-Wesley, 1992, pp. 316-317.

## Purpose Convert NTSC values to RGB color space

```
Syntax rgbmap = ntsc2rgb(yiqmap)
RGB = ntsc2rgb(YIQ)
```


## Description

## Class Support

The input image or colormap must be of class double. The output is of class double.

## Examples Convert RGB image to NTSC and back.

```
RGB = imread('board.tif');
NTSC = rgb2ntsc(RGB);
RGB2 = ntsc2rgb(NTSC);
```

See Also

```
rgb2ntsc | rgb2ind | ind2rgb | ind2gray
```

Purpose Open R-Set file
Syntax openrset(filename)
Description openrset (filename) opens the reduced resolution dataset (R-Set) specified by filename for viewing.
See Also imtool | rsetwrite

## ordfilt2

| Purpose | 2-D order-statistic filtering |
| ---: | :--- |
| Syntax | B$=\operatorname{ordfilt2(A,~order,~domain)~}$ |
|  | $B=\operatorname{ordfilt2(A,~order,~domain,~S)~}$ |
|  | $B=\operatorname{ordfilt2(\ldots ,~padopt)~}$ |

## Description

## Class <br> Support

Tips
$B=$ ordfilt2(A, order, domain) replaces each element in $A$ by the orderth element in the sorted set of neighbors specified by the nonzero elements in domain.
$B=$ ordfilt2(A, order, domain, $S$ ) where $S$ is the same size as domain, uses the values of $S$ corresponding to the nonzero values of domain as additive offsets.

B = ordfilt2(..., padopt) controls how the matrix boundaries are padded. Set padopt to 'zeros' (the default) or 'symmetric'. If padopt is 'zeros', $A$ is padded with 0 's at the boundaries. If padopt is 'symmetric', A is symmetrically extended at the boundaries.

The class of A can be logical, uint8, uint16, or double. The class of B is the same as the class of $A$, unless the additive offset form of ordfilt2 is used, in which case the class of $B$ is double.
domain is equivalent to the structuring element used for binary image operations. It is a matrix containing only 1's and 0's; the 1's define the neighborhood for the filtering operation.

For example, $B=\operatorname{ordfilt2}(A, 5$, ones $(3,3))$ implements a 3 -by- 3 median filter; $B=\operatorname{ordfilt2}(A, 1$, ones $(3,3))$ implements a 3 -by- 3 minimum filter; and $B=$ ordfilt2 $(A, 9$, ones $(3,3))$ implements a 3 -by-3 maximum filter. $B=\operatorname{ordfilt2(A,1,[010;1001;~010])~}$ replaces each element in A by the minimum of its north, east, south, and west neighbors.

The syntax that includes S (the matrix of additive offsets) can be used to implement grayscale morphological operations, including grayscale dilation and erosion.

## Performance Considerations

When working with large domain matrices that do not contain any zero-valued elements, ordfilt2 can achieve higher performance if A is in an integer data format (uint8, int8, uint16, int16). The gain in speed is larger for uint8 and int8 than for the 16 -bit data types. For 8 -bit data formats, the domain matrix must contain seven or more rows. For 16 -bit data formats, the domain matrix must contain three or more rows and 520 or more elements.

## Examples

## References

[1] Haralick, Robert M., and Linda G. Shapiro, Computer and Robot Vision, Volume I, Addison-Wesley, 1992.
[2] Huang, T.S., G.J.Yang, and G.Y.Tang. "A fast two-dimensional median filtering algorithm.", IEEE transactions on Acoustics, Speech and Signal Processing, Vol ASSP 27, No. 1, February 1979

## See Also <br> medfilt2

## Purpose Convert optical transfer function to point-spread function

## Syntax <br> Description

Class
Support

## Examples

## See Also

PSF = otf2psf(OTF)
PSF = otf2psf(OTF, OUTSIZE)
PSF = otf2psf(0TF) computes the inverse Fast Fourier Transform (IFFT) of the optical transfer function (OTF) array and creates a point-spread function (PSF), centered at the origin. By default, the PSF is the same size as the OTF.

PSF = otf2psf(OTF, OUTSIZE) converts the OTF array into a PSF array, where OUTSIZE specifies the size of the output point-spread function. The size of the output array must not exceed the size of the OTF array in any dimension.

To center the PSF at the origin, otf2psf circularly shifts the values of the output array down (or to the right) until the $(1,1)$ element reaches the central position, then it crops the result to match dimensions specified by OUTSIZE.

Note that this function is used in image convolution/deconvolution when the operations involve the FFT.

OTF can be any nonsparse, numeric array. PSF is of class double.

```
PSF = fspecial('gaussian',13,1);
OTF = psf2otf(PSF,[31 31]); % PSF --> OTF
PSF2 = otf2psf(OTF,size(PSF)); % OTF --> PSF2
subplot(1,2,1); surf(abs(OTF)); title('|OTF|');
axis square; axis tight
subplot(1,2,2); surf(PSF2); title('Corresponding PSF');
axis square; axis tight
```

```
psf2otf | circshift | padarray
```

| Purpose | Pad array |
| :---: | :---: |
| Syntax | $\begin{aligned} & B=\text { padarray }(A, \text { padsize }) \\ & B=\text { padarray }(A, \text { padsize, padval) } \\ & B=\text { padarray }(A, \text { padsize, padval, direction }) \end{aligned}$ |
| Description | B = padarray(A, padsize) pads array A with 0's (zeros). padsize is a vector of nonnegative integers that specifies both the amount of padding to add and the dimension along which to add it. The value of an element in the vector specifies the amount of padding to add. The order of the element in the vector specifies the dimension along which to add the padding. <br> For example, a padsize value of [2 3] means add 2 elements of padding along the first dimension and 3 elements of padding along the second dimension. By default, paddarray adds padding before the first element and after the last element along the specified dimension. <br> $B$ = padarray(A, padsize, padval) pads array A where padval specifies the value to use as the pad value. padarray uses the value 0 (zero) as the default. padval can be a scalar that specifies the pad value directly or one of the following text strings that specifies the method padarray uses to determine the values of the elements added as padding. |
|  | Value $\quad$ Meaning |
|  | 'circular' Pad with circular repetition of elements within the <br> dimension. |
|  | 'replicate' ${ }^{\text {' }}$ Pad by repeating border elements of array. |
|  | 'symmetric' $\quad$ Pad array with mirror reflections of itself. |
|  | $B=$ padarray(A, padsize, padval, direction) pads A in the direction specified by the string direction. direction can be one of the following strings. The default value is enclosed in braces (\{\}). |


| Value | Meaning |
| :--- | :--- |
| \{'both' \} | Pads before the first element and after the last array <br> element along each dimension. This is the default. |
| 'post' | Pad after the last array element along each dimension. |
| 'pre' | Pad before the first array element along each dimension. |

## Class Support

## Examples

When padding with a constant value, A can be numeric or logical. When padding using the 'circular', 'replicate', or 'symmetric' methods, $A$ can be of any class. $B$ is of the same class as $A$.

## Example 1

Add three elements of padding to the beginning of a vector. The padding elements, indicated by the gray shading, contain mirror copies of the array elements.

```
a = [ 1 2 3 4 ];
b = padarray(a,[0 3],'symmetric','pre')
b == 3
```


## Example 2

Add three elements of padding to the end of the first dimension of the array and two elements of padding to the end of the second dimension. The example uses the value of the last array element as the padding value.

```
A = [1 2; 3 4];
B = padarray(A,[3 2],'replicate','post')
            1 2 2 2
            3
    3
    3 4
    3
B =
```


## Example 3

Add three elements of padding to the vertical and horizontal dimensions of a three-dimensional array. Use default values for the pad value and direction.
$A=\left[\begin{array}{ll}12 ; & 4]\end{array}\right.$
$B=[56 ; 78] ;$
$C=\operatorname{cat}(3, A, B)$
$C(:,:, 1)=$
12
34
$C(:,:, 2)=$
56
$7 \quad 8$
D = padarray (C,[llll)

| 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 | 1 | 2 | 0 | 0 | 0 |
| 0 | 0 | 0 | 3 | 4 | 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 |

$D(:,:, 1)=$

| 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 | 5 | 6 | 0 | 0 | 0 |
| 0 | 0 | 0 | 7 | 8 | 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 |

See Also circshift | imfilter

## Purpose

Convert parallel-beam projections to fan-beam
Syntax
$F=\operatorname{para2fan}(P, D)$
I = para2fan(..., param1, val1, param2, val2,...)
[F, fan_positions, fan_rotation_angles] = fan2para(...)

## Description

$F=$ para2fan ( $P, D$ ) computes the fan-beam data (sinogram) $F$ from the parallel-beam data (sinogram) P. Each column of P contains the parallel-beam sensor samples at one rotation angle. D is the distance in pixels from the center of rotation to the center of the sensors.

The sensors are assumed to have a one-pixel spacing. The parallel-beam rotation angles are assumed to be spaced equally to cover $[0,180]$ degrees. The calculated fan-beam rotation angles cover $[0,360)$ with the same spacing as the parallel-beam rotation angles. The calculated fan-beam angles are equally spaced with the spacing set to the smallest angle implied by the sensor spacing.
I = para2fan(..., param1, val1, param2, val2,...) specifies parameters that control various aspects of the para2fan conversion. Parameter names can be abbreviated, and case does not matter. Default values are enclosed in braces like this: \{default\}. Parameters include

| Parameter | Description |
| :--- | :--- |
| 'FanCoverage' | String specifying the range through which the beams <br> are rotated. <br> Possible values: \{ 'cycle' $\}$ or 'minimal' ' <br> See ifanbeam for details. |
| 'FanRotationIncrement' | Positive real scalar specifying the rotation angle <br> increment of the fan-beam projections in degrees. |
|  | If 'FanCoverage' is 'cycle ', <br> 'FanRotationIncrement ' must be a factor of 360. <br> If 'FanRotationIncrement' is not specified, then it is <br> set to the same spacing as the parallel-beam rotation <br> angles. |


| Parameter | Description |
| :---: | :---: |
| 'FanSensorGeometry' | Text string specifying how sensors are positioned. <br> Possible values: \{'arc'\} or 'line' <br> See fanbeam for details. |
| 'FanSensorSpacing' | Positive real scalar specifying the spacing of the fan beams. Interpretation of the value depends on the setting of 'FanSensorGeometry': <br> If 'FanSensorGeometry' is 'arc', the value defines the angular spacing in degrees. Default value is 1. <br> If 'FanSensorGeometry' is 'line', the value defines the linear spacing in pixels. <br> If 'FanSensorSpacing' is not specified, the default is the smallest value implied by 'ParallelSensorSpacing' such that <br> If 'FanSensorGeometry' is 'arc', 'FanSensorSpacing' is <br> 180/PI*ASIN(PSPACE/D) <br> where PSPACE is the value of 'ParallelSensorSpacing'. <br> If 'FanSensorGeometry' is 'line', 'FanSensorSpacing' is D*ASIN (PSPACE/D) |

$\left.\begin{array}{l|l}\hline \text { Parameter } & \text { Description } \\ \hline \text { 'Interpolation' } & \begin{array}{l}\text { Text string specifying the type of interpolation used } \\ \text { between the parallel-beam and fan-beam data. } \\ \text { 'nearest ' — Nearest-neighbor }\end{array} \\ & \begin{array}{l}\text { \{'linear' \} — Linear } \\ \text { 'spline' — Piecewise cubic spline }\end{array} \\ & \begin{array}{l}\text { 'pchip' — Piecewise cubic Hermite (PCHIP) } \\ \text { 'cubic' — Same as 'pchip' }\end{array} \\ \hline \text { 'ParallelCoverage' } & \begin{array}{l}\text { Text string specifying the range of rotation. } \\ \text { 'cycle' -- Parallel data covers 360 degrees }\end{array} \\ & \text { \{'halfcycle' \} — Parallel data covers 180 degrees }\end{array}\right]$
[F, fan_positions, fan_rotation_angles] = fan2para(...) returns the fan-beam sensor measurement angles in fan_positions, if 'FanSensorGeometry' is 'arc'. If 'FanSensorGeometry' is 'line', fan_positions contains the fan-beam sensor positions along the line of sensors. fan_rotation_angles contains rotation angles.

## Class Support

## Examples

See Also
$P$ and $D$ can be double or single, and must be nonsparse. The other numeric input arguments must be double. The output arguments are double.

Generate parallel-beam projections

```
ph = phantom(128);
theta = 0:180;
[P,xp] = radon(ph,theta);
imshow(theta,xp,P,[],'n'), axis normal
title('Parallel-Beam Projections')
xlabel('0 (degrees)')
ylabel('x''')
colormap(hot), colorbar
```

Convert to fan-beam projections

```
[F,Fpos,Fangles] = para2fan(P,100);
figure, imshow(Fangles,Fpos,F,[],'n'), axis normal
title('Fan-Beam Projections')
xlabel('0 (degrees)')
ylabel('Sensor Locations (degrees)')
colormap(hot), colorbar
```

fan2para | fanbeam | iradon | ifanbeam | phantom | radon

## Purpose

Create head phantom image
Syntax
$P=$ phantom(def, $n$ )
$P=$ phantom(E, n)
[P, E] = phantom(...)

## Description

$P=$ phantom(def, $n$ ) generates an image of a head phantom that can be used to test the numerical accuracy of radon and iradon or other two-dimensional reconstruction algorithms. P is a grayscale intensity image that consists of one large ellipse (representing the brain) containing several smaller ellipses (representing features in the brain).
def is a string that specifies the type of head phantom to generate. Valid values are

- 'Shepp-Logan' - Test image used widely by researchers in tomography
- 'Modified Shepp-Logan' (default) - Variant of the Shepp-Logan phantom in which the contrast is improved for better visual perception
n is a scalar that specifies the number of rows and columns in P. If you omit the argument, $n$ defaults to 256 .
$P=$ phantom $(E, n)$ generates a user-defined phantom, where each row of the matrix E specifies an ellipse in the image. E has six columns, with each column containing a different parameter for the ellipses. This table describes the columns of the matrix.

| Column | Parameter | Meaning |
| :--- | :--- | :--- |
| Column 1 | A | Additive intensity value of the ellipse |
| Column 2 | a | Length of the horizontal semiaxis of the <br> ellipse |
| Column 3 | b | Length of the vertical semiaxis of the <br> ellipse |
| Column 4 | x0 | $x$-coordinate of the center of the ellipse |


| Column | Parameter | Meaning |
| :--- | :--- | :--- |
| Column 5 | y0 | $y$-coordinate of the center of the ellipse |
| Column 6 | phi | Angle (in degrees) between the horizontal <br> semiaxis of the ellipse and the $x$-axis of <br> the image |

For purposes of generating the phantom, the domains for the $x$ - and $y$-axes span $[-1,1]$. Columns 2 through 5 must be specified in terms of this range.
$[P, E]=$ phantom (...) returns the matrix E used to generate the phantom.

## Class <br> Support

Tips $\begin{aligned} & \text { For any given pixel in the output image, the pixe } \\ & \text { sum of the additive intensity values of all ellipses } \\ & \text { of. If a pixel is not part of any ellipse, its value is } \\ & \text { The additive intensity value A for an ellipse can b } \\ & \text { if it is negative, the ellipse will be darker than th } \\ & \text { Note that, depending on the values of A, some pix } \\ & \text { outside the range [0,1]. } \\ & \text { Examples } \\ & \begin{array}{l}\text { P = phantom ('Modified Shepp-Logan ' , 200) ; } \\ \text { imshow (P) }\end{array}\end{aligned}$


References $\quad$ [1] Jain, Anil K., Fundamentals of Digital Image Processing, Englewood

Cliffs, NJ, Prentice Hall, 1989, p. 439.
See Also radon | iradon

Purpose
Syntax
Description

Convert region of interest (ROI) polygon to region mask

BW = poly2mask(x, y, m, n)
BW = poly2mask(x,y,m,n) computes a binary region of interest (ROI) mask, BW, from an ROI polygon, represented by the vectors $x$ and $y$. The size of BW is m-by-n. poly2mask sets pixels in BW that are inside the polygon ( $\mathrm{X}, \mathrm{Y}$ ) to 1 and sets pixels outside the polygon to 0 .
poly2mask closes the polygon automatically if it isn't already closed.

## Note on Rectangular Polygons

When the input polygon goes through the middle of a pixel, sometimes the pixel is determined to be inside the polygon and sometimes it is determined to be outside (see Algorithm for details). To specify a polygon that includes a given rectangular set of pixels, make the edges of the polygon lie along the outside edges of the bounding pixels, instead of the center of the pixels.

