

Package ‘biOps’

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Type Package

Title Image processing and analysis

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Maintainer ORPHANED

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Description This package includes several methods for image processing and analysis. It provides geometric, arithmetic, logic, morphologic (supported on one channel images only), look-up tables, edge detection (including Roberts, Sobel, Kirsch, Marr-Hildreth and Canny, among others) and convolution masks operations (predefined commons masks already defined and user defined applications). Isodata and k-means classification methods are also provided (standard, kd-tree and brute force methods implemented). Fast Fourier Transform methods and filters also available if fftw3 installed. Supports jpeg and tiff images so far (more image support in future versions). libtiff and libjpeg libraries installed required.

SystemRequirements libjpeg; optionally libtiff and fftw3

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biOps-package	<i>Basic image operations and image processing</i>
---------------	--

Description

This package includes arithmetic, logic, look up table and geometric operations. Some image processing functions, for edge detection (several algorithms including roberts, sobel, kirsch, marr-hildreth, canny) and operations by convolution masks (with predefined as well as user defined masks) are provided. Supported file formats are jpeg and tiff (it requires libtiff and libjpeg libraries installed).

Details

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r_dec_intensity	Decrease intensity
r_gamma	Gamma correct an image
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r_imgAverage	Average images
r_imgDiffer	Subtract two images
r_imgMaximum	Images maximum
r_inc_contrast	Increase contrast
r_inc_intensity	Increase intensity
r_look_up_table	Transforms an image by a given look-up table
r_negative	Negate an image
r_negative_lut	Negate an image
r_threshold	Threshold an image
readJpeg	Read jpeg file
readTiff	Read tiff file
writeJpeg	Write jpeg file
writeTiff	Write tiff file

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imagedata

Generate an imagedata

Description

This function makes an imagedata object from a matrix. This data structure is primary data structure to represent image in biOps package.

Usage

```
imagedata(mat, type=NULL, ncol=dim(mat)[1], nrow=dim(mat)[2])
```

Arguments

mat	array, matrix or vector
type	"rgb" or "grey"
ncol	width of image
nrow	height of image

Details

For grey scale image, matrix should be given in the form of 2 dimensional matrix. First dimension is row, and second dimension is column.

For rgb image, matrix should be given in the form of 3 dimensional array (row, column, channel). `mat[,1]`, `mat[,2]`, `mat[,3]` are red plane, green plane and blue plane, respectively.

You can omit 'type' specification if you give a proper array or matrix.

Value

return an imagedata object

See Also

[plot.imagedata](#) [print.imagedata](#)

Examples

```
p <- q <- seq(-1, 1, length=20)
r <- 1 - outer(p^2, q^2, "+") / 2
plot(imagedata(r))
```

`imageType`*Get information on color type of imagedata*

Description

This function returns color type ("rgb" or "grey") of a given imagedata.

Usage

```
imageType(x)
```

Arguments

<code>x</code>	The image
----------------	-----------

Value

"rgb" or "grey"

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
cat("Image Type", imageType(x))  
  
## End(Not run)
```

`imgAdd`*Add two images*

Description

This function adds two images and returns a new image.

Usage

```
imgAdd(imgdata1, imgdata2)
```

Arguments

<code>imgdata1</code>	The first image
<code>imgdata2</code>	The second image

Value

return an imagedata object

Note

To add a constant *c* to an image you can just do: `>> imgdata + c`.

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgAdd(x, x)

## End(Not run)
```

`imgAND`*And two images*

Description

This function does a logic AND between two images and returns a new image.

Usage

```
imgAND(imgdata1, imgdata2)
```

Arguments

<code>imgdata1</code>	The first image
<code>imgdata2</code>	The second image

Value

return an imagedata object

See Also

[imgOR](#) [imgXOR](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgAND(x, x)

## End(Not run)
```

imgAverage	<i>Average images</i>
------------	-----------------------

Description

This function calculates the average of the given images and returns a new image.

Usage

```
imgAverage(imgdata_list)
```

Arguments

imgdata_list An image list

Value

return an imagedata object

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgAverage(list(x, x))  
  
## End(Not run)
```

imgAverageShrink	<i>Shrink an image</i>
------------------	------------------------

Description

This function shrinks an image using the average and returns a new image.

Usage

```
imgAverageShrink(imgdata, x_scale, y_scale)
```

Arguments

imgdata	The image
x_scale	The horizontal scale factor
y_scale	The vertical scale factor

Value

return an imagedata object

Note

The scale factors are expected to be less than 1.

See Also

[imgMedianShrink](#) [imgNearestNeighborScale](#) [imgBilinearScale](#) [imgCubicScale](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgAverageShrink(x, 0.5, 0.5)  
  
## End(Not run)
```

imgBilinearRotate	<i>Rotate an image</i>
-------------------	------------------------

Description

This function rotates an image using bilinear interpolation and returns a new image.

Usage

```
imgBilinearRotate(imgdata, angle)
```

Arguments

imgdata	The image
angle	The clockwise deg angle to rotate

Value

return an imagedata object

See Also

[imgRotate](#) [imgNearestNeighborRotate](#) [imgCubicRotate](#) [imgSplineRotate](#) [imgRotate90Clockwise](#)
[imgRotate90CounterClockwise](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgBilinearRotate(x, 45)

## End(Not run)
```

imgBilinearScale	<i>Scale an image</i>
------------------	-----------------------

Description

This function scales an image using bilinear interpolation and returns a new image.

Usage

```
imgBilinearScale(imgdata, x_scale, y_scale)
```

Arguments

imgdata	The image
x_scale	The horizontal scale factor
y_scale	The vertical scale factor

Value

return an imagedata object

Note

The scale factors are expected to be greater than 1. To reduce an image use the minification functions instead.

See Also

[imgScale](#) [imgNearestNeighborScale](#) [imgCubicScale](#) [imgSplineScale](#) [imgMedianShrink](#) [imgAverageShrink](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgBilinearScale(x, 1.5, 1.5)

## End(Not run)
```

imgBinaryClosing	<i>Applies a "closing" to an image</i>
------------------	--

Description

This function applies an Dilation immediatly followed by a Erosion to the given image

Usage

```
imgBinaryClosing(imgdata, mask)
```

Arguments

imgdata	The image
mask	Mask to apply operation

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

See Also

[imgBinaryErosion](#) [imgBinaryDilation](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
mat <- matrix (0, 3, 3)
mask <- imagedata (mat, "grey", 3, 3)
y <- imgBinaryClosing(x, mask)

## End(Not run)
```

imgBinaryDilation	<i>Dilation of a binary image</i>
-------------------	-----------------------------------

Description

This function makes a dilation of a binary image with a given mask. This is, it applies the mask in every image pixel: when reached a black point, it turns every image's mask black point into black.

Usage

```
imgBinaryDilation(imgdata, mask)
```

Arguments

imgdata	The image
mask	Mask to apply operation

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
mat <- matrix(0, 3, 3)  
mask <- imagedata(mat, "grey", 3, 3)  
y <- imgBinaryDilation(x, mask)  
  
## End(Not run)
```

imgBinaryErosion	<i>Erosion of a binary image</i>
------------------	----------------------------------

Description

This function makes an erosion of a binary image with a given mask. This is, it applies the mask in every image pixel: when the mask matches completely, it turns its images' center into a black point

Usage

```
imgBinaryErosion(imgdata, mask)
```

Arguments

imgdata	The image
mask	Mask to apply operation

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
mat <- matrix (0, 3, 3)
mask <- imagedata (mat, "grey", 3, 3)
y <- imgBinaryErosion(x, mask)

## End(Not run)
```

imgBinaryOpening	<i>Applies an "opening" to an image</i>
------------------	---

Description

This function applies an erosion immediately followed by a dilation to the given image

Usage

```
imgBinaryOpening(imgdata, mask)
```

Arguments

imgdata	The image
mask	Mask to apply operation

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

See Also

[imgBinaryErosion](#) [imgBinaryDilation](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
mat <- matrix (0, 3, 3)
mask <- imagedata (mat, "grey", 3, 3)
y <- imgBinaryOpening(x, mask)

## End(Not run)
```

imgBlockMedianFilter *Filters an image*

Description

This function filters an image by the Median filter, with a block window with a given dimension

Usage

```
imgBlockMedianFilter (imgdata, dim)
```

Arguments

imgdata	The image
dim	Block's dimension (default=3)

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgBlockMedianFilter(x, 5)

## End(Not run)
```

imgBlueBand	<i>Return the image blue band</i>
-------------	-----------------------------------

Description

This function returns the blue band of the imagedata.