For example, to include pixels in columns 4 through 10 and rows 4 through 10, you might specify the polygon vertices like this:

```
x = [l4 10 10 4 4];
y = [lllllll
mask = poly2mask(x,y,12,12)
mask =
\begin{tabular}{llllllllllll}
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 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0
\end{tabular}
```

| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

In this example, the polygon goes through the center of the bounding pixels, with the result that only some of the desired bounding pixels are determined to be inside the polygon (the pixels in row 4 and column 4 and not in the polygon). To include these elements in the polygon, use fractional values to specify the outside edge of the 4th row (3.5) and the 10th row (10.5), and the outside edge of the 4th column (3.5) and the outside edge of the 10 th column (10.5) as vertices, as in the following example:

```
x = [llllllllll
y = [llllllllll}3.5 3.5 10.5 10.5 3.5];
mask = poly2mask(x,y,12,12)
mask =
```

| 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 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 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 |

## Class Support

## Examples

The class of BW is logical

```
x = [63 186 54 190 63];
y = [60 60 209 204 60];
bw = poly2mask(x,y,256,256);
```


## poly2mask

```
imshow(bw)
hold on
plot(x,y,'b','LineWidth',2)
hold off
```

Create a mask using random points.

```
x = 256*rand(1,4);
y = 256*rand(1,4);
x(end+1) = x(1);
y(end+1) = y(1);
bw = poly2mask(x,y,256,256);
imshow(bw)
hold on
plot(x,y,'b','LineWidth',2)
hold off
```

Algorithms When creating a region of interest (ROI) mask, poly2mask must determine which pixels are included in the region. This determination can be difficult when pixels on the edge of a region are only partially covered by the border line. The following figure illustrates a triangular region of interest, examining in close-up one of the vertices of the ROI. The figure shows how pixels can be partially covered by the border of a region-of-interest.


## Pixels on the Edge of an ROI Are Only Partially Covered by Border

To determine which pixels are in the region, poly2mask uses the following algorithm:

1 Divide each pixel (unit square) into a 5-by-5 grid. See "Dividing Pixels into a 5-by-5 Subpixel Grid" on page 3-718 for an illustration.

2 Adjust the position of the vertices to be on the intersections of the subpixel grid. See "Adjusting the Vertices to the Subpixel Grid" on page 3-718 for an illustration.

3 Draw a path from each adjusted vertex to the next, following the edges of the subpixel grid. See "Drawing a Path Between the Adjusted Vertices" on page 3-719 for an illustration.

4 Determine which border pixels are inside the polygon using this rule: if a pixel's central subpixel is inside the boundaries defined by the

## poly2mask

path between adjusted vertices, the pixel is considered inside the polygon. See "Determing Which Pixels Are in the Region" on page 3-720 for an illustration.

## Dividing Pixels into a 5-by-5 Subpixel Grid

The following figure shows the pixel that contains the vertex of the ROI shown previously with this 5 -by- 5 subpixel grid.


## Adjusting the Vertices to the Subpixel Grid

poly2mask adjusts each vertex of the polygon so that the vertex lies on the subpixel grid. Note how poly2mask rounds up $x$ and $y$ coordinates to find the nearest grid corner. This creates a second, modified polygon, slightly smaller, in this case, than the original ROI. A portion is shown in the following figure.


## Drawing a Path Between the Adjusted Vertices

poly2mask forms a path from each adjusted vertex to the next, following the edges of the subpixel grid. In the following figure, a portion of this modified polygon is shown by the thick dark lines.


Determing Which Pixels Are in the Region
poly2mask uses the following rule to determine which border pixels are inside the polygon: if the pixel's central subpixel is inside the modified polygon, the pixel is inside the region.

In the following figure, the central subpixels of pixels on the ROI border are shaded a dark gray color. Pixels inside the polygon are shaded a lighter gray. Note that the pixel containing the vertex is not part of the ROI because its center pixel is not inside the modified polygon.


See Also
roipoly

## Purpose Convert point-spread function to optical transfer function

Syntax $\quad$| OTF | $=\operatorname{psf} 20 \mathrm{tf}(\mathrm{PSF})$ |
| ---: | :--- |
| $0 T F$ | $=\operatorname{psf} 2 \mathrm{tf}(\mathrm{PSF}$, OUTSIZE $)$ |

Description

Class Support

Examples

See Also

OTF $=$ psf2otf(PSF) computes the fast Fourier transform (FFT) of the point-spread function (PSF) array and creates the optical transfer function array, OTF, that is not influenced by the PSF off-centering. By default, the OTF array is the same size as the PSF array.

OTF = psf2otf(PSF,OUTSIZE) converts the PSF array into an OTF array, where OUTSIZE specifies the size of the OTF array. OUTSIZE cannot be smaller than the PSF array size in any dimension.

To ensure that the OTF is not altered because of PSF off-centering, psf2otf postpads the PSF array (down or to the right) with 0's to match dimensions specified in OUTSIZE, then circularly shifts the values of the PSF array up (or to the left) until the central pixel reaches ( 1,1 ) position.

Note that this function is used in image convolution/deconvolution when the operations involve the FFT.

PSF can be any nonsparse, numeric array. OTF is of class double.

```
PSF = fspecial('gaussian',13,1);
OTF = psf2otf(PSF,[31 31]); % PSF --> OTF
subplot(1,2,1); surf(PSF); title('PSF');
axis square; axis tight
subplot(1,2,2); surf(abs(OTF)); title('Corresponding |OTF|');
axis square; axis tight
```

otf2psf | circshift | padarray

## Purpose

Quadtree decomposition
Syntax
S = qtdecomp(I)
S = qtdecomp(I, threshold)
S = qtdecomp(I, threshold, mindim)
S = qtdecomp(I, threshold, [mindim maxdim])
S = qtdecomp(I, fun)
qtdecomp divides a square image into four equal-sized square blocks, and then tests each block to see if it meets some criterion of homogeneity. If a block meets the criterion, it is not divided any further. If it does not meet the criterion, it is subdivided again into four blocks, and the test criterion is applied to those blocks. This process is repeated iteratively until each block meets the criterion. The result can have blocks of several different sizes.
$S=$ qtdecomp(I) performs a quadtree decomposition on the intensity image I and returns the quadtree structure in the sparse matrix S. If $S(k, m)$ is nonzero, then ( $k, m$ ) is the upper left corner of a block in the decomposition, and the size of the block is given by $S(k, m)$. By default, qtdecomp splits a block unless all elements in the block are equal.

S = qtdecomp(I, threshold) splits a block if the maximum value of the block elements minus the minimum value of the block elements is greater than threshold. threshold is specified as a value between 0 and 1 , even if I is of class uint8 or uint16. If I is uint8, the threshold value you supply is multiplied by 255 to determine the actual threshold to use; if I is uint16, the threshold value you supply is multiplied by 65535.

S = qtdecomp(I, threshold, mindim) will not produce blocks smaller than mindim, even if the resulting blocks do not meet the threshold condition.
$S=q t d e c o m p(I, ~ t h r e s h o l d, ~[m i n d i m ~ m a x d i m]) ~ w i l l ~ n o t ~ p r o d u c e ~$ blocks smaller than mindim or larger than maxdim. Blocks larger than maxdim are split even if they meet the threshold condition. maxdim/mindim must be a power of 2 .

S = qtdecomp(I, fun) uses the function fun to determine whether to split a block. qtdecomp calls fun with all the current blocks of size $m$-by-m stacked into an m-by-m-by-k array, where $k$ is the number of $m$-by-m blocks. fun returns a logical k-element vector, whose values are 1 if the corresponding block should be split, and 0 otherwise. (For example, if $k(3)$ is 0 , the third $m$-by-m block should not be split.) fun must be a function_handle. Parameterizing Functions, in the MATLAB Mathematics documentation, explains how to provide additional parameters to the function fun.

## Class Support

Tips

## Examples

For the syntaxes that do not include a function, the input image can be of class logical, uint8, uint16, int16, single, or double. For the syntaxes that include a function, the input image can be of any class supported by the function. The output matrix is always of class sparse.
qtdecomp is appropriate primarily for square images whose dimensions are a power of 2 , such as 128 -by- 128 or 512 -by- 512 . These images can be divided until the blocks are as small as 1-by-1. If you use qtdecomp with an image whose dimensions are not a power of 2 , at some point the blocks cannot be divided further. For example, if an image is 96 -by- 96 , it can be divided into blocks of size 48 -by- 48 , then 24 -by- 24,12 -by- 12 , 6 -by- 6 , and finally 3 -by- 3 . No further division beyond 3 -by- 3 is possible. To process this image, you must set mindim to 3 (or to 3 times a power of 2); if you are using the syntax that includes a function, the function must return 0 at the point when the block cannot be divided further.

```
I = uint8([1 1 1 1 1 2 3 6 6;...
    1121456 8;...
    111147777;...
    11111665 5;...
    20 22 20 22 1 2 3 4;...
    20 22 22 20 5 4 7 8;...
    20 22 20 20 9 12 40 12;...
    20 22 20 20 13 14 15 16]);
S = qtdecomp(I,.05);
```

```
disp(full(S));
```

View the block representation of quadtree decomposition.

```
I = imread('liftingbody.png');
S = qtdecomp(I,.27);
blocks = repmat(uint8(0),size(S));
for dim = [[512 256 128 64 32 16 8 4 2 1];
    numblocks = length(find(S==dim));
    if (numblocks > 0)
        values = repmat(uint8(1),[dim dim numblocks]);
        values(2:dim,2:dim,:) = 0;
        blocks = qtsetblk(blocks,S,dim,values);
    end
end
blocks(end,1:end) = 1;
blocks(1:end,end) = 1;
imshow(I), figure, imshow(blocks,[])
```

The following figure shows the original image and a representation of the quadtree decomposition of the image.

## qtdecomp



Image courtesy of NASA

See Also function_handle | qtgetblk | qtsetblk<br>How To<br>- "Anonymous Functions"<br>- "Parameterizing Functions"

## Purpose

Block values in quadtree decomposition
Syntax

Description

## Class <br> Support

Tips

Examples
[vals, r, c] = qtgetblk(I, S, dim)
[vals, idx] = qtgetblk(I, S, dim) left corners of the blocks.
[vals, idx] = qtgetblk(I, S, dim) returns in idx a vector S is of class sparse. the values from the second 4 -by- 4 block.
[vals, $r, c$ ] $=$ qtgetblk(I, $s$, dim) returns in vals an array containing the dim-by-dim blocks in the quadtree decomposition of I. $S$ is the sparse matrix returned by qtdecomp; it contains the quadtree structure. vals is a dim-by-dim-by-k array, where $k$ is the number of dim-by-dim blocks in the quadtree decomposition; if there are no blocks of the specified size, all outputs are returned as empty matrices. $r$ and $c$ are vectors containing the row and column coordinates of the upper containing the linear indices of the upper left corners of the blocks.

I can be of class logical, uint8, uint16, int16, single, or double.

The ordering of the blocks in vals matches the columnwise order of the blocks in I. For example, if vals is 4 -by-4-by-2, vals ( $:,:, 1$ ) contains the values from the first 4 -by- 4 block in I, and vals ( $:,:, 2$ ) contains

| $\mathrm{I}=[1$ | 1 | 1 | 1 | 2 | 3 | 6 | 6 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | 1 | 2 | 1 | 4 | 5 | 6 | 8 |
| 1 | 1 | 1 | 1 | 10 | 15 | 7 | 7 |
| 1 | 1 | 1 | 1 | 20 | 25 | 7 | 7 |
| 20 | 22 | 20 | 22 | 1 | 2 | 3 | 4 |
| 20 | 22 | 22 | 20 | 5 | 6 | 7 | 8 |
| 20 | 22 | 20 | 20 | 9 | 10 | 11 | 12 |
| 22 | 22 | 20 | 20 | 13 | 14 | 15 | 16]; |

$$
\text { [vals, } r, c \text { ] }=q \operatorname{tgetblk}(I, S, 4)
$$

See Also qtdecomp | qtsetblk

## Purpose Set block values in quadtree decomposition

```
Syntax J = qtsetblk(I, S, dim, vals)
```

Description
$J=q t s e t b l k(I, S, d i m, ~ v a l s)$ replaces each dim-by-dim block in the quadtree decomposition of I with the corresponding dim-by-dim block in vals. $S$ is the sparse matrix returned by qtdecomp; it contains the quadtree structure. vals is a dim-by-dim-by-k array, where $k$ is the number of dim-by-dim blocks in the quadtree decomposition.

Class I can be of class logical, uint8, uint16, int16, single, or double. Support
$S$ is of class sparse.
Tips The ordering of the blocks in vals must match the columnwise order of the blocks in I. For example, if vals is 4 -by- 4 -by- 2 , vals ( $:,:, 1$ ) contains the values used to replace the first 4 -by- 4 block in I, and vals(:,:,2) contains the values for the second 4 -by- 4 block.

Examples

| $\mathrm{I}=[1$ | 1 | 1 | 1 | 2 | 3 | 6 | 6 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | 1 | 2 | 1 | 4 | 5 | 6 | 8 |
| 1 | 1 | 1 | 1 | 10 | 15 | 7 | 7 |
| 1 | 1 | 1 | 1 | 20 | 25 | 7 | 7 |
| 20 | 22 | 20 | 22 | 1 | 2 | 3 | 4 |
| 20 | 22 | 22 | 20 | 5 | 6 | 7 | 8 |
| 20 | 22 | 20 | 20 | 9 | 10 | 11 | 12 |
| 22 | 22 | 20 | 20 | 13 | 14 | 15 | 16]; |
| S = qtdecomp ( $\mathrm{I}, 5$ ) ; |  |  |  |  |  |  |  |

## See Also qtdecomp | qtgetblk

## Purpose Radon transform

$$
\begin{array}{ll}
\text { Syntax } & R=\operatorname{radon}(I, \text { theta }) \\
& {[R, x p]=\operatorname{radon}(\ldots)}
\end{array}
$$

## Description

Class
Support
I can be of class double, logical, or any integer class. All other inputs and outputs are of class double.

## Examples

$R=\operatorname{radon}(I$, theta) returns the Radon transform $R$ of the intensity image I for the angle theta degrees.

The Radon transform is the projection of the image intensity along a radial line oriented at a specific angle. If theta is a scalar, R is a column vector containing the Radon transform for theta degrees. If theta is a vector, $R$ is a matrix in which each column is the Radon transform for one of the angles in theta. If you omit theta, it defaults to 0:179.
$[R, x p]=\operatorname{radon}(\ldots)$ returns a vector $x p$ containing the radial coordinates corresponding to each row of $R$.

The radial coordinates returned in xp are the values along the $x$ '-axis, which is oriented at theta degrees counterclockwise from the $x$-axis. The origin of both axes is the center pixel of the image, which is defined as
floor((size(I)+1)/2)
For example, in a 20 -by-30 image, the center pixel is $(10,15)$.

```
iptsetpref('ImshowAxesVisible','on')
```

iptsetpref('ImshowAxesVisible','on')
I = zeros(100,100);
I = zeros(100,100);
I(25:75, 25:75) = 1;
I(25:75, 25:75) = 1;
theta = 0:180;
theta = 0:180;
[R,xp] = radon(I,theta);
[R,xp] = radon(I,theta);
imshow(R,[],'Xdata',theta,'Ydata',xp,...
imshow(R,[],'Xdata',theta,'Ydata',xp,...
'InitialMagnification','fit')
'InitialMagnification','fit')
xlabel('0 (degrees)')
xlabel('0 (degrees)')
ylabel('x''')

```
ylabel('x''')
```

```
colormap(hot), colorbar
iptsetpref('ImshowAxesVisible','off')
```



References Bracewell, Ronald N., Two-Dimensional Imaging, Englewood Cliffs, NJ, Prentice Hall, 1995, pp. 505-537.

Lim, Jae S., Two-Dimensional Signal and Image Processing, Englewood Cliffs, NJ, Prentice Hall, 1990, pp. 42-45.

Algorithms
The Radon transform of an image is the sum of the Radon transforms of each individual pixel.

The algorithm first divides pixels in the image into four subpixels and projects each subpixel separately, as shown in the following figure.


Each subpixel's contribution is proportionally split into the two nearest bins, according to the distance between the projected location and the bin centers. If the subpixel projection hits the center point of a bin, the bin on the axes gets the full value of the subpixel, or one-fourth the value of the pixel. If the subpixel projection hits the border between two bins, the subpixel value is split evenly between the bins.

See Also

fan2para | fanbeam | ifanbeam | iradon | para2fan | phantom

| Purpose | Local range of image <br> Syntax <br> $J=$ = rangefilt (I) |
| :--- | :--- |
| Description |  |
| $J=$ rangefilt (I, NHOOD) |  |
| contains the range value (maximum value - minimum value) of the |  |
| 3-by-3 neighborhood around the corresponding pixel in the input image |  |
| I. The image I can have any dimension. The output image $J$ is the |  |
| same size as the input image I. |  |

then use the getnhood method to extract the neighborhood from the structuring element object.

## Examples

I = imread('liftingbody.png');
J = rangefilt(I);
imshow(I), figure, imshow(J);
(3-D) Quantify land cover changes in an RGB image. The example first converts the image to $L^{*} a^{*} b^{*}$ colorspace to separate intensity information into a single plane of the image, and then calculates the local range in each layer.

```
I = imread('autumn.tif');
cform = makecform('srgb2lab');
LAB = applycform(I, cform);
rLAB = rangefilt(LAB);
imshow(I);
figure, imshow(rLAB(:,:,1),[]);
figure, imshow(rLAB(:,:,2),[]);
figure, imshow(rLAB(:,:,3),[]);
```

See Also entropyfilt | getnhood \| imdilate | imerode \| stdfilt | strel

## Purpose Reflect structuring element <br> Syntax $\quad$ SE2 $=\operatorname{reflect}(S E)$

Description SE2 = reflect(SE) reflects a structuring element through its center. The effect is the same as if you rotated the structuring element's domain 180 degrees around its center (for a 2-D structuring element). If SE is an array of structuring element objects, then reflect(SE) reflects each element of SE, and SE2 has the same size as SE.

## Class <br> SE and SE2 are STREL objects. <br> Support

Examples $\quad$ se $=\operatorname{strel}\left(\left[\begin{array}{llllllll}0 & 0 & 1 ; 0 & 0 & 0 ; & 0 & 0\end{array}\right]\right)$
se2 = reflect(se)
se =
Flat STREL object containing 1 neighbor.
Neighborhood:
$0 \quad 0 \quad 1$
$0 \quad 0 \quad 0$
$0 \quad 0 \quad 0$
se2 =
Flat STREL object containing 1 neighbor.
Neighborhood:
$0 \quad 0 \quad 0$
$0 \quad 0 \quad 0$
100

## See Also

strel

Purpose Measure properties of image regions
Syntax $\quad \begin{aligned} \text { STATS } & =\text { regionprops }(B W, \text { properties }) \\ \text { STATS } & =\text { regionprops }(C C, \text { properties }) \\ \text { STATS } & =\text { regionprops }(L, \text { properties }) \\ \text { STATS } & =\text { regionprops }(\ldots, \text { I, properties })\end{aligned}$

## Description

## Properties

STATS = regionprops(BW, properties) measures a set of properties for each connected component (object) in the binary image, BW. The image $B W$ is a logical array; it can have any dimension.

STATS = regionprops(CC, properties) measures a set of properties for each connected component (object) in CC, which is a structure returned by bwconncomp.

STATS = regionprops(L, properties) measures a set of properties for each labeled region in the label matrix L. Positive integer elements of $L$ correspond to different regions. For example, the set of elements of $L$ equal to 1 corresponds to region 1 ; the set of elements of $L$ equal to 2 corresponds to region 2; and so on.

STATS = regionprops(..., I, properties) measures a set of properties for each labeled region in the image I. The first input to regionprops-either BW, CC, or L-identifies the regions in I. The sizes must match: size(I) must equal size(BW), CC. ImageSize, or size(L).
STATS is a structure array with length equal to the number of objects in BW, CC.NumObjects, or max (L(:)). The fields of the structure array denote different properties for each region, as specified by properties.
properties can be a comma-separated list of strings, a cell array containing strings, the single string 'all', or the string 'basic'. If properties is the string 'all', regionprops computes all the shape measurements, listed in Shape Measurements on page 3-737. If called with a grayscale image, regionprops also returns the pixel value measurements, listed in Pixel Value Measurements on page 3-737. If properties is not specified or if it is the string 'basic', regionprops computes only the 'Area', 'Centroid', and 'BoundingBox'
measurements. You can calculate the following properties on N-D inputs: 'Area', 'BoundingBox', 'Centroid', 'FilledArea', 'FilledImage', 'Image', 'PixelIdxList', 'PixelList', and 'SubarrayIdx'.

## Shape Measurements

| 'Area' | 'EulerNumber' | 'Orientation' |
| :--- | :--- | :--- |
| 'BoundingBox' | 'Extent' | 'Perimeter' |
| 'Centroid' | 'Extrema' | 'PixelIdxList' |
| 'ConvexArea' | 'FilledArea' | 'PixelList' |
| 'ConvexHull' | 'FilledImage' | 'Solidity' |
| 'ConvexImage' | 'Image' | 'SubarrayIdx' |
| 'Eccentricity' | 'MajorAxisLength' |  |
| 'EquivDiameter' | 'MinorAxisLength' |  |

Pixel Value Measurements

| 'MaxIntensity ' | 'MinIntensity' | 'WeightedCentroid' |
| :--- | :--- | :--- |
| 'MeanIntensity ' | 'PixelValues' |  |

## Definitions

'Area ' - Scalar; the actual number of pixels in the region. (This value might differ slightly from the value returned by bwarea, which weights different patterns of pixels differently.)
'BoundingBox' - The smallest rectangle containing the region, a 1-by- $Q * 2$ vector, where $Q$ is the number of image dimensions: ndims(L), ndims(BW), or numel(CC.ImageSize). BoundingBox is [ul_corner width], where:
ul_corner is in the form [x y z ...] ] and specifies the upper-left corner of the bounding box
width is in the form [x_width y_width ...] and specifies the width of the bounding box along each dimension
'Centroid' - 1-by-Q vector that specifies the center of mass of the region. Note that the first element of Centroid is the horizontal coordinate (or $x$-coordinate) of the center of mass, and the second element is the vertical coordinate (or $y$-coordinate). All other elements of Centroid are in order of dimension.

This figure illustrates the centroid and bounding box for a discontiguous region. The region consists of the white pixels; the green box is the bounding box, and the red dot is the centroid.

'ConvexHull' - p-by-2 matrix that specifies the smallest convex polygon that can contain the region. Each row of the matrix contains the $x$ - and $y$-coordinates of one vertex of the polygon. This property is supported only for 2-D input label matrices.
'ConvexImage ' - Binary image (logical) that specifies the convex hull, with all pixels within the hull filled in (i.e., set to on). (For pixels that the boundary of the hull passes through, regionprops uses the same logic as roipoly to determine whether the pixel is inside or outside the hull.) The image is the size of the bounding box of the region. This property is supported only for 2 -D input label matrices.
'ConvexArea' - Scalar that specifies the number of pixels in 'ConvexImage '. This property is supported only for 2-D input label matrices.
'Eccentricity ' - Scalar that specifies the eccentricity of the ellipse that has the same second-moments as the region. The eccentricity is the ratio of the distance between the foci of the ellipse and its major axis length. The value is between 0 and 1. ( 0 and 1 are degenerate cases; an ellipse whose eccentricity is 0 is actually a circle, while an ellipse whose eccentricity is 1 is a line segment.) This property is supported only for 2-D input label matrices.
'EquivDiameter' - Scalar that specifies the diameter of a circle with the same area as the region. Computed as sqrt(4*Area/pi). This property is supported only for 2-D input label matrices.
'EulerNumber' - Scalar that specifies the number of objects in the region minus the number of holes in those objects. This property is supported only for 2-D input label matrices. regionprops uses 8 -connectivity to compute the EulerNumber measurement. To learn more about connectivity, see "Pixel Connectivity".
'Extent ' - Scalar that specifies the ratio of pixels in the region to pixels in the total bounding box. Computed as the Area divided by the area of the bounding box. This property is supported only for 2 -D input label matrices.
'Extrema' - 8-by-2 matrix that specifies the extrema points in the region. Each row of the matrix contains the $x$ - and $y$-coordinates of one of the points. The format of the vector is [top-left top-right right-top right-bottom bottom-right bottom-left left-bottom left-top]. This property is supported only for 2-D input label matrices.
This figure illustrates the extrema of two different regions. In the region on the left, each extrema point is distinct. In the region on the right, certain extrema points (e.g., top-left and left-top) are identical.

'FilledArea' - Scalar specifying the number of on pixels in FilledImage.
'FilledImage ' - Binary image (logical) of the same size as the bounding box of the region. The on pixels correspond to the region, with all holes filled in.


Original Image, Containing a Single Region


Image Returned
'Image ' - Binary image (logical) of the same size as the bounding box of the region; the on pixels correspond to the region, and all other pixels are off.
'MajorAxisLength ' - Scalar specifying the length (in pixels) of the major axis of the ellipse that has the same normalized second central moments as the region. This property is supported only for 2-D input label matrices.
'MaxIntensity ' - Scalar specifying the value of the pixel with the greatest intensity in the region.
'MeanIntensity ' - Scalar specifying the mean of all the intensity values in the region.
'MinIntensity ' - Scalar specifying the value of the pixel with the lowest intensity in the region.
'MinorAxisLength ' - Scalar; the length (in pixels) of the minor axis of the ellipse that has the same normalized second central moments as the region. This property is supported only for 2-D input label matrices.
'Orientation' - Scalar; the angle (in degrees ranging from -90 to 90 degrees) between the $x$-axis and the major axis of the ellipse that has the same second-moments as the region. This property is supported only for 2 -D input label matrices.

This figure illustrates the axes and orientation of the ellipse. The left side of the figure shows an image region and its corresponding ellipse. The right side shows the same ellipse, with features indicated graphically:

- The solid blue lines are the axes.
- The red dots are the foci.
- The orientation is the angle between the horizontal dotted line and the major axis.

'Perimeter' - Scalar; the distance around the boundary of the region. regionprops computes the perimeter by calculating the distance between each adjoining pair of pixels around the border of the region. If the image contains discontiguous regions, regionprops returns
unexpected results. The following figure shows the pixels included in the perimeter calculation for this object.

'PixelIdxList' - p-element vector containing the linear indices of the pixels in the region.
'PixelList' - p-by-Q matrix specifying the locations of pixels in the region. Each row of the matrix has the form [ $\left.\begin{array}{lll}x & y & z\end{array} ..\right]$ ] and specifies the coordinates of one pixel in the region.
'PixelValues' - $p$-by- 1 vector, where $p$ is the number of pixels in the region. Each element in the vector contains the value of a pixel in the region.
'Solidity ' - Scalar specifying the proportion of the pixels in the convex hull that are also in the region. Computed as Area/ConvexArea. This property is supported only for 2 -D input label matrices.
'SubarrayIdx' - Cell-array containing indices such that L(idx\{:\}) extracts the elements of $L$ inside the object bounding box.
'WeightedCentroid' - $p$-by- $Q$ vector of coordinates specifying the center of the region based on location and intensity value. The first element of WeightedCentroid is the horizontal coordinate (or $x$-coordinate) of the weighted centroid. The second element
is the vertical coordinate (or $y$-coordinate). All other elements of WeightedCentroid are in order of dimension.


## Class Support

## Tips

If the first input is BW, BW must be a logical array and it can have any dimension. If the first input is CC, CC must be a structure returned by bwconncomp. If the first input is $L$, $L$ must be real, nonsparse, and contain integers. $L$ can have any numeric class and any dimension.

## Note on Terminology

You can use regionprops on contiguous regions and discontiguous regions.

Contiguous regions are also called "objects," "connected components," and "blobs." A label matrix containing contiguous regions might look like this:

```
110220 3 3
1102 2 0 3 3
```

Elements of $L$ equal to 1 belong to the first contiguous region or connected component; elements of $L$ equal to 2 belong to the second connected component; etc.

Discontiguous regions are regions that might contain multiple connected components. A label matrix containing discontiguous regions might look like this:

```
1100110}2
1110111022
```

Elements of $L$ equal to 1 belong to the first region, which is discontiguous and contains two connected components. Elements of $L$ equal to 2 belong to the second region, which is a single connected component.

## Selecting Regions Based on Certain Criteria

The function ismember is useful in conjunction with regionprops, bwconncomp, and labelmatrix for creating a binary image containing only objects or regions that meet certain criteria. For example, these

## regionprops

commands create a binary image containing only the regions whose area is greater than 80 .

```
cc = bwconncomp(BW);
stats = regionprops(cc, 'Area');
idx = find([stats.Area] > 80);
BW2 = ismember(labelmatrix(cc), idx);
```


## Using the Comma-Separated List Syntax

The comma-separated list syntax for structure arrays is very useful when you work with the output of regionprops. For example, for a field that contains a scalar, you can use this syntax to create a vector containing the value of this field for each region in the image.

For instance, if stats is a structure array with field Area, then the following two expressions are equivalent:

```
stats(1).Area, stats(2).Area, ..., stats(end).Area
and
stats.Area
```

Therefore, you can use these calls to create a vector containing the area of each region in the image.

```
stats = regionprops(L, 'Area');
allArea = [stats.Area];
```

allArea is a vector of the same length as the structure array stats.

## Performance Considerations

Most of the measurements take very little time to compute. However, there are a few measuements, listed below, that can take significantly longer, depending on the number of regions in L :

- 'ConvexHull'
- 'ConvexImage'
- 'ConvexArea'
- 'FilledImage'

Note that computing certain groups of measurements takes about the same amount of time as computing just one of them because regionprops takes advantage of intermediate computations used in both computations. Therefore, it is fastest to compute all the desired measurements in a single call to regionprops.

## Using bwlabel, bwlabeln, bwconncomp, and regionprops

The functions bwlabel, bwlabeln, and bwconncomp all compute connected components for binary images. bwconncomp replaces the use of bwlabel and bwlabeln. It uses significantly less memory and is sometimes faster than the other functions.

| Function | Input <br> Dimension | Output Form | Memory <br> Use | Connectivity |
| :--- | :--- | :--- | :--- | :--- |
| bwlabel | 2-D | Double-precision <br> label matrix | High | 4 or 8 |
| bwlabeln | N-D | Double-precision <br> label matrix | High | Any |
| bwconncomp | N-D | CC struct | Low | Any |

The output of bwlabel and bwlabeln is a double-precision label matrix. To compute a label matrix using a more memory-efficient data type, use the labelmatrix function on the output of bwconncomp:
$C C=$ bwconncomp(BW);
L = labelmatrix(CC);

To extract features from a binary image using regionprops with the default connectivity, it is no longer necessary to call bwlabel or bwlabeln first. You can simply pass the binary image directly to regionprops, which then uses the memory-efficient bwconncomp to

## regionprops

compute the connected components automatically for you. To extract features from a binary image using a nondefault connectivity, call bwconncomp first and then pass the result to regionprops:

CC = bwconncomp(BW, CONN);
S = regionprops(CC);

## Examples

Label the connected pixel components in the text. png image, compute their centroids, and superimpose the centroid locations on the image:

```
BW = imread('text.png');
s = regionprops(BW, 'centroid');
centroids = cat(1, s.Centroid);
imshow(BW)
hold on
plot(centroids(:,1), centroids(:,2), 'b*')
hold off
```

Fhe werm watershed rofors to a rudge that

See Also bwconncomp | bwlabel | bwlabeln | ismember | labelmatrix | watershed

## Purpose <br> Description

## Construction

## Properties

Mattes mutual information metric configuration object

A MattesMutualInformation object describes a mutual information metric configuration that you pass to the function imregister to solve image registration problems.
metric = registration.metric.MattesMutualInformation() constructs a MattesMutualInformation object.

## NumberOfSpatialSamples

Number of spatial samples used to compute the metric.
NumberOfSpatialSamples is a positive scalar integer value that defines the number of random pixels imregister uses to compute the metric. Your registration results are more reproducible (at the cost of performance) as you increase this value. imregister only uses NumberOfSpatialSamples when UseAllPixels = 0 (false). The default value for NumberOfSpatialSamples is 500.

## NumberOfHistogramBins

Number of histogram bins used to compute the metric.
NumberOfHistogramBins is a positive scalar integer value that defines the number of bins imregister uses to compute the joint distribution histogram. The default value is 50 , and the minimum value is 5 .

## UseAllPixels

Logical scalar that specifies whether imregister should use all pixels in the overlap region of the images to compute the metric.

You can achieve significantly better performance if you set this property to 0 (false). When UseAllPixels $=0$, the NumberOfSpatialSamples property controls the number of random pixel locations that imregister uses to compute the metric. The results of your registration might not be reproducible when UseAllPixels $=0$. This is because imregister selects a

## registration.metric.MattesMutualInformation

subset of pixels from the images to compute the metric. The default value forUseAllPixels is 1 (true).