Usage

```
imgBlueBand(x)
```

Arguments

x	The image
---	-----------

Value

grey imagedata

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
plot(imgBlueBand(x))

## End(Not run)
```

imgBlur	<i>Blurs an image</i>
---------	-----------------------

Description

This function blurs an image by convoluting with the following matrix:

1/16	1/8	1/16
1/8	1/4	1/8
1/16	1/8	1/16

Usage

```
imgBlur(imgdata)
```

Arguments

imgdata	The image
---------	-----------

Value

return an imagedata object

See Also

[imgStdBlur](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgStdBlur(x)  
  
## End(Not run)
```

imgBoost

High Boosts an image

Description

This function high boosts an image by convoluting with the following matrix:

$$\begin{bmatrix} -1/9 & -1/9 & -1/9 \\ -1/9 & (9p-1)/9 & -1/9 \\ -1/9 & -1/9 & -1/9 \end{bmatrix}$$

It increases intensity by a given proportion (p) and subtracting a lowpass filter

Usage

```
imgBoost(imgdata, proportion)
```

Arguments

imgdata	The image
proportion	Proportion of intensity to be increased (optional: default = 1 -HighPassFilter-)

Value

return an imagedata object

Note

When proportion=1, it's the same as [imgHighPassFilter](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgBoost(x, 1.2)

## End(Not run)
```

Canny Edge Detection Method

Description

This function does edge detection using the Canny algorithm.

Usage

```
imgCanny(imgdata, sigma, low=0, high=-1)
```

Arguments

imgdata	The image
sigma	The standard deviation used for the gaussian smoothing convolution
low	The lower threshold for hysteresis
high	The higher threshold for hysteresis

Value

return an imagedata object

Note

If not specified, the low and high parameters are estimated based in a histogram of the image.

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgCanny(x, 0.7)

## End(Not run)
```

imgConvolve	<i>Performs an image convolution</i>
-------------	--------------------------------------

Description

This function performs an image convolution with given mask

Usage

```
imgConvolve(imgdata, mask, bias)
```

Arguments

imgdata	The image
mask	Kernel's convolution matrix
bias	Value to be added to each pixel after method is applied (used to correct some expected behaviour). This argument is optional (default = 32)

Value

return an imagedata object

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
m <- matrix(c(1,2,1,2,4,2,1,2,1)/16, 3, 3, byrow = TRUE)  
y <- imgConvolve(x, m, 64)  
  
## End(Not run)
```

imgCrop	<i>Crops an image</i>
---------	-----------------------

Description

This function crops image.

Usage

```
imgCrop(imgdata, x_start, y_start, c_width, c_height)
```

Arguments

imgdata	The image
x_start	Upper left x coordinate of source block
y_start	Upper left y coordinate of source block
c_width	Width of the block to crop
c_height	Height of the block to crop

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgCrop(x, 100, 50, 100, 50)

## End(Not run)
```

imgCubicRotate	<i>Rotate an image</i>
----------------	------------------------

Description

This function rotates an image using cubic interpolation and returns a new image.

Usage

```
imgCubicRotate(imgdata, angle)
```

Arguments

imgdata	The image
angle	The clockwise deg angle to rotate

Value

return an imagedata object

See Also

[imgRotate](#) [imgNearestNeighborRotate](#) [imgBilinearRotate](#) [imgSplineRotate](#) [imgRotate90Clockwise](#)
[imgRotate90CounterClockwise](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgCubicRotate(x, 45)

## End(Not run)
```

imgCubicScale	<i>Scale an image</i>
---------------	-----------------------

Description

This function scales an image using cubic interpolation and returns a new image.

Usage

```
imgCubicScale(imgdata, x_scale, y_scale)
```

Arguments

imgdata	The image
x_scale	The horizontal scale factor
y_scale	The vertical scale factor

Value

return an imagedata object

Note

The scale factors are expected to be greater than 1. To reduce an image use the minification functions instead.

See Also

[imgScale](#) [imgNearestNeighborScale](#) [imgBilinearScale](#) [imgSplineScale](#) [imgMedianShrink](#)
[imgAverageShrink](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgCubicScale(x, 1.5, 1.5)

## End(Not run)
```

<code>imgDecreaseContrast</code>	<i>Decrease contrast</i>
----------------------------------	--------------------------

Description

This function decreases an image contrast, leaving each pixel value between given values.

Usage

```
imgDecreaseContrast(imgdata, min_desired, max_desired)
```

Arguments

<code>imgdata</code>	The image
<code>min_desired</code>	The min value
<code>max_desired</code>	The max value

Value

return an imagedata object

See Also

[imgIncreaseContrast](#) [r_dec_contrast](#) [r_inc_contrast](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgDecreaseContrast(x, 60, 200)  
  
## End(Not run)
```

<code>imgDecreaseIntensity</code>	<i>Decrease intensity</i>
-----------------------------------	---------------------------

Description

This function decreases an image intensity by a given factor.

Usage

```
imgDecreaseIntensity(imgdata, percentage)
```


Arguments

imgdata	The image
percentage	A non negative value representing the intensity percentage to be decreased. 1 stands for 100% (eg. 0.5 = 50%).

Value

return an imagedata object

See Also

[imgIncreaseIntensity](#) [r_dec_intensity](#) [r_inc_intensity](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgDecreaseIntensity(x, 0.3)

## End(Not run)
```

imgDiffer

Subtract two images

Description

This function subtracts two images and returns a new image, `imgdata1 - imgdata2`.

Usage

```
imgDiffer(imgdata1, imgdata2)
```

Arguments

imgdata1	The first image
imgdata2	The second image

Value

return an imagedata object

Note

To subtract a constant `c` to an image you can just do: `>> imgdata - c`.

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgDiffer(x, x)

## End(Not run)
```

imgDifferenceEdgeDetection

Enhances image edges

Description

This function enhances image's edge by the difference method. It uses a 3x3 matrix to determine the current pixel value (by getting the maximum value between the distances of matrix's opposite neighbors

Usage

```
imgDifferenceEdgeDetection(imgdata, bias)
```

Arguments

imgdata	The image
bias	Value to be added to each pixel after method is applied (used to correct some expected behaviour). This argument is optional (default = 32)

Value

return an imagedata object

See Also

[imgHomogeneityEdgeDetection](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgDifferenceEdgeDetection(x, bias=64)

## End(Not run)
```

imgDivide	<i>Divide two images</i>
-----------	--------------------------

Description

This function divides two images and returns a new image.