## Definitions

Copy
Semantics
Tips

## Mutual Information Metric

Metric used to maximize the number of coincident pixels with the same relative brightness value. This metric is best suited for images with different brightness ranges.

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

- Larger values of mutual information correspond to better registration results. You can examine the computed values of Mattes mutual information if you enable 'DisplayOptimization' when you call imregister, for example:
movingRegistered $=$ imregister(moving,fixed,'rigid',optimizer,metric,'DisplayOptimization',


## Examples Register MRI Images with MattesMutuallnformation Metric

Register two MRI images of a knee that were obtained using different protocols.

Read the images into the workspace.

```
fixed = dicomread('knee1.dcm');
moving = dicomread('knee2.dcm');
```

View the misaligned images.

```
imshowpair(fixed, moving,'Scaling','joint');
```



Create the optimizer configuration object suitable for registering images from different sensors.
optimizer $=$ registration.optimizer.OnePlusOneEvolutionary;
Create the MattesMutualInformation metric configuration object.
metric $=$ registration.metric.MattesMutualInformation
metric $=$
registration.metric.MattesMutualInformation
Properties:
NumberOfSpatialSamples: ..... 500
NumberOfHistogramBins: ..... 50UseAllPixels: 1

Tune the properties of the optimizer so that the problem will converge on a global maxima. Increase the number of iterations the optimizer will use to solve the problem.

```
optimizer.InitialRadius = 0.009;
optimizer.Epsilon = 1.5e-4;
optimizer.GrowthFactor = 1.01;
optimizer.MaximumIterations = 300;
```

Register the moving and fixed images.
movingRegistered = imregister(moving, fixed, 'affine', optimizer, metric)
View the registered images.
figure;
imshowpair(fixed, movingRegistered,'Scaling','joint');


## Algorithms

The imregister function uses an iterative process to register images. The metric you pass to imregister defines the image similarity metric for evaluating the accuracy of the registration. An image similarity metric takes two images and returns a scalar value that describes how similar the images are. The optimizer you pass to imregister defines the methodology for minimizing or maximizing the similarity metric.

Mutual information metrics are information theoretic techniques for measuring how related two variables are. These algorithms use the joint probability distribution of a sampling of pixels from two images to measure the certainty that the values of one set of pixels map to similar values in the other image. This information is a quantitative measure of how similar the images are. High mutual information implies a large

## registration.metric.MattesMutualInformation

reduction in the uncertainty (entropy) between the two distributions, signaling that the images are likely better aligned.

The Mattes mutual information algorithm uses a single set of pixel locations for the duration of the optimization, instead of drawing a new set at each iteration. The number of samples used to compute the probability density estimates and the number of bins used to compute the entropy are both user selectable. The marginal and joint probability density function is evaluated at the uniformly spaced bins using the samples. Entropy values are computed by summing over the bins. Zero-order and third-order B-spline kernels are used to compute the probability density functions of the fixed and moving images, respectively.[1]

\author{

References [1] Rahunathan, Smriti, D. Stredney, P. Schmalbrock, and B.D. Clymer. Image Registration Using Rigid Registration and Maximization of Mutual Information. Poster presented at: MMVR13. The 13th Annual Medicine Meets Virtual Reality Conference; 2005 January 26-29; Long Beach, CA. <br> [2] D. Mattes, D.R. Haynor, H. Vesselle, T. Lewellen, and W. Eubank. "Non-rigid multimodality image registration." (Proceedings paper).Medical Imaging 2001: Image Processing. SPIE Publications, 3 July 2001. pp. 1609-1620. <br> Alternatives <br> Use imregconfig to construct a metric configuration for typical image registration scenarios. <br> | See Also | registration.metric.MeanSquares \| imregister |
| :--- | :--- |
| Concepts | - Class Attributes |
|  | - Property Attributes |

}
Purpose Mean square error metric configuration object
DescriptionA MeanSquares object describes a mean square error metricconfiguration that you pass to the function imregister to solve imageregistration problems.
Constructionmetric $=$ registration.metric.MeanSquares() constructs aMeanSquares object.
Copy
Semantics
Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.
Tips

- This metric is an element-wise difference between two inputimages. The ideal value is zero. You can examinethe computed values of mean square error if you enable'DisplayOptimization' when you call imregister. For example,movingRegistered = imregister(moving,fixed,'rigid',optimizer, metric
Examples Register Remote Sensing Images with MeanSquares Metric
Create a MeanSquares object and use it to register two images capturedwith different sensors.
In general, imregister doesn't support perspective transformations. However it returns good results for this problem, which uses a similarity transformation.
Read the images into the workspace.

```
fixed = imread('westconcordorthophoto.png');
moving = rgb2gray(imread('westconcordaerial.png'));
```

View the misaligned images.

```
imshowpair(fixed, moving,'Scaling','joint');
```


## registration.metric.MeanSquares



Create the optimizer configuration object suitable for registering images from different sensors.
optimizer = registration.optimizer.OnePlusOneEvolutionary;
Create the MeanSquares metric configuration object. Even though the images came from different sensors, they have an intensity relationship similar enough to use mean square error as the similarity metric.
metric = registration.metric.MeanSquares
metric =

## registration.metric.MeanSquares

## registration.metric.MeanSquares <br> This class has no properties.

Increase MaximumIterations property of the optimizer to allow for more iterations.
optimizer.MaximumIterations = 1000;
Register the moving and fixed images.
movingRegistered = imregister(moving, fixed, 'similarity', optimizer

View the registered images.
figure;
imshowpair(fixed, movingRegistered,'Scaling','joint');

## registration.metric.MeanSquares



Algorithms

The imregister function uses an iterative process to register images. The metric you pass to imregister defines the image similarity metric for evaluating the accuracy of the registration. An image similarity metric takes two images and returns a scalar value that describes how similar the images are. The optimizer you pass to imregister defines the methodology for minimizing or maximizing the similarity metric.

The mean squares image similarity metric is computed by squaring the difference of corresponding pixels in each image and taking the mean of the those squared differences.

Use imregconfig to construct a metric configuration for typical image registration scenarios.

See Also registration.metric.MattesMutualInformation I imregister

## registration.optimizer.OnePlusOneEvolutionary

| Purpose | One-plus-one evolutionary optimizer configuration object |
| :--- | :--- |
| Description | A OnePlusOneEvolutionary object describes a one-plus-one <br> evolutionary optimization configuration that you pass to the function <br> imregister to solve image registration problems. |
| Construction | optimizer = registration. optimizer. OnePlusOneEvolutionary () <br> Constructs a OnePlusOneEvolutionary object. |
| Properties $\quad$GrowthFactor <br> Growth factor of the search radius. <br> GrowthFactor is a positive scalar value that the optimizer <br> uses to control the rate at which the search radius grows in <br> parameter space. If you set GrowthFactor to a large value, <br> the optimization is fast, but it might result in finding only the <br> metric's local extrema. If you set GrowthFactor to a small value, <br> the optimization is slower, but it is likely to converge on a better <br> solution. The default value of GrowthFactor is 1.05. |  |

## Epsilon

Minimum size of the search radius.
Epsilon is a positive scalar value that controls the accuracy of convergence by adjusting the minimum size of the search radius. If you set Epsilon to a small value, the optimization of the metric is more accurate, but the computation takes longer. If you set Epsilon to a large value, the computation time deceases at the expense of accuracy. The default value of Epsilon is 1.5e-6.

## InitialRadius

Initial size of search radius.
InitialRadius is a positive scalar value that controls the initial search radius of the optimizer. If you set InitialRadius to a large value, the computation time decreases. However, overly large
values of InitialRadius might result in an optimization that fails to converge. The default value of InitialRadius is 6.25e-3.

## Maximumlterations

Maximum number of optimizer iterations.
MaximumIterations is a positive scalar integer value that determines the maximum number of iterations the optimizer performs at any given pyramid level. The registration could converge before the optimizer reaches the maximum number of iterations. The default value of MaximumIterations is 100 .

## Copy Semantics

## Examples Register MRI Images with OnePlusOneEvolutionary Optimizer

Register two MRI images of a knee that were obtained using different protocols.

Read the images into the workspace.

```
fixed = dicomread('knee1.dcm');
moving = dicomread('knee2.dcm');
```

View the misaligned images.

```
imshowpair(fixed, moving,'Scaling','joint');
```


## registration.optimizer.OnePlusOneEvolutionary



Create the optimizer configuration object suitable for registering images from different sensors.

```
optimizer = registration.optimizer.OnePlusOneEvolutionary
optimizer =
    registration.optimizer.OnePlusOneEvolutionary
    Properties:
        GrowthFactor: 1.050000e+00
                Epsilon: 1.500000e-06
            InitialRadius: 6.250000e-03
        MaximumIterations: 100
```

Create the MattesMutualInformation metric configuration object.
metric = registration.metric.MattesMutualInformation;
Tune the properties of the optimizer so that the problem will converge on a global maxima. Increase the number of iterations the optimizer will use to solve the problem.

```
optimizer.InitialRadius = 0.009;
optimizer.Epsilon = 1.5e-4;
optimizer.GrowthFactor = 1.01;
optimizer.MaximumIterations = 300;
```

Register the moving and fixed images.

```
movingRegistered = imregister(moving, fixed, 'affine', optimizer, met!
```

View the registered images.
figure
imshowpair(fixed, movingRegistered,'Scaling','joint');

## registration.optimizer.OnePlusOneEvolutionary



Algorithms
The imregister function uses an iterative process to register images. The metric you pass to imregister defines the image similarity metric for evaluating the accuracy of the registration. An image similarity metric takes two images and returns a scalar value that describes how similar the images are. The optimizer you pass to imregister defines the methodology for minimizing or maximizing the similarity metric.

An evolutionary algorithm iterates to find a set of parameters that produce the best possible registration result. It does this by perturbing, or mutating, the parameters from the last iteration (the parent). If the new (child) parameters yield a better result, then the child becomes the new parent whose parameters are perturbed, perhaps more aggressively. If the parent yields a better result, it remains the parent and the next perturbation is less aggressive.

References

Alternatives Use imregconfig to construct an optimizer configuration for typical image registration scenarios.

## See Also <br> registration.optimizer.RegularStepGradientDescent | imregister

## Concepts - Class Attributes

- Property Attributes


## registration.optimizer.RegularStepGradientDescent

## Purpose Regular step gradient descent optimizer configuration object <br> Description <br> Construction <br> optimizer = registration.optimizer.RegularStepGradientDescent() constructs a RegularStepGradientDescent object. <br> Properties <br> GradientMagnitudeTolerance

Gradient magnitude tolerance.
GradientMagnitudeTolerance is a positive scalar value that controls the optimization process. When the value of the gradient is smaller than GradientMagnitudeTolerance, it is an indication that the optimizer might have reached a plateau. The default value of GradientMagnitudeTolerance is 1e-4.

## MinimumStepLength

Tolerance for convergence.
MinimumStepLength is a positive scalar value that controls the accuracy of convergence. If you set MinimumStepLength to a small value, the optimization takes longer to compute, but it is likely to converge on a more accurate metric value. The default value of MinimumStepLength is $1 \mathrm{e}-5$.

## MaximumStepLength

Initial step length.
MaximumStepLength is a positive scalar value that controls the initial step length used in optimization. If you set MaximumStepLength to a large value, the computation time decreases. However, the optimizer might fail to converge if you set MaximumStepLength to an overly large value. The default value of MaximumStepLength is 0.0625 .

## Maximumlterations

Maximum number of iterations.
MaximumIterations is a positive scalar integer value that determines the maximum number of iterations the optimizer performs at any given pyramid level. The registration could converge before the optimizer reaches the maximum number of iterations. The default value of MaximumIterations is 100.

## RelaxationFactor

Step length reduction factor.
RelaxationFactor is a scalar value between 0 and 1 that defines the rate at which the optimizer reduces step size during convergence. Whenever the optimizer determines that the direction of the gradient changed, it reduces the size of the step length. If your metric is noisy, you can set RelaxationFactor to a larger value. This leads to a more stable convergence at the expense of computation time. The default value of RelaxationFactor is 0.5 .

## Copy Semantics

## Examples

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB Programming Fundamentals documentation.

## Register Images with RegularStepGradientDescent Optimizer

Create a RegularStepGradientDescent object and use it to register two images captured with the same device.

Read the reference image and create an unregistered copy.

```
fixed = imread('pout.tif');
moving = imrotate(fixed, 5, 'bilinear', 'crop');
```

View the misaligned images.

```
imshowpair(fixed, moving,'Scaling','joint');
```


## registration.optimizer.RegularStepGradientDescent



Create the optimizer configuration object suitable for registering images from the same device.
optimizer = registration.optimizer.RegularStepGradientDescent
Create the metric configuration object.
metric = registration.metric.MeanSquares;
Now modify the optimizer configuration to get more precision.
optimizer. MaximumIterations $=300$;
optimizer.MinimumStepLength = 5e-4;
Perform the registration.
movingRegistered = imregister(moving,fixed,'rigid',optimizer,metric);
View registered images.

```
figure
imshowpair(fixed, movingRegistered,'Scaling','joint');
```



## Algorithms

The imregister function uses an iterative process to register images. The metric you pass to imregister defines the image similarity metric for evaluating the accuracy of the registration. An image similarity metric takes two images and returns a scalar value that describes how similar the images are. The optimizer you pass to imregister defines the methodology for minimizing or maximizing the similarity metric.

The regular step gradient descent optimization adjusts the transformation parameters so that the optimization follows the gradient of the image similarity metric in the direction of the extrema. It uses constant length steps along the gradient between computations until the gradient changes direction, at which point the step length is halved.
Use imregconfig to construct an optimizer configuration for typical image registration scenarios.

## registration.optimizer.RegularStepGradientDescent

$\begin{array}{ll}\text { See Also } & \text { registration.optimizer.OnePlusOneEvolutionary I imregister } \\ \text { Concepts } & \text { - Class Attributes } \\ & \text { - Property Attributes }\end{array}$
Purpose Convert RGB image or colormap to grayscale
Syntax

I = rgb2gray (RGB)

newmap $=$ rgb2gray(map)
Description
Class
Support
Examples Convert an RGB image to a grayscale image.

```
I = imread('board.tif');
J = rgb2gray(I);
figure, imshow(I), figure, imshow(J);
```

Convert the colormap to a grayscale colormap.

```
[X,map] = imread('trees.tif');
gmap = rgb2gray(map);
figure, imshow(X,map), figure, imshow(X,gmap);
```


## Algorithms

rgb2gray converts RGB values to grayscale values by forming a weighted sum of the $R, G$, and $B$ components:
0.2989 * $R+0.5870 * G+0.1140$ * $B$

Note that these are the same weights used by the rgb2ntsc function to compute the $Y$ component.

See Also
ind2gray | mat2gray | ntsc2rgb | rgb2ind | rgb2ntsc

## Purpose Convert RGB color values to NTSC color space

```
Syntax yiqmap = rgb2ntsc(rgbmap)
YIQ = rgb2ntsc(RGB)
```


## Description

yiqmap $=$ rgb2ntsc(rgbmap) converts the m-by-3 RGB values in rgbmap to NTSC color space. yiqmap is an m-by-3 matrix that contains the NTSC luminance ( $Y$ ) and chrominance ( $I$ and $Q$ ) color components as columns that are equivalent to the colors in the RGB colormap.

YIQ = rgb2ntsc(RGB) converts the truecolor image RGB to the equivalent NTSC image YIQ.

Tips
In the NTSC color space, the luminance is the grayscale signal used to display pictures on monochrome (black and white) televisions. The other components carry the hue and saturation information.
rgb2ntsc defines the NTSC components using

$$
\left[\begin{array}{l}
Y \\
I \\
Q
\end{array}\right]=\left[\begin{array}{rrr}
0.299 & 0.587 & 0.114 \\
0.596 & -0.274 & -0.322 \\
0.211 & -0.523 & 0.312
\end{array}\right]\left[\begin{array}{l}
R \\
G \\
B
\end{array}\right]
$$

## Class <br> Support

RGB can be of class uint8, uint16, int16, single, or double. RGBMAP can be double. The output is double.

See Also ntsc2rgb | rgb2ind | ind2rgb | ind2gray

Purpose Convert RGB color values to YCbCr color space
Syntax $\quad$ ycbcrmap $=r g b 2 y c b c r($ map $)$
$\mathrm{YCBCR}=\operatorname{rgb2ycbcr}(\mathrm{RGB})$

Description

Class Support

Examples Convert RGB image to YCbCr .
RGB $=$ imread('board.tif');
YCBCR $=$ rgb2ycbcr(RGB);
Convert RGB color space to YCbCr.

```
```

map = jet(256);

```
```

map = jet(256);
newmap = rgb2ycbcr(map);

```
```

newmap = rgb2ycbcr(map);

```
```


## References

 array. Cb and Cr are in the range [4112 61680]. is of the same class as the input image.ycbcrmap $=$ rgb2ycbcr(map) converts the RGB values in map to the YCbCr color space. map must be an M-by-3 array. ycbermap is an M-by-3 matrix that contains the YCbCr luminance $(Y)$ and chrominance ( Cb and $C r$ ) color values as columns. Each row in ycbcfmap represents the equivalent color to the corresponding row in the RGB colormap, map.