Usage

```
imgDivide(imgdata1, imgdata2)
```

Arguments

imgdata1	The first image
imgdata2	The second image

Value

return an imagedata object

Note

To divide an image by a constant c you can just do: `>> imgdata / c.`

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgDivide(x, x)  
  
## End(Not run)
```

imgEKMeans	<i>Image clustering</i>
------------	-------------------------

Description

This function performs an unsupervised classification through the k-means algorithm. It is an enhanced implementation, that avoid some comparisons based on kept information about distances and centroids of previous iterations.

Usage

```
imgEKMeans (imgdata, k, maxit=10)
```

Arguments

imgdata	The image
k	Number of clusters
maxit	Max number of iterations

Value

return an imagedata object, the result of the classification

See Also

[imgKMeans](#) [imgKDKMeans](#) [imgIsoData](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgEKMeans(x, 4)

## End(Not run)
```

imgFFT

Fast Fourier Transformation of an image

Description

This function applies a Fast Fourier Transformation on an imagedata.

Usage

```
imgFFT(imgdata, shift = TRUE)
```

Arguments

imgdata	The image
shift	If TRUE (default), the transformation origin is centered

Value

return a complex matrix

See Also

[imgFFTInv](#) [imgFFTShift](#) [imgFFTiShift](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgFFT(x)

## End(Not run)
```

imgFFTBandPass	<i>Apply a band pass filter on a fft matrix</i>
----------------	---

Description

This function returns the band passed filter on a fft matrix (this matrix should be shifted).

Usage

```
imgFFTBandPass(fft_matrix, r1, r2)
```

Arguments

fft_matrix	The complex matrix of an fft transformation
r1	The inner radius of the frequency filter
r2	The outer radius of the frequency filter

Value

return an imagedata

See Also

[imgFFT](#) [imgFFTInv](#) [imgFFTLowPass](#) [imgFFTHighPass](#) [imgFFTBandStop](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgFFT(x, FALSE)
i <- imgFFTBandPass(t, 25, 70)

## End(Not run)
```

imgFFTBandStop	<i>Apply a band stop filter on a fft matrix</i>
----------------	---

Description

This function returns the band stop filter on a fft matrix (this matrix should be shifted).

Usage

```
imgFFTBandStop(fft_matrix, r1, r2)
```

Arguments

fft_matrix	The complex matrix of an fft transformation
r1	The inner radius of the frequency filter
r2	The outer radius of the frequency filter

Value

return an imagedata

See Also

[imgFFT](#) [imgFFTInv](#) [imgFFTLowPass](#) [imgFFTHighPass](#) [imgFFTBandPass](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgFFT(x, FALSE)
i <- imgFFTBandStop(t, 25, 70)

## End(Not run)
```

imgFFTConvolve	<i>Apply a convolution filter on an imagedata through fft transformation</i>
----------------	--

Description

This function returns the imagedata that results from the convolution, using fft transformation that let you convolve with bigger masks.

Usage

```
imgFFTConvolve(imgdata, mask)
```

Arguments

imgdata	The image
mask	The convolution mask

Value

return an imagedata

See Also

[imgFFT](#) [imgFFTInv](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
data <- c(-1,-1,-1,-1,9,-1,-1,-1,-1)
m <- matrix(data, 3, 3, byrow = TRUE)
i <- imgFFTConvolve(x, m)

## End(Not run)
```

imgFFTHighPass	<i>Apply a high pass filter on a fft matrix</i>
----------------	---

Description

This function returns the high passed filter on a fft matrix (this matrix should be shifted).

Usage

```
imgFFTHighPass(fft_matrix, r)
```

Arguments

fft_matrix	The complex matrix of an fft transformation
r	The radius of the frequency filter

Value

return an imagedata

See Also

[imgFFT](#) [imgFFTInv](#) [imgFFTLowPass](#) [imgFFTBandPass](#) [imgFFTBandStop](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgFFT(x, FALSE)
i <- imgFFTHighPass(t, 25)

## End(Not run)
```

imgFFTInv

*Fast Fourier Inverse Transformation to an image***Description**

This function applies a Fast Fourier Inverse Transformation on a complex matrix and return an imagedata.

Usage

```
imgFFTInv(fft_matrix, shift = TRUE)
```

Arguments

fft_matrix	The image
shift	If TRUE, the transformation origin is moved to the top-left before the inverse

Value

return an imagedata

See Also

[imgFFT](#) [imgFFTShift](#) [imgFTiShift](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgFFT(x)
i <- imgFFTInv(t)

## End(Not run)
```

imgFFTiShift	<i>Inverse of the imgFFTShift</i>
--------------	-----------------------------------

Description

This function returns the inverse shifted matrix, useful in fft transformation.

Usage

```
imgFFTiShift(imgmatrix)
```

Arguments

imgmatrix A matrix (could be an image or a fft matrix)

Value

return a matrix

See Also

[imgFFT](#) [imgFFTInv](#) [imgFFTShift](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgFFTShift(x)
i <- imgFFTiShift(t)

## End(Not run)
```

imgFFTLowPass	<i>Apply a low pass filter on a fft matrix</i>
---------------	--

Description

This function returns the low passed filter on a fft matrix (this matrix should be shifted).

Usage

```
imgFFTLowPass(fft_matrix, r)
```

Arguments

fft_matrix The complex matrix of an fft transformation
r The radius of the frequency filter

Value

return an imagedata

See Also

[imgFFT](#) [imgFFTInv](#) [imgFFTHighPass](#) [imgFTTBandPass](#) [imgFTTBandStop](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgFFT(x, FALSE)
i <- imgFTTLowPass(t, 25)

## End(Not run)
```

imgFFTPhase

Image representation of the fft matrix phase

Description

This function returns the respective phase of the given complex matrix (ie the result of a fft transformation).

Usage

```
imgFTTPhase(fft_matrix)
```

Arguments

fft_matrix The complex matrix of an fft transformation

Value

return an imagedata

See Also

[imgFFT](#) [imgFFTInv](#) [imgFTTSpectrum](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgFFT(x)
i <- imgFTTPhase(t)

## End(Not run)
```

`imgFFTShift`*Shift a matrix and leave top-left value in the center*

Description

This function returns the shifted matrix, useful in fft transformation.

Usage

```
imgFFTShift(imgmatrix)
```

Arguments

`imgmatrix` A matrix (could be an image or a fft matrix)

Value

return a matrix

See Also

[imgFFT](#) [imgFFTInv](#) [imgFFTiShift](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgFFT(x, FALSE)
i <- imgFFTShift(t)

## End(Not run)
```

`imgFFTSpectrum`*Image representation of the fft matrix spectrum*

Description

This function returns the respective spectrum of the given complex matrix (ie the result of a fft transformation).

Usage

```
imgFFTSpectrum(fft_matrix)
```

Arguments

`fft_matrix` The complex matrix of an fft transformation

Value

return an imagedata

See Also

[imgFFT](#) [imgFFTIInv](#) [imgFFTPhase](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgFFT(x)
i <- imgFFTSpectrum(t)

## End(Not run)
```

imgFreiChen	<i>Frei-Chen Edge Detection Method</i>
-------------	--

Description

This function enhances image’s edges by convoluting with the Frei-Chen method matrices:

	H_r				H_c	
1	0	-1		-1	$-\sqrt{2}$	-1
$\sqrt{2}$	0	$-\sqrt{2}$		0	0	0
1	0	-1		1	$\sqrt{2}$	1

Usage

```
imgFreiChen(imgdata)
```

Arguments

imgdata The image

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgFreiChen(x)

## End(Not run)
```

imgGamma	<i>Gamma correct an image</i>
----------	-------------------------------

Description

This function applies gamma operation to a given image. Each pixel value is taken to the inverse of gamma_value-th exponent.

Usage

```
imgGamma(imgdata, gamma_value)
```

Arguments

imgdata	The image
gamma_value	A non negative value representing operation gamma value

Value

return an imagedata object

See Also

[r_gamma](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgGamma(x, 1.3)  
  
## End(Not run)
```

imgGaussianNoise	<i>Add gaussian noise</i>
------------------	---------------------------

Description

This function adds gaussian noise to an image.

Usage

```
imgGaussianNoise(imgdata, mean, variance)
```

Arguments

imgdata	The image
mean	The gaussian mean
variance	The gaussian variance

Value

return an imagedata object

See Also

[imgSaltPepperNoise](#)

Examples

```
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgGaussianNoise(x, 0, 120)
```

imgGetRGBFromBands *Return an RGB image*

Description

This function returns the RGB image compositing the given bands.

Usage

```
imgGetRGBFromBands(R, G, B)
```

Arguments

R	A one-band image for the Red band
G	A one-band image for the Green band
B	A one-band image for the Blue band

Value

RGB imagedata

Examples

```
## Not run: x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
r <- imgRedBand(x)
g <- imgGreenBand(x)
b <- imgBlueBand(x)
rgb <- imgGetRGBFromBands(r, g, b)

## End(Not run)
```

imgGrayScaleClosing	<i>Applies a “closing” to an image</i>
---------------------	--

Description

This function applies an Dilation immediatly followed by a Erosion to the given image

Usage

```
imgGrayScaleClosing(imgdata, mask)
```

Arguments

imgdata	The image
mask	Mask to apply operation

Value

return an imagedata object

Note

This function accepts gray scale images and will fail with color ones.

See Also

[imgGrayScaleErosion](#) [imgGrayScaleDilation](#) [imgBinaryErosion](#) [imgBinaryDilation](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
mat <- matrix (0, 3, 3)
mask <- imagedata (mat, "grey", 3, 3)
y <- imgGrayScaleClosing(x, mask)

## End(Not run)
```

imgGrayScaleDilation	<i>Dilation of a gray scale image</i>
----------------------	---------------------------------------

Description

This function makes a dilation of a gray scale image with a given mask. This is, it applies the mask in every image pixel and sets current point to the maximum of the sums of the corresponding pair of pixel values in the mask and image.

Usage

```
imgGrayScaleDilation(imgdata, mask)
```

Arguments

imgdata	The image
mask	Mask to apply operation

Value

return an imagedata object

Note

This function accepts gray scale images and will fail with color ones.

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
mat <- matrix (0, 3, 3)
mask <- imagedata (mat, "grey", 3, 3)
y <- imgGrayScaleDilation(x, mask)

## End(Not run)
```

imgGrayScaleErosion	<i>Erosion of a gray scale image</i>
---------------------	--------------------------------------

Description

This function makes a dilation of a gray scale image with a given mask. This is, it applies the mask in every image pixel and sets current point to the minimum of the sums of the corresponding pair of pixel values in the mask and image.

Usage

```
imgGrayScaleErosion(imgdata, mask)
```

Arguments

imgdata	The image
mask	Mask to apply operation

Value

return an imagedata object

Note

This function accepts gray scale images and will fail with color ones.

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
mat <- matrix (0, 3, 3)
mask <- imagedata (mat, "grey", 3, 3)
y <- imgGrayScaleErosion(x, mask)

## End(Not run)
```

imgGrayScaleOpening	<i>Applies an “opening” to an image</i>
---------------------	---

Description

This function applies an erosion immediately followed by a dilation to the given image

Usage

```
imgGrayScaleOpening(imgdata, mask)
```

Arguments

imgdata	The image
mask	Mask to apply operation

Value

return an imagedata object

Note

This function accepts gray scale images and will fail with color ones.

See Also

[imgGrayScaleErosion](#) [imgGrayScaleDilation](#) [imgBinaryErosion](#) [imgBinaryDilation](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
mat <- matrix (125, 3, 3)
mask <- imagedata (mat, "grey", 3, 3)
y <- imgGrayScaleOpening(x, mask)

## End(Not run)
```

imgGreenBand	<i>Return the image green band</i>
--------------	------------------------------------

Description

This function returns the green band of the imagedata.

Usage

```
imgGreenBand(x)
```

Arguments

x	The image
---	-----------

Value

grey imagedata

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
plot(imgGreenBand(x))

## End(Not run)
```

<code>imgHighPassFilter</code>	<i>Sharpens an image</i>
--------------------------------	--------------------------

Description

This function sharpens an image by convoluting with the following matrix:

-1/9 -1/9 -1/9
-1/9 8/9 -1/9
-1/9 -1/9 -1/9

Usage

imgHighPassFilter (imgdata)

Arguments

imgdata The image

Value

return an imagedata object

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgHighPassFilter(x)  
  
## End(Not run)
```

imgHistogram	<i>Return the image histogram</i>
--------------	-----------------------------------

Description

This function returns the image pixel values histogram.

Usage

imgHistogram(x, main='Image Histogram', col='Midnight Blue', ...)

Arguments

x The image
main The histogram title
col The histogram bars color
... Same options of hist function

Value

histogram object

See Also[hist](#)**Examples**

```
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
h <- imgHistogram(x)
```

`imgHomogeneityEdgeDetection`*Enhances image edges*

Description

This function enhances image's edge by the homogeneity method. It uses a 3x3 matrix to determine the current pixel value (by getting the maximum value between the distances of the pixel and its neighbors)

Usage

```
imgHomogeneityEdgeDetection(imgdata, bias)
```

Arguments

<code>imgdata</code>	The image
<code>bias</code>	Value to be added to each pixel after method is applied (used to correct some expected behaviour). This argument is optional (default = 32)

Value

return an imagedata object

See Also[imgHomogeneityEdgeDetection](#)**Examples**

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgHomogeneityEdgeDetection(x, bias=64)

## End(Not run)
```

`imgHorizontalMirroring`*Horizontal mirror an image*

Description

This function flips an image about the y axis.

Usage

```
imgHorizontalMirroring(imgdata)
```

Arguments

<code>imgdata</code>	The image
----------------------	-----------

Value

return an imagedata object

See Also

[imgVerticalMirroring](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgHorizontalMirroring(x)  
  
## End(Not run)
```

`imgIncreaseContrast` *Increase contrast*

Description

This function increases an image contrast, augmenting pixel values differences between given limits (in a linear fashion).

Usage

```
imgIncreaseContrast(imgdata, min_limit, max_limit)
```

Arguments

imgdata	The image
min_limit	The minimum limit to apply lineal modification
max_limit	The maximum limit to apply lineal modification

Value

return an imagedata object

See Also

[imgDecreaseContrast](#) [r_inc_contrast](#) [r_dec_contrast](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgIncreaseContrast(x, 60, 200)  
  
## End(Not run)
```

imgIncreaseIntensity *Increase intensity*

Description

This function increases an image intensity by a given factor.

Usage

```
imgIncreaseIntensity(imgdata, percentage)
```

Arguments

imgdata	The image
percentage	A non negative value representing the intensity percentage to be increased. 1 stands for 100% (eg. 0.5 = 50%)

Value

return an imagedata object

See Also

[imgDecreaseIntensity](#) [r_inc_intensity](#) [r_dec_intensity](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgIncreaseIntensity(x, 0.3)

## End(Not run)
```

imgIsoData

*Image clustering***Description**

This function performs an unsupervised classification through the k-means algorithm. It is an enhanced implementation, that avoid some comparisons based on kept information about distances and centroids of previous iterations.

Usage

```
imgIsoData (imgdata, k, min_dist=1, min_elems=1, split_sd=0.1, iter_start=5, max_merge=2, max_iter=
```

Arguments

imgdata	The image
k	Number of clusters
min_dist	Minimum distance between cluster centroids
min_elems	Minimum elements per cluster
split_sd	Standard deviation threshold for splitting operation
iter_start	Maximum number of forgy iterations
max_merge	Maximum of merge operations per iteration
max_iter	Maximum number of iterations

Value

return an imagedata object, the result of the classification

See Also

[imgKMeans](#) [imgEKMeans](#) [imgKDKMeans](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgIsoData(x, 4)

## End(Not run)
```


imgKDKMeans

*Image clustering***Description**

This function performs an unsupervised classification through the k-means algorithm. This implementation uses kd-trees for nearest neighbor queries. It is useful for big values of k.