YCBCR $=$ rgb2ycbcr(RGB) converts the truecolor image RGB to the equivalent image in the YCbCr color space. RGB must be a M-by-N-by-3

If the input is uint8, $Y C B C R$ is uint8, where $Y$ is in the range [ 16 235], and Cb and Cr are in the range [ 16 240]. If the input is a double, Y is in the range [16/255 235/255] and Cb and Cr are in the range [16/255 $240 / 255$ ]. If the input is uint16, $Y$ is in the range [4112 60395] and

If the input is an RGB image, it can be of class uint8, uint16, or double. If the input is a colormap, it must be double. The output image
[1] Poynton, C. A.A Technical Introduction to Digital Video, John Wiley \& Sons, Inc., 1996, p. 175.
[2] Rec. ITU-R BT.601-5, Studio Encoding Parameters of Digital Television for Standard 4:3 and Wide-screen 16:9 Aspect Ratios, (1982-1986-1990-1992-1994-1995), Section 3.5.

See Also ntsc2rgb | rgb2ntsc | ycbcr2rgb

## roicolor

Purpose Select region of interest (ROI) based on color

```
Syntax \(\quad B W=\operatorname{roicolor}(A\), low, high \()\)
BW = roicolor(A, v)
```

Description

Class
Support
Examples
roicolor selects a region of interest ( ROI ) within an indexed or intensity image and returns a binary image. (You can use the returned image as a mask for masked filtering using roifilt2.)

BW = roicolor(A, low, high) returns an ROI selected as those pixels that lie within the colormap range [low high].
$B W=(A>=$ low $) \&(A<=~ h i g h)$
BW is a binary image with 0's outside the region of interest and 1's inside.
$B W=\operatorname{roicolor}(A, v)$ returns an $R O I$ selected as those pixels in $A$ that match the values in vector v . BW is a binary image with 1's where the values of A match the values of $v$.

The input image A must be numeric. The output image BW is of class logical.
load clown
$B W=$ roicolor (X, 10, 20) ;
imshow (X, map)
figure,imshow(BW)


See Also roifilt2 | roipoly

Purpose
Fill in specified region of interest (ROI) polygon in grayscale image
Syntax

```
J = roifill
J = roifill(I)
J = roifill(I, c, r)
J = roifill(I, BW)
[J,BW] = roifill(...)
J = roifill(x, y, I, xi, yi)
[x, y, J, BW, xi, yi] = roifill(...)
```


## Description

Use roifill to fill in a specified region of interest (ROI) polygon in a
grayscale image. roifill smoothly interpolates inward from the pixel values on the boundary of the polygon by solving Laplace's equation. The boundary pixels are not modified. roifill can be used, for example, to erase objects in an image.
$J=$ roifill creates an interactive polygon tool, associated with the image displayed in the current figure, called the target image. You use the mouse to define the ROI - see "Interactive Behavior" on page $3-777$. When you are finished defining the ROI, fill in the area specified by the ROI by double-clicking inside the region or by right-clicking anywhere inside the region and selecting Fill Area from the context menu. roifill returns the image, $J$, which is the same size as I with the region filled in (see "Examples" on page 3-780).

Note If you do not specify an output argument, roifill displays the filled image in a new figure.
$J=$ roifill(I) displays the image I and creates an interactive polygon tool associated with the image.
$J=$ roifill(I, $c, r$ ) fills in the polygon specified by $c$ and $r$, which are equal-length vectors containing the row-column coordinates of the pixels on vertices of the polygon. The kth vertex is the pixel ( $\mathrm{r}(\mathrm{k}), \mathrm{c}(\mathrm{k})$ ).
$J=$ roifill(I, BW) uses BW (a binary image the same size as I) as a mask. roifill fills in the regions in I corresponding to the nonzero pixels in BW. If there are multiple regions, roifill performs the interpolation on each region independently.
$[J, B W]=$ roifill (...) returns the binary mask used to determine which pixels in I get filled. BW is a binary image the same size as I with 1's for pixels corresponding to the interpolated region of I and 0's elsewhere.
$J=$ roifill(x, $y, ~ I, ~ x i, ~ y i) ~ u s e s ~ t h e ~ v e c t o r s ~ x ~ a n d ~ y ~ t o ~ e s t a b l i s h ~$ a nondefault spatial coordinate system. xi and yi are equal-length vectors that specify polygon vertices as locations in this coordinate system.
[x, y, J, BW, xi, yi] = roifill(...) returns the XData and YData in $x$ and $y$, the output image in $J$, the mask image in $B W$, and the polygon coordinates in xi and yi. xi and yi are empty if the roifill(I, $B W$ ) form is used.

## Interactive Behavior

When you call roifill with an interactive syntax, the pointer changes to a cross hairs shape $\Psi_{\text {when you move it over the target image. }}$ Using the mouse, you specify a region-of-interest by selecting vertices of a polygon. You can change the size or shape of the polygon using the mouse. The following figure illustrates a polygon defined by multiple vertices. For more information about all the interactive capabilities of roifill, see the table that follows.


| Interactive <br> Behavior | Description |
| :--- | :--- |
| Closing the polygon. <br> (Completing the <br> region-of-interest.) | Use any of the following mechanisms: <br> - Move the pointer over the initial vertex of <br> the polygon that you selected. The shape <br> changes to a circle $\bigcirc$. Click either mouse <br> button. |

- Double-click the left mouse button. This action creates a vertex at the point under the mouse and draws a straight line connecting this vertex with the initial vertex.
- Click the right mouse button. This action draws a line connecting the last vertex

| Interactive Behavior | Description |
| :---: | :---: |
|  | selected with the initial vertex; it does not create a new vertex. |
| Deleting the polygon | Press Backspace, Escape or Delete, or right-click inside the region and select Cancel from the context menu. <br> Note: If you delete the ROI, the function returns empty values. |
| Moving the polygon | Move the pointer inside the region. The pointer changes to a fleur Click and drag the mouse to move the polygon. |
| Changing the color of the polygon | Move the pointer inside the region. Right-click and select Set color from the context menu. |
| Adding a new vertex. | Move the pointer over an edge of the polygon and press the $\mathbf{A}$ key. The shape of the pointer changes $\uparrow$. Click the left mouse button to create a new vertex at that position on the line. |
| Moving a vertex. (Reshaping the region-of-interest.) | Move the pointer over a vertex. The pointer changes to a circle $\bigcirc$. Click and drag the vertex to its new position. |


| Interactive <br> Behavior | Description |
| :--- | :--- |
| Deleting a vertex. | Move the pointer over a vertex. The pointer <br> changes to a circle $\bigcirc$. Right-click and select <br> Delete Vertex from the context menu. This <br> action deletes the vertex and adjusts the shape <br> of the polygon, drawing a new straight line <br> between the two vertices that were neighbors <br> of the deleted vertex. |
| Retrieving the <br> coordinates of the <br> vertices | Move the pointer inside the region. Right-click <br> and select Copy position from the context <br> menu to copy the current position to the <br> Clipboard. Position is an $n$-by-2 array <br> containing the $x$ - and $y$-coordinates of each <br> vertex, where $n$ is the number of vertices you <br> selected. |

## Class Support

## Examples

The input image I can of class uint8, uint16, int16, single, or double. The input binary mask BW can be any numeric class or logical. The output binary mask BW is always logical. The output image $J$ is of the same class as I. All other inputs and outputs are of class double.

This example uses roifill to fill a region in the input image, I. For more examples, especially of the interactive syntaxes, see "Filling an ROI".

```
I = imread('eight.tif');
c = [222 272 300 270 221 194];
r = [21 21 75 121 121 75];
J = roifill(I,c,r);
imshow(I)
figure, imshow(J)
```



See Also
impoly | roifilt2 | roipoly
Purpose Filter region of interest (ROI) in image
Syntax

J = roifilt2(h, I, BW)

J = roifilt2(I, BW, fun)

Class

## Examples

$J=$ roifilt2(h, I, BW) filters the data in I with the two-dimensional linear filter $h$. BW is a binary image the same size as I that defines an ROI used as a mask for filtering. roifilt2 returns an image that consists of filtered values for pixels in locations where BW contains 1's, and unfiltered values for pixels in locations where BW contains 0's. For this syntax, roifilt2 calls filter2 to implement the filter.
$J=$ roifilt2(I, BW, fun) processes the data in I using the function fun. The result $J$ contains computed values for pixels in locations where BW contains 1's, and the actual values in I for pixels in locations where BW contains 0's. fun must be a function handle. Parameterizing Functions, in the MATLAB Mathematics documentation, explains how to provide additional parameters to the function fun.

For the syntax that includes a filter h , the input image can be logical or numeric, and the output array $J$ has the same class as the input image. For the syntax that includes a function, I can be of any class supported by fun, and the class of $J$ depends on the class of the output from fun.

This example continues the roipoly example, filtering the region of the image I specified by the mask BW. The roifilt2 function returns the filtered image $J$, shown in the following figure.

I = imread('eight.tif');
c = [222 272300270221 194];
$r=\left[\begin{array}{lllll}21 & 21 & 75 & 121 & 121 \\ 75\end{array}\right] ;$
BW = roipoly(I, c,r);
H = fspecial('unsharp');
J = roifilt2(H,I,BW);
figure, imshow(I), figure, imshow(J)


See Also filter2 | function_handle | imfilter | roipoly
How To . "Anonymous Functions"

- "Parameterizing Functions"


## roipoly

Purpose Specify polygonal region of interest (ROI)

```
Syntax \(\quad B W=\) roipoly
BW = roipoly(I)
BW = roipoly(I, c, r)
BW = roipoly(x, y, I, xi, yi)
[BW, xi, yi] = roipoly(...)
[x, y, BW, xi, yi] = roipoly(...)
```


## Description

Use roipoly to specify a polygonal region of interest (ROI) within an image. roipoly returns a binary image that you can use as a mask for masked filtering.

BW = roipoly creates an interactive polygon tool, associated with the image displayed in the current figure, called the target image. With the polygon tool active, the pointer changes to cross hairs $\mathcal{T}_{\text {when you }}$ move the pointer over the image in the figure. Using the mouse, you specify the region by selecting vertices of the polygon. You can move or resize the polygon using the mouse. The following figure illustrates a polygon defined by multiple vertices. The following table describes all the interactive behavior of the polygon tool.


When you are finished positioning and sizing the polygon, create the mask by double-clicking, or by right-clicking inside the region and selecting Create mask from the context menu. roipoly returns the mask as a binary image, BW, the same size as I. In the mask image, roipoly sets pixels inside the region to 1 and pixels outside the region to 0 .
$\left.\begin{array}{l|l}\hline \begin{array}{l}\text { Interactive } \\ \text { Behavior }\end{array} & \text { Description } \\ \hline \begin{array}{l}\text { Closing the polygon. } \\ \text { (Completing the } \\ \text { region-of-interest.) }\end{array} & \begin{array}{l}\text { Use any of the following mechanisms: } \\ \text { - Move the pointer over the initial vertex of } \\ \text { the polygon that you selected. The pointer } \\ \text { changes to a circle } \bigcirc \text {. Click either mouse } \\ \text { button. } \\ \text { - Double-click the left mouse button. This } \\ \text { action creates a vertex at the point under } \\ \text { the mouse pointer and draws a straight } \\ \text { line connecting this vertex with the initial } \\ \text { vertex. }\end{array} \\ \text { - Right-click the mouse. This draws a line } \\ \text { connecting the last vertex selected with } \\ \text { the initial vertex; it does not create a new } \\ \text { vertex at the point under the mouse. }\end{array}\right]$

## roipoly

| Interactive <br> Behavior | Description |
| :--- | :--- |
| Moving a vertex. <br> (Reshaping the <br> region-of-interest.) | Move the pointer over a vertex. The pointer <br> changes to a circle $\bigcirc$. Click and drag the <br> vertex to its new position. |
| Adding a new vertex. | Move the pointer over an edge of the polygon <br> and press the A key. The pointer changes <br> shape to \&. Click the left mouse button to <br> create a new vertex at that point on the edge. |
| Deleting a vertex. <br> Reshaping the <br> region-of-interest.) | Move the pointer over the vertex. The pointer <br> changes to a circle $\bigcirc$. Right-click and <br> select Delete vertex from the context menu. <br> roipoly draws a new straight line between <br> the two vertices that were neighbors of the <br> deleted vertex. |
| Changing the color of <br> the polygon | Move the pointer anywhere inside the <br> boundary of the region and click the right <br> mouse button. Select Set color from the <br> context menu. |
| Retrieving the <br> coordinates of the <br> vertices | Move the pointer inside the region. Right-click <br> and select Copy position from the context <br> menu to copy the current position to the <br> Clipboard. The position is an $n$-by-2 array <br> containing the $x$ - and $y$-coordinates of each <br> vertex, where $n$ is the number of vertices. |

Note If you call roipoly without specifying any output arguments, roipoly displays the resulting mask image in a new figure window.

BW = roipoly(I) displays the image I and creates an interactive polygon tool associated with that image.

BW = roipoly(I, c, r) returns the ROI specified by the polygon described by vectors $c$ and $r$, which specify the column and row indices of each vertex, respectively. $c$ and $r$ must be the same size.
$B W=$ roipoly (x, y, I, xi, yi) uses the vectors $x$ and $y$ to establish a nondefault spatial coordinate system. xi and yi are equal-length vectors that specify polygon vertices as locations in this coordinate system.
[BW, xi, yi] = roipoly(...) returns the $x$ - and $y$-coordinates of the polygon vertices in $x i$ and $y i$.

Note roipoly always produces a closed polygon. If the points specified describe a closed polygon (i.e., if the last pair of coordinates is identical to the first pair), the length of xi and yi is equal to the number of points specified. If the points specified do not describe a closed polygon, roipoly adds a final point having the same coordinates as the first point. (In this case the length of xi and yi is one greater than the number of points specified.)
[x, y, BW, xi, yi] = roipoly(...) returns the XData and YData in $x$ and $y$, the mask image in $B W$, and the polygon coordinates in $x i$ and $y i$.

## Class <br> Support

Tips

The input image I can be of class uint8, uint16, int16, single, or double. The output image BW is of class logical. All other inputs and outputs are of class double.

For any of the roipoly syntaxes, you can replace the input image I with two arguments, $m$ and $n$, that specify the row and column dimensions of an arbitrary image. For example, these commands create a 100-by-200 binary mask.

```
c = [112 112 79 79];
r = [37 66 66 37];
BW = roipoly(100,200, c,r);
```


## roipoly

If you specify $m$ and $n$ with an interactive form of roipoly, an $m$-by- $n$ black image is displayed, and you use the mouse to specify a polygon within this image.

## Examples

See Also

Use roipoly to create a mask image, BW, the same size as the input image, I. The example in roifilt2 continues this example, filtering the specified region in the image. For more examples, especially of the interactive syntaxes, see "Specifying a Region of Interest (ROI)".

```
I = imread('eight.tif');
c = [222 272 300 270 221 194];
r = [21 21 75 121 121 75];
BW = roipoly(I,c,r);
figure, imshow(I)
figure, imshow(BW)
```



```
impoly | poly2mask| roifilt2 | roicolor | roifill
```


## Purpose <br> Syntax <br> Description

Create reduced resolution data set from image file

Tips

```
rsetfile = rsetwrite(File_Name)
rsetfile = rsetwrite(File_Name, output_filename)
rsetfile = rsetwrite(adapter, output_filename)
```

rsetfile = rsetwrite(File_Name), where File_Name is a TIFF or NITF image file, creates a reduced resolution data set (R-Set) from the specified file. The R-Set file is written to the current working directory with a name based on the input file name. For example, if File_Name is 'VeryLargeImage.tiff', rsetfile will be 'VeryLargeImage.rset'. If an image file contains multiple images, only the first one is used.
rsetfile = rsetwrite(File_Name, output_filename) creates an R -Set from the specified image file, using output filename as the name of the new file. In this case, rsetfile and output_filename contain the same string.
rsetfile = rsetwrite(adapter, output_filename) creates an R -Set from the specified Image Adapter object, adapter. Image Adapters are user-defined classes that provide rsetwrite a common API for reading a particular image file format. See the documentation for ImageAdapter for more details.
rsetwrite creates an R-Set file by dividing an image into spatial tiles and resampling the image at different resolution levels. When you open the R-Set file in the Image Tool and zoom in, you view tiles at a higher resolution. When you zoom out, you view tiles at a lower resolution. In this way, clarity of the image and memory usage are balanced for optimal performance. The R-Set file contains a compressed copy of the full-resolution data.