Usage

```
imgKDKMeans (imgdata, k, maxit=10)
```

Arguments

imgdata	The image
k	Number of clusters
maxit	Max number of iterations

Value

return an imagedata object, the result of the classification

See Also

[imgKMeans](#) [imgEKMeans](#) [imgIsoData](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgKDKMeans(x, 4)

## End(Not run)
```

imgKirsch

*Kirsch Edge Detection Method***Description**

This function enhances image's edges by convoluting with the Kirsch method. Base matrix is:

5	-3	-3
5	0	-3
5	-3	-3

Usage

```
imgKirsch(imgdata)
```

Arguments

imgdata	The image
---------	-----------

Value

return an imagedata object

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgKirsch(x)  
  
## End(Not run)
```

imgKMeans

<i>Image clustering</i>

Description

This function performs an unsupervised classification through the k-means algorithm. It is an straightforward implementation.

Usage

```
imgKMeans (imgdata, k, maxit=10)
```

Arguments

imgdata	The image
k	Number of clusters
maxit	Max number of iterations

Value

return an imagedata object, the result of the classification

See Also

[imgEKMeans](#) [imgKDKMeans](#) [imgIsoData](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgKMeans(x, 4)

## End(Not run)
```

imgMarrHildreth	<i>Marr-Hildreth Edge Detection Method</i>
-----------------	--

Description

This function does edge detection using the Marr-Hildreth algorithm.

Usage

```
imgMarrHildreth(imgdata, sigma)
```

Arguments

imgdata	The image
sigma	The standard deviation of Gaussian for convolution

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgMarrHildreth(x, 2)

## End(Not run)
```

imgMaximum	<i>Calculates image maximum</i>
------------	---------------------------------

Description

This function calculates the maximum of the given images and returns a new image.

Usage

```
imgMaximum(imgdata_list)
```

Arguments

imgdata_list An image list

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgMaximum(list(x, x))

## End(Not run)
```

imgMaximumFilter *Filters an image*

Description

This function filters an image by the Maximum filter, with a block window with a given dimension

Usage

```
imgMaximumFilter (imgdata, dim)
```

Arguments

imgdata The image
dim Block's dimension (default=3)

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgMaximumFilter(x, 5)

## End(Not run)
```

imgMedianShrink	<i>Shrink an image</i>
-----------------	------------------------

Description

This function shrinks an image using the median and returns a new image.

Usage

```
imgMedianShrink(imgdata, x_scale, y_scale)
```

Arguments

imgdata	The image
x_scale	The horizontal scale factor
y_scale	The vertical scale factor

Value

return an imagedata object

Note

The scale factors are expected to be less than 1.

See Also

[imgAverageShrink](#) [imgNearestNeighborScale](#) [imgBilinearScale](#) [imgCubicScale](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgMedianShrink(x, 0.5, 0.5)  
  
## End(Not run)
```

imgMinimumFilter	<i>Filters an image</i>
------------------	-------------------------

Description

This function filters an image by the Minimum filter, with a block window with a given dimension

Usage

```
imgMinimumFilter (imgdata, dim)
```

Arguments

imgdata	The image
dim	Block's dimension (default=3)

Value

return an imagedata object

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgMinimumFilter(x, 5)  
  
## End(Not run)
```

imgMultiply	<i>Multiply two images</i>
-------------	----------------------------

Description

This function multiplies two images and returns a new image.

Usage

```
imgMultiply(imgdata1, imgdata2)
```

Arguments

imgdata1	The first image
imgdata2	The second image

Value

return an imagedata object

Note

To multiply an image by a constant c you can just do: »> imgdata * c.

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgMultiply(x, x)  
  
## End(Not run)
```

imgNDilationErosion	<i>Dilation/Erosion multiple apply</i>
---------------------	--

Description

This function applies n dilations followed by n erosions to the given image. Smoothes of irregularities of N pixels in size

Usage

```
imgNDilationErosion(imgdata, mask, n)
```

Arguments

imgdata	The image
mask	Mask to apply operation
n	Times to apply each operation

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

See Also

[imgBinaryErosion](#) [imgBinaryDilation](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
mat <- matrix (0, dim, dim)
mask <- imagedata (mat, "grey", dim, dim)
y <- imgNDilationErosion(x, mask, 5)

## End(Not run)
```

imgNearestNeighborRotate

Rotate an image

Description

This function rotates an image using nearest neighbor interpolation and returns a new image.

Usage

```
imgNearestNeighborRotate(imgdata, angle)
```

Arguments

imgdata	The image
angle	The clockwise deg angle to rotate

Value

return an imagedata object

See Also

[imgRotate](#) [imgBilinearRotate](#) [imgCubicRotate](#) [imgSplineRotate](#) [imgRotate90Clockwise](#) [imgRotate90CounterClockwise](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgNearestNeighborRotate(x, 45)

## End(Not run)
```

`imgNearestNeighborScale`*Scale an image*

Description

This function scales an image using nearest neighbor interpolation and returns a new image.

Usage

```
imgNearestNeighborScale(imgdata, x_scale, y_scale)
```

Arguments

<code>imgdata</code>	The image
<code>x_scale</code>	The horizontal scale factor
<code>y_scale</code>	The vertical scale factor

Value

return an imagedata object

Note

The scale factors are expected to be greater than 1. To reduce an image use the minification functions instead.

See Also

[imgScale](#) [imgBilinearScale](#) [imgCubicScale](#) [imgSplineScale](#) [imgMedianShrink](#) [imgAverageShrink](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgNearestNeighborScale(x, 1.5, 1.5)  
  
## End(Not run)
```

imgNegative	<i>Negate an image</i>
-------------	------------------------

Description

This function negates an image.

Usage

```
imgNegative(imgdata)
```

Arguments

imgdata	The image
---------	-----------

Value

return an imagedata object

See Also

[r_negative](#) [r_negative_lut](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgNegative(x)

## End(Not run)
```

imgNErosionDilation	<i>Erosion/Dilation multiple apply</i>
---------------------	--

Description

This function applies n erosions followed by n dilations to the given image. Approaches an N depth opening

Usage

```
imgNErosionDilation(imgdata, mask, n)
```

Arguments

imgdata	The image
mask	Mask to apply operation
n	Times to apply each operation

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

See Also

[imgBinaryErosion](#) [imgBinaryDilation](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
mat <- matrix (0, dim, dim)
mask <- imagedata (mat, "grey", dim, dim)
y <- imgNErosionDilation(x, mask, 5)

## End(Not run)
```

imgNormalize

Normalization for vector and matrix

Description

This function normalizes image so that the minimum value is 0 and the maximum value is 1.

Usage

```
imgNormalize(x)
```

Arguments

x	The image
---	-----------

Value

Data of the same type as 'x', in which minimum value is 0 and maximum value is 255.

Examples

```
## Not run:
data(logo)
plot(imgNormalize(logo))

## End(Not run)
```

imgOR

Or two images

Description

This function does a logic OR between two images and returns a new image.

Usage

```
imgOR(imgdata1, imgdata2)
```

Arguments

imgdata1	The first image
imgdata2	The second image

Value

return an imagedata object

See Also

[imgAND](#) [imgXOR](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgOR(x, x)

## End(Not run)
```

imgPadding	<i>Pad an image to the given dimensions</i>
------------	---

Description

This function returns an imagedata padded to the given dimensions, leaving the input imagedata in the center of the result.

Usage

```
imgPadding(imgdata, n, m = n)
```

Arguments

imgdata	The image
n	The new width
m	The new height

Value

return an imagedata

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
t <- imgPadding(x, 350)

## End(Not run)
```

imgPrewitt	<i>Prewitt Edge Detection Method</i>
------------	--------------------------------------

Description

This function enhaces image's edges by convoluting with the Prewitt method matrices:

	H_r				H_c	
1	0	-1		-1	-1	-1
1	0	-1		0	0	0
1	0	-1		1	1	1

Usage

```
imgPrewitt(imgdata)
```

Arguments

imgdata The image

Value

return an imagedata object

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgPrewitt(x)  
  
## End(Not run)
```

imgPrewittCompassGradient

Prewitt Compass Gradient Edge Detection Method

Description

This function enhances image's edges by convoluting with the Prewitt method. Base matrix is:

$$\begin{bmatrix} 1 & 1 & -1 \\ 1 & -2 & -1 \\ 1 & 1 & -1 \end{bmatrix}$$
Usage

```
imgPrewittCompassGradient(imgdata)
```

Arguments

imgdata The image

Value

return an imagedata object

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgPrewittCompassGradient(x)
```

```
## End(Not run)
```

imgRedBand	<i>Return the image red band</i>
------------	----------------------------------

Description

This function returns the red band of the imagedata.

Usage

```
imgRedBand(x)
```

Arguments

x	The image
---	-----------

Value

grey imagedata

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
plot(imgRedBand(x))  
  
## End(Not run)
```

imgRGB2Grey	<i>Convert color imagedata to grey imagedata</i>
-------------	--

Description

This function convert color imagedata to grey imagedata.

Usage

```
imgRGB2Grey(x, coefs=c(0.30, 0.59, 0.11))
```

Arguments

x	The image
coefs	The coefficients for red, green and blue bands

Value

grey imagedata

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
plot(imgRGB2Grey(x))

## End(Not run)
```

imgRoberts	<i>Roberts Edge Detection Method</i>
------------	--------------------------------------

Description

This function enhaces image’s edges by convoluting with the Roberts method matrices:

	H_r				H_c	
	0	0	-1		-1	0
	0	1	0		0	1
	0	0	0		0	0

Usage

```
imgRoberts(imgdata)
```

Arguments

imgdata The image

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgRoberts(x)

## End(Not run)
```

imgRobinson3Level	<i>Robinson 3-level Edge Detection Method</i>
-------------------	---

Description

This function enhances image's edges by convoluting with the Robinson 3-level method. Base matrix is:

$$\begin{bmatrix} 1 & 0 & -1 \\ 1 & 0 & -1 \\ 1 & 0 & -1 \end{bmatrix}$$
Usage

```
imgRobinson3Level(imgdata)
```

Arguments

imgdata	The image
---------	-----------

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgRobinson3Level(x)

## End(Not run)
```

imgRobinson5Level	<i>Robinson 5-level Edge Detection Method</i>
-------------------	---

Description

This function enhances image's edges by convoluting with the Robinson 5-level method. Base matrix is:

$$\begin{bmatrix} 1 & 0 & -1 \\ 2 & 0 & -2 \\ 1 & 0 & -1 \end{bmatrix}$$

Usage

imgRobinson5Level(imgdata)

Arguments

imgdata The image

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgRobinson5Level(x)

## End(Not run)
```

imgRotate	<i>Rotate an image</i>
-----------	------------------------

Description

This function rotates an image using the given interpolation and returns a new image.

Usage

imgRotate(imgdata, angle, interpolation)

Arguments

imgdata The image
angle The clockwise deg angle to rotate
interpolation The interpolation method: nearestneighbor | bilinear | cubic | spline

Value

return an imagedata object

See Also

[imgNearestNeighborRotate](#) [imgBilinearRotate](#) [imgCubicRotate](#) [imgSplineRotate](#) [imgRotate90Clockwise](#)
[imgRotate90CounterClockwise](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgRotate(x, 45, 'spline')

## End(Not run)
```

imgRotate90Clockwise	<i>Rotate an image</i>
----------------------	------------------------

Description

This function rotates the image 90 degrees clockwise.

Usage

```
imgRotate90Clockwise(imgdata)
```

Arguments

imgdata	The image
---------	-----------

Value

return an imagedata object

See Also

[imgRotate90CounterClockwise](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgRotate90Clockwise(x)

## End(Not run)
```

```
imgRotate90CounterClockwise
```

Rotate an image

Description

This function rotates the image 90 degrees counter-clockwise.

Usage

```
imgRotate90CounterClockwise(imgdata)
```

Arguments

imgdata	The image
---------	-----------

Value

return an imagedata object

See Also

[imgRotate90Clockwise](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgRotate90CounterClockwise(x)

## End(Not run)
```

```
imgSaltPepperNoise
```

Add salt and pepper noise

Description

This function adds salt and pepper noise to an image.

Usage

```
imgSaltPepperNoise(imgdata, percent)
```

Arguments

imgdata	The image
percent	The percent of noise to add

Value

return an imagedata object

See Also

[imgGaussianNoise](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgSaltPepperNoise(x, 30)

## End(Not run)
```

imgScale

Scale an image

Description

This function scales an image using the given interpolation and returns a new image.

Usage

```
imgScale(imgdata, x_scale, y_scale, interpolation)
```

Arguments

imgdata	The image
x_scale	The horizontal scale factor
y_scale	The vertical scale factor
interpolation	The interpolation method: nearestneighbor bilinear cubic spline

Value

return an imagedata object

Note

The scale factors are expected to be greater than 1. To reduce an image use the minification functions instead.

See Also

[imgNearestNeighborScale](#) [imgBilinearScale](#) [imgCubicScale](#) [imgSplineScale](#) [imgMedianShrink](#)
[imgAverageShrink](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgScale(x, 1.5, 1.5, 'bilinear')

## End(Not run)
```

imgSharpen	<i>Sharpens an image with selected mask</i>
------------	---

Description

This function sharpens an image by convoluting with one of the following matrices:

1				2				3			1
0	-1	0		-1	-1	-1		1	-2	1	
-1	5	-1		-1	9	-1		-2	5	-2	
0	-1	0		-1	-1	-1		1	-2	1	

Usage

```
imgSharpen (imgdata, mask)
```

Arguments

imgdata	The image
mask	The matrix to be used in the convolution. Must be one of 1, 2, 3 (default=1)

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgSharpen(x, 2)

## End(Not run)
```

imgShenCastan	<i>Shen-Castan Edge Detection Method</i>
---------------	--

Description

This function does edge detection using the Shen-Castan algorithm.

Usage

imgShenCastan(imgdata, smooth_factor=0.9, thin_factor=2, adapt_window=7, thresh_ratio=0.8, do_hyste

Arguments

- imgdata The image
- smooth_factor The smooth factor
- thin_factor The thinning factor
- adapt_window The size of the window for adaptive gradient
- thresh_ratio The percentage of pixels to be above high threshold
- do_hysteresis If true, do hysteresis

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgShenCastan(x)

## End(Not run)
```

imgSobel	<i>Sobel Edge Detection Method</i>
----------	------------------------------------

Description

This function enhaces image’s edges by convoluting with the Sobel method matrices:

	H__r				H__c		
1	0	-1		-1	-2	-1	
2	0	-2		0	0	0	
1	0	-1		1	2	1	

Usage

imgSobel(imgdata)

Arguments

- imgdata The image

Value

return an imagedata object

Examples

```
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgSobel(x)
```

imgSplineRotate	<i>Rotate an image</i>
-----------------	------------------------

Description

This function rotates an image using b-spline interpolation and returns a new image.