Because R-Set creation can be time consuming, a progress bar shows the status of the operation. If you cancel the operation, processing stops, no file is written, and the rsetfile variable will be empty.
rsetwrite supports NITF image files that are uncompressed and Version 2.0 or higher. It does not support NITF files with more than

## rsetwrite

three bands or with floating point data. Images with more than one data band are OK if they contain unsigned integer data.

While it is possible to create an R-Set from an image where the dimensions are smaller than the size of a single $R$-Set tile, the resulting R -set file will likely be larger and take longer to load than the original file. The current size of an R-Set tile is $512 \times 512$ pixels.

## Examples Example 1: Create an R-Set File

Visualize a very large image by using an R-Set. Replace 'MyReallyBigImage.tif' in the example below with the name of your file:

```
big_file = 'MyReallyBigImage.tif';
rset_file = rsetwrite(big_file);
imtool(rset_file)
```


## Example 2: Convert TIFF Files to R-Set Files

Create R-Set files for every TIFF in a directory containing very large images. Put the R-Set files into a temporary directory:

```
d = dir('*.tif*');
image_dir = pwd;
cd(tempdir)
for p = 1:numel(d)
    big_file = fullfile(image_dir, d(p).name);
    rsetwrite(big_file);
end
```

See Also imread | imtool
Purpose Standard deviation of matrix elements
Syntax

b = std2(A)
Description $b=s t d 2(A)$ computes the standard deviation of the values in $A$.
Class A can be numeric or logical. $B$ is a scalar of class double. SupportAlgorithms std2 computes the standard deviation of the array $A$ using $s t d(A(:))$.See Also corr2 | mean2 | std | mean

| Purpose | Local standard deviation of image |
| :--- | :--- |
| Syntax | $J=$ stdfilt(I) <br> $J=$ stdfilt (I, NHOOD) |
| Description | $J=$ stdfilt(I) returns the array $J$, where each output pixel |
| contains the standard deviation of the 3-by-3 neighborhood around the |  |
| corresponding pixel in the input image I. I can have any dimension. |  |
| The output image $J$ is the same size as the input image I. |  |
| For pixels on the borders of I, stdfilt uses symmetric padding. In |  |
| symmetric padding, the values of padding pixels are a mirror reflection |  |
| of the border pixels in I. |  |

Purpose
Syntax

Description

Create morphological structuring element (STREL)

```
SE = strel(shape, parameters)
SE = strel('arbitrary', NHOOD)
SE = strel('arbitrary', NHOOD, HEIGHT)
SE = strel('ball', R, H, N)
SE = strel('diamond', R)
SE = strel('disk', R, N)
SE = strel('line', LEN, DEG)
SE = strel('octagon', R)
SE = strel('pair', OFFSET)
SE = strel('periodicline', P, V)
SE = strel('rectangle', MN)
SE = strel('square', W)
```

SE = strel(shape, parameters) creates a structuring element, SE, of the type specified by shape. This table lists all the supported shapes. Depending on shape, strel can take additional parameters. See the syntax descriptions that follow for details about creating each type of structuring element.

Flat Structuring Elements

| 'arbitrary' | 'pair' |
| :--- | :--- |
| 'diamond' | 'periodicline' |
| 'disk' | 'rectangle' |
| 'line' | 'square' |
| 'octagon' |  |

## Nonflat Structuring Elements

| 'arbitrary ' | 'ball' |
| :--- | :--- |

SE = strel('arbitrary', NHOOD) creates a flat structuring element where NHOOD specifies the neighborhood. NHOOD is a matrix containing 1 's and 0's; the location of the 1's defines the neighborhood for the
morphological operation. The center (or origin) of NHOOD is its center element, given by floor ((size (NHOOD)+1)/2). You can omit the 'arbitrary' string and just use strel(NHOOD).


SE = strel('arbitrary', NHOOD, HEIGHT) creates a nonflat structuring element, where NHOOD specifies the neighborhood. HEIGHT is a matrix the same size as NHOOD containing the height values associated with each nonzero element of NHOOD. The HEIGHT matrix must be real and finite valued. You can omit the 'arbitrary' string and just use strel(NHOOD, HEIGHT).

SE = strel('ball', R, H, N) creates a nonflat, ball-shaped structuring element (actually an ellipsoid) whose radius in the $\mathrm{X}-\mathrm{Y}$ plane is R and whose height is H . Note that R must be a nonnegative integer, H must be a real scalar, and N must be an even nonnegative integer. When $N$ is greater than 0 , the ball-shaped structuring element is approximated by a sequence of $N$ nonflat, line-shaped structuring elements. When $N$ equals 0 , no approximation is used, and the structuring element members consist of all pixels whose centers are no greater than $R$ away from the origin. The corresponding height values are determined from the formula of the ellipsoid specified by R and H. If $N$ is not specified, the default value is 8 .

Note Morphological operations run much faster when the structuring element uses approximations ( $\mathrm{N}>0$ ) than when it does not ( $\mathrm{N}=0$ ).

SE = strel('diamond', R) creates a flat, diamond-shaped structuring element, where R specifies the distance from the structuring element origin to the points of the diamond. R must be a nonnegative integer scalar.


SE = strel('disk', R, N) creates a flat, disk-shaped structuring element, where R specifies the radius. R must be a nonnegative integer. $N$ must be $0,4,6$, or 8 . When $N$ is greater than 0 , the disk-shaped structuring element is approximated by a sequence of $N$ periodic-line structuring elements. When $N$ equals 0 , no approximation is used, and the structuring element members consist of all pixels whose centers are no greater than $R$ away from the origin. If $N$ is not specified, the default value is 4 .

Note Morphological operations run much faster when the structuring element uses approximations ( $\mathrm{N}>0$ ) than when it does not ( $\mathrm{N}=0$ ). However, structuring elements that do not use approximations ( $\mathrm{N}=$ 0 ) are not suitable for computing granulometries. Sometimes it is necessary for strel to use two extra line structuring elements in the approximation, in which case the number of decomposed structuring elements used is $\mathrm{N}+2$.
SE $=$

| 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| 0 | 1 | 1 | 1 | 1 | 1 | 0 |
| 0 | 1 | $R=31$ | 1 | 1 | 1 | 0 |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 0 | 1 | 1 | 1 | 1 | 1 | 0 |
| 0 | 1 | 1 | 1 | 1 | 1 | 0 |
| 0 | 0 | 0 | 1 | 0 | 0 | 0 |

SE = strel('line', LEN, DEG) creates a flat linear structuring element that is symmetric with respect to the neighborhood center. DEG specifies the angle (in degrees) of the line as measured in a counterclockwise direction from the horizontal axis. LEN is approximately the distance between the centers of the structuring element members at opposite ends of the line.


SE = strel('octagon', R) creates a flat, octagonal structuring element, where R specifies the distance from the structuring element origin to the sides of the octagon, as measured along the horizontal and vertical axes. R must be a nonnegative multiple of 3 .


SE = strel('pair', OFFSET) creates a flat structuring element containing two members. One member is located at the origin. The second member's location is specified by the vector OFFSET. OFFSET must be a two-element vector of integers.


SE = strel('periodicline', P, V) creates a flat structuring element containing $2 * \mathrm{P}+1$ members. V is a two-element vector containing integer-valued row and column offsets. One structuring element member is located at the origin. The other members are located at $1 * \mathrm{~V},-1 * \mathrm{~V}, 2 * \mathrm{~V},-2 * \mathrm{~V}, \ldots, \mathrm{P} * \mathrm{~V},-\mathrm{P} * \mathrm{~V}$.


SE = strel('rectangle', MN) creates a flat, rectangle-shaped structuring element, where MN specifies the size. MN must be a two-element vector of nonnegative integers. The first element of MN is the number of rows in the structuring element neighborhood; the second element is the number of columns.


HIII $=\left[\begin{array}{ll}3 & 5\end{array}\right]$

SE = strel('square', W) creates a square structuring element whose width is $W$ pixels. $W$ must be a nonnegative integer scalar.


Notes

Methods

For all shapes except 'arbitrary', structuring elements are constructed using a family of techniques known collectively as structuring element decomposition. The principle is that dilation by some large structuring elements can be computed faster by dilation with a sequence of smaller structuring elements. For example, dilation by an 11-by-11 square structuring element can be accomplished by dilating first with a 1-by-11 structuring element and then with an 11-by- 1 structuring element. This results in a theoretical performance improvement of a factor of 5.5 , although in practice the actual performance improvement is somewhat less. Structuring element decompositions used for the 'disk' and 'ball' shapes are approximations; all other decompositions are exact.

This table lists the methods supported by the STREL object.

| Method | Description |
| :--- | :--- |
| getheight | Get height of structuring element |
| getneighbors | Get structuring element neighbor locations and <br> heights |
| getnhood | Get structuring element neighborhood |
| getsequence | Extract sequence of decomposed structuring <br> elements |
| isflat | Return true for flat structuring element |
| reflect | Reflect structuring element |
| translate | Translate structuring element |

Examples<br>\section*{Algorithms}

See Also imdilate | imerode

## References

 pp. 1057-1063, 1996.se1 $=$ strel('square',11) $\quad \% 11$-by-11 square
se2 $=$ strel('line',10,45) $\%$ length 10 , angle 45 degrees
se3 $=$ strel('disk',15) $\quad$ \% disk, radius 15
se4 $=$ strel('ball', 15,5$) \quad$ \% ball, radius 15 , height 5

The method used to decompose diamond-shaped structuring elements is known as "logarithmic decomposition" [1].

The method used to decompose disk structuring elements is based on the technique called "radial decomposition using periodic lines" [2], [3]. For details, see the MakeDiskStrel subfunction in toolbox/images/images/@strel/strel.m.

The method used to decompose ball structuring elements is the technique called "radial decomposition of spheres" [2].
[1] van den Boomgard, R, and R. van Balen, "Methods for Fast Morphological Image Transforms Using Bitmapped Images," Computer Vision, Graphics, and Image Processing: Graphical Models and Image Processing, Vol. 54, Number 3, pp. 252-254, May 1992.
[2] Adams, R., "Radial Decomposition of Discs and Spheres," Computer Vision, Graphics, and Image Processing: Graphical Models and Image Processing, Vol. 55, Number 5, pp. 325-332, September 1993.
[3] Jones, R., and P. Soille, "Periodic lines: Definition, cascades, and application to granulometrie," Pattern Recognition Letters, Vol. 17,

Purpose Find limits to contrast stretch image
Syntax $\quad \begin{aligned} \text { LOW_HIGH } & =\text { stretchlim(I) } \\ \text { LOW_HIGH } & =\operatorname{stretchlim(I,~TOL)~} \\ \text { LOW_HIGH } & =\text { stretchlim(RGB, TOL) }\end{aligned}$
Description
LOW_HIGH = stretchlim(I) returns LOW_HIGH, a two-element vector of pixel values that specify lower and upper limits that can be used for contrast stretching image I. By default, values in LOW_HIGH specify the bottom $1 \%$ and the top $1 \%$ of all pixel values. The gray values returned can be used by the imadjust function to increase the contrast of an image.

LOW_HIGH = stretchlim(I, TOL) where TOL is a two-element vector [LOW_FRACT HIGH_FRACT] that specifies the fraction of the image to saturate at low and high pixel values.

If TOL is a scalar, LOW_FRACT = TOL, and HIGH_FRACT = 1 -
LOW_FRACT, which saturates equal fractions at low and high pixel values.
If you omit the argument, TOL defaults to [0.01 0.99], saturating $2 \%$.
If TOL = 0, LOW_HIGH = [min(I(:)); max(I(:))].
LOW_HIGH = stretchlim(RGB, TOL) returns a 2 -by-3 matrix of intensity pairs to saturate each plane of the RGB image. TOL specifies the same fractions of saturation for each plane.

Note If TOL is too big, such that no pixels would be left after saturating low and high pixel values, stretchlim returns [ $\left.\begin{array}{ll}0 & 1\end{array}\right]$.

## Class <br> Support

Examples
The input image can be of class uint8, uint16, int16, double, or single. The output limits returned, LOW_HIGH, are of class double and have values between 0 and 1 .

```
I = imread('pout.tif');
J = imadjust(I,stretchlim(I),[]);
```

imshow(I), figure, imshow(J)


See Also
brighten | histeq | imadjust

## subimage

Purpose Display multiple images in single figure

Syntax |  | subimage $(X$, map $)$ |
| :--- | :--- |
|  | subimage $(I)$ |
|  | subimage $(B W)$ |
|  | subimage $(R G B)$ |
|  | subimage $(x, y . .)$. |
|  | $h=\operatorname{subimage}(\ldots)$ |

## Description

## Class

Support

## Examples

See Also

You can use subimage in conjunction with subplot to create figures with multiple images, even if the images have different colormaps. subimage works by converting images to truecolor for display purposes, thus avoiding colormap conflicts.
subimage ( $X$, map) displays the indexed image $X$ with colormap map in the current axes.
subimage (I) displays the intensity image $I$ in the current axes.
subimage ( $B W$ ) displays the binary image $B W$ in the current axes.
subimage (RGB) displays the truecolor image RGB in the current axes.
subimage (x, y...) displays an image using a nondefault spatial coordinate system.
$\mathrm{h}=$ subimage (...) returns a handle to an image object.
The input image can be of class logical, uint8, uint16, or double.

```
load trees
[X2,map2] = imread('forest.tif');
subplot(1,2,1), subimage(X,map)
subplot(1,2,2), subimage(X2,map2)
```

imshow | subplot

## Purpose

Apply spatial transformation to N-D array

## Syntax

Description
$B=$ tformarray (A, T, R, TDIMS_A, TDIMS_B, TSIZE_B, TMAP_B, F)
$B=$ tformarray (A, T, R, TDIMS_A, TDIMS_B, TSIZE_B, TMAP_B, F) applies a spatial transformation to array A to produce array B. The tformarray function is like imtransform, but is intended for problems involving higher-dimensioned arrays or mixed input/output dimensionality, or requiring greater user control or customization. (Anything that can be accomplished with imtransform can be accomplished with a combination of maketform, makeresampler, findbounds, and tformarray; but for many tasks involving 2-D images, imtransform is simpler.)

This table provides a brief description of all the input arguments. See the following section for more detail about each argument. (Click an argument in the table to move to the appropriate section.)

| Argument | Description |
| :--- | :--- |
| A | Input array or image |
| T | Spatial transformation structure, called a TFORM, <br> typically created with maketform |
| R | Resampler structure, typically created with <br> makeresampler |
| TDIMS_A | Row vector listing the input transform dimensions |
| TDIMS_B | Row vector listing the output transform dimensions |
| TSIZE_B | Output array size in the transform dimensions |
| TMAP_B | Array of point locations in output space; can be used as <br> an alternative way to specify a spatial transformation |
| F | Array of fill values |

A can be any nonsparse numeric array, and can be real or complex.

T is a TFORM structure that defines a particular spatial transformation. For each location in the output transform subscript space (as defined by TDIMS_B and TSIZE_B), tformarray uses T and the function tforminv to compute the corresponding location in the input transform subscript space (as defined by TDIMS_A and size(A)).
If $T$ is empty, tformarray operates as a direct resampling function, applying the resampler defined in $R$ to compute values at each transform space location defined in TMAP_B (if TMAP_B is nonempty), or at each location in the output transform subscript grid.
$R$ is a structure that defines how to interpolate values of the input array at specified locations. $R$ is usually created with makeresampler, which allows fine control over how to interpolate along each dimension, as well as what input array values to use when interpolating close to the edge of the array.

TDIMS_A and TDIMS_B indicate which dimensions of the input and output arrays are involved in the spatial transformation. Each element must be unique, and must be a positive integer. The entries need not be listed in increasing order, but the order matters. It specifies the precise correspondence between dimensions of arrays $A$ and $B$ and the input and output spaces of the transformer T. length (TDIMS_A) must equal T.ndims_in, and length(TDIMS_B) must equal T.ndims_out.

For example, if $T$ is a $2-\mathrm{D}$ transformation, TDIMS_A = [2 1], and TDIMS_B = [llll $\left.\begin{array}{ll}1 & 2\end{array}\right]$, then the column dimension and row dimension of A correspond to the first and second transformation input-space dimensions, respectively. The row and column dimensions of B correspond to the first and second output-space dimensions, respectively.