Usage

```
imgSplineRotate(imgdata, angle)
```

Arguments

imgdata	The image
angle	The clockwise deg angle to rotate

Value

return an imagedata object

See Also

[imgRotate](#) [imgNearestNeighborRotate](#) [imgBilinearRotate](#) [imgCubicRotate](#) [imgRotate90Clockwise](#)
[imgRotate90CounterClockwise](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgSplineRotate(x, 45)

## End(Not run)
```

imgSplineScale	<i>Scale an image</i>
----------------	-----------------------

Description

This function scales an image using b-spline interpolation and returns a new image.

Usage

```
imgSplineScale(imgdata, x_scale, y_scale)
```

Arguments

imgdata	The image
x_scale	The horizontal scale factor
y_scale	The vertical scale factor

Value

return an imagedata object

Note

The scale factors are expected to be greater than 1. To reduce an image use the minification functions instead.

See Also

[imgScale](#) [imgNearestNeighborScale](#) [imgBilinearScale](#) [imgCubicScale](#) [imgMedianShrink](#) [imgAverageShrink](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgSplineScale(x, 1.5, 1.5)  
  
## End(Not run)
```

imgStdBinaryClosing *Fixed mask binary closing*

Description

This function applies a Binary Closing with a 0-squared mask, with given dimension

Usage

```
imgStdBinaryClosing(imgdata, dim)
```

Arguments

imgdata	The image
dim	mask's dimension (default = 3)

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

See Also

[imgStdBinaryErosion](#) [imgStdBinaryDilation](#) [imgBinaryClosing](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgStdBinaryClosing(x, 4)

## End(Not run)
```

imgStdBinaryDilation *Fixed mask binary dilation*

Description

This function makes a dilation of a binary image with a 0-squared mask, with given dimension.

Usage

```
imgStdBinaryDilation(imgdata, dim)
```

Arguments

imgdata	The image
dim	mask's dimension (default = 3)

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

See Also

[imgStdBinaryDilation](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgStdBinaryDilation(x, 4)  
  
## End(Not run)
```

imgStdBinaryErosion	<i>Fixed mask binary erosion</i>
---------------------	----------------------------------

Description

This function makes an erosion of a binary image with a 0-squared mask, with given dimension.

Usage

```
imgStdBinaryErosion(imgdata, dim)
```

Arguments

imgdata	The image
dim	mask's dimension (default = 3)

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

See Also[imgStdBinaryErosion](#)**Examples**

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgStdBinaryErosion(x, 4)

## End(Not run)
```

imgStdBinaryOpening	<i>Fixed mask binary opening</i>
---------------------	----------------------------------

Description

This function applies a Binary Opening with a 0-squared mask, with given dimension

Usage

```
imgStdBinaryOpening(imgdata, dim)
```

Arguments

imgdata	The image
dim	mask's dimension (default = 3)

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

See Also[imgStdBinaryErosion](#) [imgStdBinaryDilation](#) [imgBinaryOpening](#)**Examples**

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgStdBinaryOpening(x, 4)

## End(Not run)
```

imgStdBlur	<i>Blurs an image</i>
------------	-----------------------

Description

This function blurs an image by convoluting with a average square matrix

Usage

```
imgStdBlur(imgdata, dim)
```

Arguments

imgdata	The image
dim	Square matrix dimension (optional, default = 5)

Value

return an imagedata object

See Also

[imgBlur](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgStdBlur(x, 3)  
  
## End(Not run)
```

imgStdNDilationErosion	<i>Fixed mask NDilationErosion</i>
------------------------	------------------------------------

Description

This function applies dilation n times and then erosion n times, with a 0-squared matrix with a given dimension.

Usage

```
imgStdNDilationErosion(imgdata, n, dim=3)
```

Arguments

imgdata	The image
n	Times to apply each operation
dim	mask's dimension (default = 3)

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

See Also

[imgNDilationErosion](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgStdNDilationErosion(x, 4, 5)

## End(Not run)
```

imgStdNErosionDilation

Fixed mask NErosionDilation

Description

This function applies erosion n times and then dilation n times, with a 0-squared matrix with a given dimension.

Usage

```
imgStdNErosionDilation(imgdata, n, dim=3)
```

Arguments

imgdata	The image
n	Times to apply each operation
dim	mask's dimension (default = 3)

Value

return an imagedata object

Note

This function accepts binary images only and will treat gray scale ones as binary images.

See Also

[imgNErosionDilation](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgStdNErosionDilation(x, 4, 5)

## End(Not run)
```

imgThreshold	<i>Threshold an image</i>
--------------	---------------------------

Description

This function thresholds an image using a given filter.

Usage

```
imgThreshold(imgdata, thr_value)
```

Arguments

imgdata	The image
thr_value	Filter value for thresholding

Value

return an imagedata object

See Also

[r_threshold](#)

Examples

```
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgThreshold(x, 80)
```

imgTranslate	<i>Translate an image block</i>
--------------	---------------------------------

Description

This function translates an image block and returns a new image.

Usage

```
imgTranslate(imgdata, x_start, y_start, x_end, y_end, t_width, t_height)
```

Arguments

imgdata	The image
x_start	Upper left x coordinate of source block
y_start	Upper left y coordinate of source block
x_end	Upper left x coordinate of destination block
y_end	Upper left y coordinate of destination block
t_width	Width of the block to move
t_height	Height of the block to move

Value

return an imagedata object

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgTranslate(x, 100, 100, 200, 200, 50, 50)

## End(Not run)
```

imgUnsharpen	<i>Unsharpens an image with selected mask</i>
--------------	---

Description

This function unsharpens an image by convoluting with one of the following matrices:

1		2		3	1
0 -1 0		-1 -1 -1		1 -2 1	
-1 5 -1		-1 9 -1		-2 5 -2	
0 -1 0		-1 -1 -1		1 -2 1	

Performs a difference between original image and sharpen convolved image with the specified mask

Usage

```
imgUnsharpen (imgdata, mask)
```

Arguments

imgdata	The image
mask	The matrix to be used in the convolution. Must be one of 1, 2, 3 (default=1)

Value

return an imagedata object

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- imgUnsharpen(x, 2)  
  
## End(Not run)
```

<i>imgVerticalMirroring</i>	<i>Vertical mirror an image</i>
-----------------------------	---------------------------------

Description

This function flips an image about the x axis.

Usage

```
imgVerticalMirroring(imgdata)
```

Arguments

imgdata	The image
---------	-----------

Value

return an imagedata object

See Also

[imgHorizontalMirroring](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgVerticalMirroring(x)

## End(Not run)
```

imgXOR	<i>Xor two images</i>
--------	-----------------------

Description

This function does a logic XOR between two images and returns a new image.

Usage

```
imgXOR(imgdata1, imgdata2)
```

Arguments

- imgdata1 The first image
- imgdata2 The second image

Value

return an imagedata object

See Also

[imgOR](#) [imgAND](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- imgXOR(x, x)

## End(Not run)
```

logo	<i>R logo imagedata</i>
------	-------------------------

Description

The imagedata object of R logo of the size 101x77.

Usage

```
data(logo)
```

Format

```
imagedata
```

Examples

```
## Not run:  
data(logo)  
plot(logo)  
  
## End(Not run)
```

plot.imagedata	<i>Plotting an imagedata object</i>
----------------	-------------------------------------

Description

This function outputs an imagedata object as an image.

Usage

```
## S3 method for class 'imagedata'  
plot(x, ...)
```

Arguments

x	The image
...	Plotting options

See Also

[imagedata](#)

Examples

```
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
x
plot(x)
```

print.imagedata	<i>Print information on a given imagedata object</i>
-----------------	--

Description

This function outputs information on a given imagedata object.

Usage

```
## S3 method for class 'imagedata'
print(x, ...)
```

Arguments

x	The image
...	Ignored

See Also

[imagedata](#)

readJpeg	<i>Read jpeg file</i>
----------	-----------------------

Description

This function reads a jpeg image file and return an imagedata object.

Usage

```
readJpeg(filename)
```

Arguments

filename	filename of JPEG image
----------	------------------------

Value

return an imagedata object

See Also[imagedata](#)**Examples**

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
plot(x)

## End(Not run)
```

readTiff*Read tiff file*

Description

This function reads a tiff image file and return an imagedata object.

Usage

```
readTiff(filename)
```

Arguments

filename filename of TIFF image

Value

return an imagedata object

See Also[imagedata](#)**Examples**

```
## Not run:
x <- readTiff(system.file("samples", "violet.tif", package="biOps"))
plot(x)

## End(Not run)
```

r_dec_contrast	<i>Decrease contrast</i>
----------------	--------------------------

Description

This function decreases an image contrast, leaving each pixel value between given values.

Usage

```
r_dec_contrast(imgdata, min_desired, max_desired)
```

Arguments

imgdata	The image
min_desired	The min value
max_desired	The max value

Value

return an imagedata object

Note

This is the R implementation of imgDecreaseContrast.

See Also

[imgDecreaseContrast](#) [imgIncreaseContrast](#) [r_inc_contrast](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- r_dec_contrast(x, 60, 200)  
  
## End(Not run)
```

r_dec_intensity	<i>Decrease intensity</i>
-----------------	---------------------------

Description

This function decreases an image intensity by a given factor.

Usage

```
r_dec_intensity(imgdata, percentage)
```

Arguments

imgdata	The image
percentage	A non negative value representing the intensity percentage to be decreased. 1 stands for 100% (eg. 0.5 = 50%).

Value

return an imagedata object

Note

This is the R implementation of imgDecreaseIntensity.

See Also

[imgDecreaseIntensity](#) [imgIncreaseIntensity](#) [r_inc_intensity](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- r_dec_intensity(x, 0.3)  
  
## End(Not run)
```

r_gamma	<i>Gamma correct an image</i>
---------	-------------------------------

Description

This function applies gamma operation to a given image. Each pixel value is taken to the inverse of gamma_value-th exponent

Usage

```
r_gamma(imgdata, gamma_value)
```

Arguments

imgdata	The image
gamma_value	A non negative value representing operation gamma value

Value

return an imagedata object

Note

This is the R implementation of imgGamma.

See Also

[imgGamma](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- r_gamma(x, 1.3)  
  
## End(Not run)
```

r_imgAdd	<i>Add two images</i>
----------	-----------------------

Description

This function adds two images and returns a new image.

Usage

```
r_imgAdd(imgdata1, imgdata2)
```

Arguments

imgdata1	The first image
imgdata2	The second image

Value

return an imagedata object

Note

This is the R implementation of imgAdd.

See Also

[imgAdd](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- r_imgAdd(x, x)  
  
## End(Not run)
```

r_imgAverage	<i>Average images</i>
--------------	-----------------------

Description

This function calculates the average of the given images and returns a new image.

Usage

```
r_imgAverage(imgdata_list)
```

Arguments

imgdata_list An image list

Value

return an imagedata object

Note

This is the R implementation of imgAverage.

See Also

[imgAverage](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- r_imgAverage(list(x, x))

## End(Not run)
```

r_imgDiffer	<i>Subtract two images</i>
-------------	----------------------------

Description

This function subtracts two images and returns a new image, imgdata1 - imgdata2.

Usage

```
r_imgDiffer(imgdata1, imgdata2)
```

Arguments

imgdata1 The first image
imgdata2 The second image

Value

return an imagedata object

Note

This is the R implementation of imgDiffer.

See Also[imgDiffer](#)**Examples**

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- r_imgDiffer(x, x)

## End(Not run)
```

r_imgMaximum	<i>Images maximum</i>
--------------	-----------------------

Description

This function calculates the maximum of the given images and returns a new image.

Usage

```
r_imgMaximum(imgdata_list)
```

Arguments

imgdata_list An image list

Value

return an imagedata object

Note

This is the R implementation of imgAverage.

See Also[imgMaximum](#)**Examples**

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- r_imgMaximum(list(x, x))

## End(Not run)
```

r_inc_contrast	<i>Increase contrast</i>
----------------	--------------------------

Description

This function increases an image contrast, augmenting pixel values differences between given limits (in a linear fashion).

Usage

```
r_inc_contrast(imgdata, min_limit, max_limit)
```

Arguments

imgdata	The image
min_limit	The minimum limit to apply lineal modification
max_limit	The maximum limit to apply lineal modification

Value

return an imagedata object

Note

This is the R implementation of imgIncreaseContrast.

See Also

[imgIncreaseContrast](#) [imgDecreaseContrast](#) [r_dec_contrast](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- r_inc_contrast(x, 60, 200)  
  
## End(Not run)
```

r_inc_intensity	<i>Increase intensity</i>
-----------------	---------------------------

Description

This function increases an image intensity by a given factor.

Usage

```
r_inc_intensity(imgdata, percentage)
```

Arguments

imgdata	The image
percentage	A non negative value representing the intensity percentage to be increased. 1 stands for 100% (eg. 0.5 = 50%).

Value

return an imagedata object

Note

This is the R implementation of imgIncreaseIntensity.

See Also

[imgIncreaseIntensity](#) [imgDecreaseIntensity](#) [r_dec_intensity](#)

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
y <- r_inc_intensity(x, 0.3)  
  
## End(Not run)
```

r_look_up_table	<i>Transforms an image by a given look-up table</i>
-----------------	---

Description

This function applies a transformation to an image using a given look-up table.

Usage

```
r_look_up_table(imgdata, table)
```

Arguments

imgdata	The image
table	Look up table which determines the image operation to be applied

Value

return an imagedata object

Examples

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
lut <- seq(255, 0, by=-1)  
y <- r_threshold(x, lut)  
  
## End(Not run)
```

r_negative	<i>Negate an image</i>
------------	------------------------

Description

This function negates an image.

Usage

```
r_negative(imgdata)
```

Arguments

imgdata	The image
---------	-----------

Value

return an imagedata object

Note

This is the R implementation of imgNegative.

See Also

[imgNegative](#) [r_negative_lut](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- r_negative(x)

## End(Not run)
```

r_negative_lut	<i>Negate an image</i>
----------------	------------------------

Description

This function negates an image.

Usage

```
r_negative_lut(imgdata)
```

Arguments

imgdata The image

Value

return an imagedata object

Note

This is the R implementation of imgNegative using look up tables.

See Also

[imgNegative](#) [r_negative](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- r_negative_lut(x)

## End(Not run)
```

r_threshold	<i>Threshold an image</i>
-------------	---------------------------

Description

This function thresholds an image using a given filter.

Usage

```
r_threshold(imgdata, thr_value)
```

Arguments

imgdata	The image
thr_value	Filter value for thresholding

Value

return an imagedata object

Note

This is the R implementation of imgThreshold.

See Also

[imgThreshold](#)

Examples

```
## Not run:
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))
y <- r_threshold(x, 80)

## End(Not run)
```

writeJpeg	<i>Write jpeg file</i>
-----------	------------------------

Description

This function writes an imagedata object into a jpeg image file.

Usage

```
writeJpeg(filename, imgdata)
```


Arguments

filename	filename of JPEG image
imgdata	imagedata to write

See Also[readJpeg](#)**Examples**

```
## Not run:  
x <- readJpeg(system.file("samples", "violet.jpg", package="biOps"))  
writeJpeg("new_image.jpg", x)  
  
## End(Not run)
```

writeTiff	<i>Write tiff file</i>
-----------	------------------------

Description

This function writes an imagedata object into a tiff image file.

Usage

```
writeTiff(filename, imgdata)
```

Arguments

filename	filename of TIFF image
imgdata	imagedata to write

See Also[readTiff](#)**Examples**

```
## Not run:  
x <- readTiff(system.file("samples", "violet.tif", package="biOps"))  
writeTiff("new_image.tif", x)  
  
## End(Not run)
```

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