TSIZE_B specifies the size of the array $B$ along the output-space transform dimensions. Note that the size of B along nontransform dimensions is taken directly from the size of A along those dimensions. If, for example, $T$ is a 2-D transformation, size (A) = [480 6403 10], TDIMS_B is [2 1], and TSIZE_B is [300 200], then size(B) is [200 300 3].

TMAP_B is an optional array that provides an alternative way of specifying the correspondence between the position of elements of $B$ and the location in output transform space. TMAP_B can be used, for example, to compute the result of an image warp at a set of arbitrary locations in output space. If TMAP_B is not empty, then the size of TMAP_B takes the form

```
[D1 D2 D3 ... DN L]
```

where $N$ equals length (TDIMS_B). The vector [D1 D2 ... DN] is used in place of TSIZE_B. If TMAP_B is not empty, then TSIZE_B should be [ ].

The value of $L$ depends on whether or not $T$ is empty. If $T$ is not empty, then L is T.ndims_out, and each L-dimension point in TMAP_B is transformed to an input-space location using $T$. If $T$ is empty, then $L$ is length (TDIMS_A), and each L-dimensional point in TMAP_B is used directly as a location in input space.
$F$ is a double-precision array containing fill values. The fill values in $F$ can be used in three situations:

- When a separable resampler is created with makeresampler and its padmethod is set to either 'fill' or 'bound'.
- When a custom resampler is used that supports the 'fill' or 'bound' pad methods (with behavior that is specific to the customization).
- When the map from the transform dimensions of B to the transform dimensions of A is deliberately undefined for some points. Such points are encoded in the input transform space by NaNs in either TMAP_B or in the output of TFORMINV.

In the first two cases, fill values are used to compute values for output locations that map outside or near the edges of the input array. Fill values are copied into $B$ when output locations map well outside the input array. See makeresampler for more information about 'fill' and 'bound'.

F can be a scalar (including NaN ), in which case its value is replicated across all the nontransform dimensions. F can also be a nonscalar,

## Class Support

Examples Create a 2-by-2 checkerboard image where each square is 20 pixels wide, then transform it with a projective transformation. Use a pad method of 'circular' when creating a resampler, so that the output appears to be a perspective view of an infinite checkerboard. Swap the output dimensions. Specify a 100-by-100 output image. Leave TMAP_B empty, since TSIZE_B is specified. Leave the fill value empty, since it won't be needed.

```
I = checkerboard(20,1,1);
```

```
figure; imshow(I)
T = maketform('projective',[1 1; 41 1; 41 41; 1 41],...
    [5 5; 40 5; 35 30; -10 30]);
R = makeresampler('cubic','circular');
J = tformarray(I,T,R,[1 2],[2 1],[100 100],[],[]);
figure; imshow(J)
```


## See Also

findbounds | imtransform | makeresampler | maketform

## Purpose Apply forward spatial transformation

```
Syntax
[X, Y] = tformfwd(T, U, V)
[X1, X2, X3,...] = tformfwd(T, U1, U2, U3,...)
X = tformfwd(T, U)
X = tformfwd( \(\mathrm{T}, \mathrm{U}\) )
[X1, X2, X3,...] = tformfwd(T, U)
X = tformfwd(T, U1, U2, U3,...)
\(X=\) tformfwd \((U, T)\)
```


## Description

[X, Y] = tformfwd(T, U, V) applies the 2D-to-2D spatial transformation defined in $T$ to coordinate arrays U and V , mapping the point $[U(k) V(k)]$ to the point $[X(k) Y(k)]$.

T is a TFORM struct created with maketform, fliptform, or cp2tform. Both T.ndims_in and T.ndims_out must equal $2 . U$ and $V$ are typically column vectors matching in length. In general, $U$ and $V$ can have any dimensionality, but must have the same size. In any case, $X$ and $Y$ will have the same size as $U$ and $V$.
[X1, X2, X3,...] = tformfwd(T, U1, U2, U3,...) applies the ndims_in-to-ndims_out spatial transformation defined in TFORM structure $T$ to the coordinate arrays U1, U2, . . , UNDIMS_IN (where NDIMS_IN = T.ndims_in and NDIMS_OUT = T.ndims_out). The number of output arguments must equal NDIMS_OUT. The transformation maps the point
[U1(k) U2(k) ... UNDIMS_IN(k)]
to the point
[X1(k) X2(k) ... XNDIMS_OUT(k)].
$\mathrm{U} 1, \mathrm{U} 2, \mathrm{U} 3, \ldots$ can have any dimensionality, but must be the same size.
$\mathrm{X} 1, \mathrm{X} 2, \mathrm{X} 3, \ldots$ must have this size also.
X = tformfwd(T, U) applies the ndims_in-to-ndims_out spatial transformation defined in TFORM structure $T$ to each row of $U$, where
$U$ is an M-by-NDIMS_IN matrix. It maps the point $U(k,:)$ to the point $X(k,:) . X$ is an M-by-NDIMS_OUT matrix.
$X=$ tformfwd $(T, U)$, where $U$ is an $(N+1)$-dimensional array, maps the point $U(k 1, k 2, \ldots, k N,:)$ to the point $X(k 1, k 2, \ldots, k N,:)$. size ( $\mathrm{U}, \mathrm{N}+1$ ) must equal NDIMS_IN. X is an ( $\mathrm{N}+1$ )-dimensional array, with size( $\mathrm{X}, \mathrm{I}$ ) equal to size( $\mathrm{U}, \mathrm{I}$ ) for $\mathrm{I}=1, \ldots, \mathrm{~N}$ and $\operatorname{size(X,N+1)~}$ equal to NDIMS_OUT.
[X1, X2, X3,...] = tformfwd(T, U) maps an ( $\mathrm{N}+1$ )-dimensional array to NDIMS_OUT equally sized N -dimensional arrays.

X = tformfwd(T, U1, U2, U3,...) maps NDIMS_IN N-dimensional arrays to one ( $\mathrm{N}+1$ )-dimensional array.

## Note

Examples

## See Also

$X=$ tformfwd $(U, T)$ is an older form of the two-argument syntax that remains supported for backward compatibility.

Create an affine transformation that maps the triangle with vertices $(0,0),(6,3),(-2,5)$ to the triangle with vertices $(-1,-1),(0,-10),(4,4)$.

```
u = [ 0 6 - -2]';
v = [ 0 3 5]';
x = [-1 0 4]';
y = [-1 -10 4]';
tform = maketform('affine',[u v],[x y]);
```

Validate the mapping by applying tformfwd. Results should equal [ $\mathrm{x}, \mathrm{y}$ ]
[xm, ym] = tformfwd(tform, u, v)

```
cp2tform | fliptform | maketform | tforminv
```

Purpose Apply inverse spatial transformation

```
Syntax
[U,V] = tforminv(T, X, Y) [U1, U2, U3, ...] = tforminv(T, X1, X2, X3, ...) U = tforminv(T, X)
[U1, U2, U3, ...] = tforminv(T,X)
\(U=\operatorname{tforminv}(T, X 1, X 2, X 3, \ldots)\)
```


## Description

$[\mathrm{U}, \mathrm{V}]=\operatorname{tforminv}(\mathrm{T}, \mathrm{X}, \mathrm{Y})$ applies the 2D-to-2D inverse transformation defined in TFORM structure $T$ to coordinate arrays $X$ and $Y$, mapping the point $[X(k) Y(k)]$ to the point $[U(k) V(k)]$. Both T.ndims_in and T.ndims_out must equal 2. X and Y are typically column vectors matching in length. In general, $X$ and $Y$ can have any dimensionality, but must have the same size. In any case, $U$ and $V$ will have the same size as $X$ and $Y$.
[U1, U2, U3, ...] = tforminv( $\mathrm{T}, \mathrm{X} 1, \mathrm{X} 2, \mathrm{X} 3, \ldots$ ) applies the NDIMS_OUT-to-NDIMS_IN inverse transformation defined in TFORM structure T to the coordinate arrays $\mathrm{X} 1, \mathrm{X} 2, \ldots, \mathrm{XNDIMS}$ _OUT (where NDIMS_IN = T.ndims_in and NDIMS_OUT = T.ndims_out). The number of output arguments must equal NDIMS_IN. The transformation maps the point
[X1(k) X2(k) ... XNDIMS_OUT(k)]
to the point
[U1 (k) U2 (k) ... UNDIMS_IN(k)].
$\mathrm{X} 1, \mathrm{X} 2, \mathrm{X} 3, \ldots$ can have any dimensionality, but must be the same size.
$\mathrm{U} 1, \mathrm{U} 2, \mathrm{U} 3, \ldots$ have this size also.
U = tforminv ( $T, X$ ) applies the NDIMS_OUT-to-NDIMS_IN inverse transformation defined in TFORM structure $T$ to each row of $X$, where $X$ is an M-by-NDIMS_OUT matrix. It maps the point $X(k,:)$ to the point $\mathrm{U}(\mathrm{k},: \mathrm{s})$. U is an M-by-NDIMS_IN matrix.
$U=$ tforminv $(T, X)$, where $X$ is an ( $\mathrm{N}+1$ )-dimensional array, maps the point $X(k 1, k 2, \ldots, k N,:)$ to the point $U(k 1, k 2, \ldots, k N,:)$. size ( $\mathrm{X}, \mathrm{N}+1$ ) must equal NDIMS_OUT. U is an ( $\mathrm{N}+1$ )-dimensional array, with size ( $\mathrm{U}, \mathrm{I}$ ) equal to $\operatorname{size}(\mathrm{X}, \mathrm{I})$ for $\mathrm{I}=1, \ldots, \mathrm{~N}$ and $\operatorname{size}(\mathrm{U}, \mathrm{N}+1)$ equal to NDIMS_IN.
[U1, U2, U3, ...] = tforminv(T,X) maps an (N+1)-dimensional array to NDIMS_IN equally-sized N-dimensional arrays.

U = tforminv(T,X1,X2,X3,...) maps NDIMS_OUT N-dimensional arrays to one ( $\mathrm{N}+1$ )-dimensional array.

## Note

Examples
$U=\operatorname{tforminv}(X, T)$ is an older form of the two-argument syntax that remains supported for backward compatibility.

Create an affine transformation that maps the triangle with vertices $(0,0),(6,3),(-2,5)$ to the triangle with vertices $(-1,-1),(0,-10),(4,4)$.

```
u = [ 0 6 - -2]';
v = [ 0 3 5]';
x = [-1 0 4]';
y = [-1 -10 4]';
tform = maketform('affine',[u v],[x y]);
```

Validate the mapping by applying tforminv. Results should equal [u, v].
[um, vm] = tforminv(tform, $x, y)$
See Also
cp2tform | tformfwd | maketform | fliptform

## tonemap

Purpose
Render high dynamic range image for viewing

## Syntax

Description
RGB = tonemap(HDR)
RGB = tonemap(HDR, param1, val1, ...)
RGB = tonemap (HDR) converts the high dynamic range image HDR to a lower dynamic range image, RGB, suitable for display, using a process called tone mapping. Tone mapping is a technique used to approximate the appearance of high dynamic range images on a display with a more limited dynamic range.

RGB = tonemap(HDR, param1, val1, ...) performs tone mapping where parameters control various aspects of the operation. The following table lists these parameters.

| Parameter | Description |
| :--- | :--- |
| 'AdjustLightness' | A two-element vector in the form [ low high] <br> that specifies the overall lightness of the <br> rendered image. low and high are luminance <br> values of the low dynamic range image, in <br> the range [0, 1]. These values are passed <br> to imadjust. |
| 'AdjustSaturation' | A numeric value that specifies the saturation <br> of colors in the rendered image. When the <br> value is greater than 1, the colors are more <br> saturated. When the value is in the range [0, <br> 1) colors are less saturated. |
| 'NumberOfTiles' | A two-element vector of the form [rows cols] <br> that specifies the number of tiles used during <br> the adaptive histogram equalization part of <br> the tone mapping operation. rows and cols <br> specify the number of tile rows and columns. <br> Both rows and cols must be at least 2. The <br> total number of image tiles is equal to rows * <br> cols. A larger number of tiles results in an |


| Parameter | Description |
| :--- | :--- |
|  | image with greater local contrast. The default <br> for rows and cols is 4. |

## Class Support <br> Examples

The high dynamic range image HDR must be a m-by-n-by-3 single or double array. The output image RGB is an m-by-n-by- 3 uint8 image.

Load a high dynamic range image, convert it to a low dynamic range image while deepening shadows and increasing saturation, and display the results.

```
hdr = hdrread('office.hdr');
imshow(hdr)
rgb = tonemap(hdr, 'AdjustLightness', [0.1 1], ...
    'AdjustSaturation', 1.5);
figure;
imshow(rgb)
```

See Also
adapthisteq | hdrread | stretchlim

## translate

Purpose Translate structuring element (STREL)

## Syntax $\quad$ SE2 $=$ translate $(S E, V)$

Description SE2 = translate (SE, V) translates the structuring element SE in N-D space. SE is an array of structuring elements, created using the strel function.

V is an N -element vector that specifies the offsets of the desired translation in each dimension, relative to the structuring element's origin. If you specify an array, translate reshapes the array into a vector.

SE2 is an array of structuring elements the same size as SE. Each individual structuring element in SE2 is the translation of the corresponding structuring element in SE .

## Class <br> Support

SE and SE2 are STREL objects; V is a vector of doubles that must contain only integers.

Examples Translate a 3 -by- 3 structuring element.
se = strel(ones(3))
se2 $=$ translate(se,[-2 -2])
The following figure shows the original structuring element and the translated structuring element.


Dilating with a translated version of strel(1) is a way to translate an input image in space by an integer number of pixels. This example translates the cameraman. tif image down and to the right by 25 pixels.

```
I = imread('cameraman.tif');
se = translate(strel(1), [25 25]);
J = imdilate(I,se);
imshow(I), title('Original')
figure, imshow(J), title('Translated');
```



See Also strel | reflect

## truesize

## Purpose Adjust display size of image

## Syntax truesize(fig,[mrows ncols])

Description truesize(fig, [mrows ncols]) adjusts the display size of an image. fig is a figure containing a single image or a single image with a colorbar. [mrows ncols] is a 1 -by- 2 vector that specifies the requested screen area (in pixels) that the image should occupy.
truesize(fig) uses the image height and width for [mrows ncols]. This results in the display having one screen pixel for each image pixel.

If you do not specify a figure, truesize uses the current figure.

## Examples Fit image to figure window.

imshow(checkerboard,'InitialMagnification','fit')
Resize image and figure to show image at its 80 -by- 80 pixel size.
truesize
See Also imshow | iptsetpref | iptgetpref

# Purpose Compute new values of A based on lookup table (LUT) <br> <br> Syntax <br> <br> Syntax <br> <br> B = uintlut (A,LUT) 

 <br> <br> B = uintlut (A,LUT)}
uintlut has been removed. Use intlut instead.

Class
Support

Examples

See Also

A must be uint8 or uint16. If A is uint8, then LUT must be a uint8 vector with 256 elements. If $A$ is uint16, then LUT must be a uint16 vector with 65536 elements. B has the same size and class as A.

```
A = uint8([1 2 3 4; 5 6 7 8;9 10 11 12]);
LUT = repmat(uint8([0 150 200 255]),1,64);
B = uintlut(A,LUT);
imshow(A,[]), figure, imshow(B);
```

See AlsO impixel | improfile

## viscircles

Purpose Create circle

```
Syntax viscircles(centers,radii)
viscircles(ax,centers,radii)
h = viscircles(ax,centers,radii)
h = viscircles(__,Name,Value)
```


## Description

Input
Arguments
viscircles(centers, radii) draws circles with specified centers and radii onto the current axes.
viscircles(ax, centers, radii) draws circles onto the axes specified by ax.
$h=$ viscircles(ax,centers, radii) returns a vector of hggroup handles to each circle. These handles are children of the axes object, ax.
h = viscircles( __, Name, Value) specifies additional options with one or more Name, Value pair arguments, using any of the previous syntaxes.

## centers - Coordinates of circle centers

two-column matrix
Coordinates of circle centers, specified as a P-by-2 matrix, such as that obtained from imfindcircles. The $x$-coordinates of the circle centers are in the first column and the $y$-coordinates are in the second column. The coordinates can be integers (of any numeric type) or floating-point values (of type double or single).

## Data Types

single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32 | uint64

## radii - Circle radii

column vector

Circle radii, specified as a column vector such as that returned by imfindcircles. The radius value at radii(j) corresponds to the circle with center coordinates centers( $\mathrm{j},:$ ). The values of radii can be nonnegative integers (of any numeric type) or floating-point values (of type double or single).

## Data Types

single | double | int8 | int16 | int32 | int64 | uint8 | uint16 | uint32 | uint64

## ax - Axes in which to draw circles

handle
Axes in which to draw circles, specified as a handle object returned by gca or axes.

## Data Types

double

## Name-Value Pair Arguments

Specify 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 and value pair arguments in any order as Name1, Value1, . . . , NameN, ValueN.
Example: 'EdgeColor', 'b' specifies blue circle edges, using the short name for blue.

## EdgeColor - Color of circle edge

[R G B] | short name | long name | 'red' (default) | 'none'
Color of circle edges, specified as the comma-separated pair consisting of 'EdgeColor', followed by any ColorSpec value or 'none'.
Example: 'EdgeColor','b' specifies blue circle edges.

## LineStyle - Line style of circle edge

## ' - ' (default)

## viscircles

Line style of circle edge, specified as the comma-separated pair consisting of 'LineStyle' and any line specifier in the table below.

| Specifier | Line Style |
| :---: | :---: |
| , -' | Solid line (default) |
| ', -' | Dashed line |
| ':' | Dotted line |
| ', .' | Dash-dot line |
| 'none' | No line |

Example: 'LineStyle','--' specifies a dashed line at each circle edge.

## LineWidth - Width of circle edge

double | 2 (default)
Width of circle edge expressed in points, where each point equals $1 / 72$ of an inch, specified as the comma-separated pair consisting of 'LineWidth' followed by a positive floating-point double value.

Example: 'LineWidth', 4 specifies a 4 -point line width.

## Output Arguments

## Examples

## h - Handles of the circles

vector
Handles of the circles, returned as a vector of hggroup object handles. These handles are children of the axes object ax.

## Draw Edge Lines Around Both Bright and Dark Circles in an Image

Read the image into the workspace and display it.

```
A = imread('circlesBrightDark.png');
imshow(A)
```



Define the radius range.
Rmin = 30;
Rmax $=65$;
Find all the bright circles in the image within the radius range.
[centersBright, radiiBright] = imfindcircles(A,[Rmin Rmax],'ObjectPola
Find all the dark circles in the image within the radius range.
[centersDark, radiiDark] = imfindcircles(A,[Rmin Rmax],'ObjectPolarit
Draw blue lines at bright circle edges.

## viscircles

viscircles(centersBright, radiiBright,'EdgeColor','b');


Draw red dashed lines at dark circle edges.
viscircles(centersDark, radiiDark,'LineStyle','--');


See Also
imfindcircles | imdistline | imtool

## Purpose <br> Display image as texture-mapped surface

Syntax $\quad$| $\operatorname{warp}(X$, map $)$ |  |
| :--- | :--- |
|  | $\operatorname{warp}(I, n)$ |
|  | $\operatorname{warp}(B W)$ |
|  | $\operatorname{warp}(R G B)$ |
|  | $\operatorname{warp}(z, \ldots)$ |
|  | $\operatorname{warp}(x, y, z .)$. |
|  | $h=\operatorname{warp}(\ldots)$ |

Description

Class
Support
Tips Texture-mapped surfaces are generally rendered more slowly than images.

See Also imshow | image | imagesc | surf

## Purpose Watershed transform

Syntax

Description

L = watershed(A)
L = watershed(A, conn)
$L=$ watershed $(A)$ computes a label matrix identifying the watershed regions of the input matrix $A$, which can have any dimension. The elements of $L$ are integer values greater than or equal to 0 . The elements labeled 0 do not belong to a unique watershed region. These are called watershed pixels. The elements labeled 1 belong to the first watershed region, the elements labeled 2 belong to the second watershed region, and so on.

By default, watershed uses 8-connected neighborhoods for 2-D inputs and 26 -connected neighborhoods for 3 -D inputs. For higher dimensions, watershed uses the connectivity given by conndef(ndims(A),'maximal').

L = watershed (A, conn) specifies the connectivity to be used in the watershed computation. conn can have any of the following scalar values.

| Value | Meaning |
| :--- | :--- |
| Two-dimensional connectivities |  |
| 4 | 4-connected neighborhood |
| 8 | 8 -connected neighborhood |
| Three-dimensional connectivities |  |
| 6 | 6 -connected neighborhood |
| 18 | 18 -connected neighborhood |
| 26 | 26-connected neighborhood |

Connectivity can be defined in a more general way for any dimension by using for conn a 3-by-3-by- ...-by-3 matrix of 0's and 1's. The 1 -valued
elements define neighborhood locations relative to the center element of conn. Note that conn must be symmetric about its center element.

## Remarks

The watershed transform algorithm used by this function changed in version 5.4 (R2007a) of the Image Processing Toolbox software. The previous algorithm occasionally produced labeled watershed basins that were not contiguous. If you need to obtain the same results as the previous algorithm, use the function watershed_old.

## Class

A can be a numeric or logical array of any dimension, and it must be nonsparse. The output array $L$ is of class double.

## Examples

## 2-D Example

1 Make a binary image containing two overlapping circular objects.

```
center1 = -10;
center2 = -center1;
dist = sqrt(2*(2*center1)^2);
radius = dist/2 * 1.4;
lims = [floor(center1-1.2*radius) ceil(center2+1.2*radius)];
[x,y] = meshgrid(lims(1):lims(2));
bw1 = sqrt((x-center1).^2 + (y-center1).^2) <= radius;
bw2 = sqrt((x-center2).^2 + (y-center2).^2) <= radius;
bw = bw1 | bw2;
figure, imshow(bw,'InitialMagnification','fit'), title('bw')
```

2 Compute the distance transform of the complement of the binary image.

D = bwdist(~bw);
figure, imshow(D,[],'InitialMagnification','fit')
title('Distance transform of ~bw')

3 Complement the distance transform, and force pixels that don't belong to the objects to be at - Inf.

```
D = -D;
D(~bw) = - Inf;
```

4 Compute the watershed transform and display the resulting label matrix as an RGB images.
$\mathrm{L}=$ watershed(D);
rgb = label2rgb(L,'jet',[.5 .5 .5]); figure, imshow(rgb,'InitialMagnification','fit') title('Watershed transform of $D^{\prime}$ )

## 3-D Example

1 Make a 3-D binary image containing two overlapping spheres.

```
center1 = -10;
center2 = -center1;
dist = sqrt(3*(2*center1)^2);
radius = dist/2 * 1.4;
lims = [floor(center1-1.2*radius) ceil(center2+1.2*radius)];
[x,y,z] = meshgrid(lims(1):lims(2));
bw1 = sqrt((x-center1).^2 + (y-center1).^2 + ...
    (z-center1).^2) <= radius;
bw2 = sqrt((x-center2).^2 + (y-center2).^2 + ...
    (z-center2).^2) <= radius;
bw = bw1 | bw2;
figure, isosurface(x,y,z,bw,0.5), axis equal, title('BW')
xlabel x, ylabel y, zlabel z
xlim(lims), ylim(lims), zlim(lims)
view(3), camlight, lighting gouraud
```

2 Compute the distance transform.

```
D = bwdist(~bw);
figure, isosurface(x,y,z,D,radius/2), axis equal
title('Isosurface of distance transform')
xlabel x, ylabel y, zlabel z
xlim(lims), ylim(lims), zlim(lims)
```

```
view(3), camlight, lighting gouraud
```

3 Complement the distance transform, force nonobject pixels to be - Inf, and then compute the watershed transform.

```
D = -D;
D(~bw) = -Inf;
L = watershed(D);
figure
isosurface(x,y,z,L==2,0.5)
isosurface(x,y,z,L==3,0.5)
axis equal
title('Segmented objects')
xlabel x, ylabel y, zlabel z
xlim(lims), ylim(lims), zlim(lims)
view(3), camlight, lighting gouraud
```


## Algorithms

References

See Also
watershed uses the Fernand Meyer algorithm [1].
[1] Meyer, Fernand, "Topographic distance and watershed lines," Signal Processing , Vol. 38, July 1994, pp. 113-125.
bwlabel | bwlabeln | bwdist | regionprops

## Purpose $X Y Z$ color values of standard illuminants

Syntax $\quad x y z=$ whitepoint (string)
xyz = whitepoint
Description
$x y z=$ whitepoint(string) returns xyz, a three-element row vector of $X Y Z$ values scaled so that $Y=1$. string specifies the white reference illuminant. The following table lists all the possible values for string. The default value is enclosed in braces (\{\}).

| Value | Description |
| :--- | :--- |
| 'a' | CIE standard illuminant A |
| ' $^{\prime}$ ' | CIE standard illuminant C |
| ${ }^{\prime}$ d50' | CIE standard illuminant D50 |
| 'd55' | CIE standard illuminant D55 |
| 'd65' | CIE standard illuminant D65 |
| \{'icc ' \} | ICC standard profile connection space illuminant; a <br> 16-bit fractional approximation of D50 |

xyz = whitepoint is the same as xyz = whitepoint('icc').
Class string is a character array. xyz is of class double.
Support
Examples Return the $X Y Z$ color space representation of the default white reference illuminant 'icc'.
wp_icc = whitepoint
wp_icc =

$$
0.9642 \quad 1.0000 \quad 0.8249
$$

See Also $\begin{aligned} & \text { applycform | lab2double | lab2uint8 | lab2uint16 | makecform | } \\ & \text { xyz2double | xyz2uint16 }\end{aligned}$

## Purpose

2-D adaptive noise-removal filtering

Note The syntax wiener2(I, [m n],[mblock nblock], noise) has been removed. Use the wiener2 ( $\mathrm{I},[\mathrm{m} \mathrm{n}$ ], noise) syntax instead.

```
Syntax
J = wiener2(I,[m n], noise)
[J,noise] = wiener2(I,[m n])
```

Description

Class Support

## Examples

Algorithms
wiener2 lowpass-filters a grayscale image that has been degraded by constant power additive noise. wiener2 uses a pixelwise adaptive Wiener method based on statistics estimated from a local neighborhood of each pixel.

J = wiener2(I, [m n], noise) filters the image I using pixelwise adaptive Wiener filtering, using neighborhoods of size m-by-n to estimate the local image mean and standard deviation. If you omit the [ $\mathrm{m} n$ ] argument, $m$ and $n$ default to 3 . The additive noise (Gaussian white noise) power is assumed to be noise.
[J,noise] = wiener2(I, [m n]) also estimates the additive noise power before doing the filtering. wiener2 returns this estimate in noise.

The input image I is a two-dimensional image of class uint8, uint16, int16, single, or double. The output image $J$ is of the same size and class as I.

For an example, see "Removing Noise By Adaptive Filtering".
wiener2 estimates the local mean and variance around each pixel.

$$
\mu=\frac{1}{N M} \sum_{n_{1}, n_{2} \in \eta} a\left(n_{1}, n_{2}\right)
$$

and

$$
\sigma^{2}=\frac{1}{N M} \sum_{n_{1}, n_{2} \in \eta} a^{2}\left(n_{1}, n_{2}\right)-\mu^{2},
$$

where $\eta$ is the $N$-by- $M$ local neighborhood of each pixel in the image A. wiener2 then creates a pixelwise Wiener filter using these estimates,

$$
b\left(n_{1}, n_{2}\right)=\mu+\frac{\sigma^{2}-v^{2}}{\sigma^{2}}\left(a\left(n_{1}, n_{2}\right)-\mu\right),
$$

where $v^{2}$ is the noise variance. If the noise variance is not given, wiener2 uses the average of all the local estimated variances.

## References

See Also
filter2 | medfilt2

## Purpose

Convert $X Y Z$ color values to double
Syntax $\quad x y x d=x y z 2 d o u b l e(X Y Z)$
Description
xyxd = xyz2double (XYZ) converts an M-by-3 or M-by-N-by-3 array of XYZ color values to double. xyzd has the same size as XYZ.

The Image Processing Toolbox software follows the convention that double-precision $X Y Z$ arrays contain 1931 CIE $X Y Z$ values. $X Y Z$ arrays that are uint16 follow the convention in the ICC profile specification (ICC.1:2001-4, www.color.org) for representing $X Y Z$ values as unsigned 16 -bit integers. There is no standard representation of $X Y Z$ values as unsigned 8 -bit integers. The ICC encoding convention is illustrated by this table.

| Value $(\mathbf{X}, \mathbf{Y}$, or $\mathbf{Z})$ | uint16 Value |
| :--- | :--- |
| 0.0 | 0 |
| 1.0 | 32768 |
| $1.0+(32767 / 32768)$ | 65535 |

## Class <br> Support

Examples
Convert uint16-encoded $X Y Z$ values to double.
xyz2double(uint16([100 32768 65535]))
ans =

$$
0.0031 \quad 1.0000 \quad 2.0000
$$

See Also applycform | lab2double | lab2uint16 | lab2uint8 | makecform | whitepoint | xyz2uint16

## xyz2uint 16

## Purpose Convert $X Y Z$ color values to uint16

## Syntax $\quad$ xyz16 $=$ xyz2uint16 (xyz)

Description
xyz16 = xyz2uint16(xyz) converts an M-by-3 or M-by-N-by-3 array of $X Y Z$ color values to uint16. xyz16 has the same size as xyz.

The Image Processing Toolbox software follows the convention that double-precision $X Y Z$ arrays contain 1931 CIE $X Y Z$ values. $X Y Z$ arrays that are uint16 follow the convention in the ICC profile specification (ICC.1:2001-4, www.color.org) for representing XYZ values as unsigned 16 -bit integers. There is no standard representation of XYZ values as unsigned 8 -bit integers. The ICC encoding convention is illustrated by this table.

| Value (X,Y, or $\mathbf{Z})$ | uint 16 Value |
| :--- | :--- |
| 0.0 | 0 |
| 1.0 | 32768 |
| $1.0+(32767 / 32768)$ | 65535 |

## Class Support

$x y z$ is a uint16 or double array that must be real and nonsparse. xyz16 is uint8.

Examples Convert $X Y Z$ values to uint16 encoding.
xyz2uint16([0.1 0.5 1.0])
ans =
32771638432768
See Also
applycform | lab2double | lab2uint16 | lab2uint8 | makecform | whitepoint | xyz2double

## Purpose Convert YCbCr color values to RGB color space

```
Syntax rgbmap = ycbcr2rgb(ycbcrmap)
RGB = ycbcr2rgb(YCBCR)
```

Description

## Class Support

## Examples

## References

## See Also

rgbmap $=$ ycbcr2rgb(ycbcrmap) converts the YCbCr values in the colormap ycbermap to the RGB color space. If ycbcrmap is M-by-3 and contains the YCbCr luminance $(\mathrm{Y})$ and chrominance ( Cb and Cr ) color values as columns, rgbmap is returned as an M-by- 3 matrix that contains the red, green, and blue values equivalent to those colors.

RGB = ycbcr2rgb(YCBCR) converts the YCbCr image YCBCR to the equivalent truecolor image RGB.

If the input is a YCbCr image, it can be of class uint8, uint16, or double. The output image is of the same class as the input image. If the input is a colormap, the input and output colormaps are both of class double.

Convert image from RGB space to YCbCr space and back.

```
rgb = imread('board.tif');
ycbcr = rgb2ycbcr(rgb);
rgb2 = ycbcr2rgb(ycbcr);
```

[1] Poynton, C. A.A Technical Introduction to Digital Video, John Wiley \& Sons, Inc., 1996, p. 175.
[2] Rec. ITU-R BT.601-5, Studio Encoding Parameters of Digital Television for Standard 4:3 and Wide-screen 16:9 Aspect Ratios, (1982-1986-1990-1992-1994-1995), Section 3.5.
ntsc2rgb | rgb2ntsc | rgb2ycbcr

## ycbcr2rgb

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[^0]:    Algorithms

    References

    See Also
    bwlabel uses the general procedure outlined in reference [1], pp. 40-48:
    1 Run-length encode the input image.
    2 Scan the runs, assigning preliminary labels and recording label equivalences in a local equivalence table.

    3 Resolve the equivalence classes.
    4 Relabel the runs based on the resolved equivalence classes.
    [1] Haralick, Robert M., and Linda G. Shapiro, Computer and Robot Vision, Volume I, Addison-Wesley, 1992, pp. 28-48.

[^1]:    Class Support

    ## Examples

    BW = imread('circles.png');
    imshow(BW);

[^2]:    Bayer Pattern Encoded Image

[^3]:    See Also
    fan2para | ifanbeam | iradon | para2fan | phantom | radon

[^4]:    See Also
    imshow | imtool | iptgetpref | iptsetpref

[^5]:    See Also isnitf | nitfread

