Package ‘imager’

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Type Package
Title Image Processing Library Based on 'CImg'
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Description Fast image processing for images in up to 4 dimensions (two spatial
dimensions, one time/depth dimension, one colour dimension). Provides most
traditional image processing tools (filtering, morphology, transformations,
etc.) as well as various functions for easily analysing image data using R. The
package wraps 'CImg', <http://cimg.eu>, a simple, modern C++ library for image
processing.
License LGPL-3
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R topics documented:

add.colour .......................................................... 5
as.cimg .......................................................... 6
as.cimg.array .................................................. 7
as.cimg.data.frame ........................................... 8
as.cimg.function ............................................. 9
as.cimg.raster .................................................. 10
as.data.frame.cimg .......................................... 11
as.data.frame.imlist ......................................... 12
as.data.frame.pixset ......................................... 12
as.igraph.cimg .................................................. 13
as.igraph.pixset ............................................... 14
as.imlist.list .................................................. 15
as.pixset .......................................................... 16
as.raster.cimg ................................................... 17
at ................................................................. 18
autocrop .......................................................... 19
bbox .............................................................. 20
blur_anisotropic .................................................. 21
boats .............................................................. 22
boundary ........................................................... 23
boxblur ............................................................ 23
boxblur_xy .......................................................... 24
bucketfill ........................................................... 25
cannyEdges ........................................................ 26
capture.plot ..................................................... 27
center.stencil .................................................... 27
channels .......................................................... 28
ci ................................................................. 28
cimg .............................................................. 29
cimg.dimensions ............................................... 30
cimg.extract ..................................................... 31
cimg.use.openmp ............................................... 32
cimg2im ........................................................... 33
circles .............................................................. 33
clean .............................................................. 34
colorise ............................................................ 35
common_pixsets .................................................. 36
contours ........................................................... 38
coord.index ....................................................... 39
correlate ........................................................... 39
crop.borders ...................................................... 40
deriche ............................................................ 41
diffusion_tensors ................................................ 42
displacement ....................................................... 42
display ............................................................. 43
display.cimg ....................................................... 43
topics documented:

- `display.list` .................................................. 44
- `distance_transform` ........................................ 45
- `draw_circle` .................................................. 45
- `draw_rect` .................................................... 46
- `draw_text` .................................................... 47
- `erode` ......................................................... 48
- `extract_patches` ............................................. 50
- `FFT` ........................................................... 51
- `flatten.alpha` ............................................... 52
- `frames` ........................................................ 53
- `get.locations` ................................................ 53
- `get.stencil` .................................................. 54
- `get_gradient` ................................................ 55
- `get_hessian` .................................................. 55
- `grab` ............................................................. 56
- `grayscale` .................................................... 57
- `grow` ............................................................ 57
- `gsdim` ........................................................... 58
- `haar` ............................................................. 59
- `highlight` ...................................................... 60
- `hough_circle` .................................................. 60
- `hough_line` .................................................... 61
- `idply` .......................................................... 62
- `iply` ............................................................. 63
- `ilply` ............................................................ 63
- `im2cimg` ....................................................... 64
- `imager` .......................................................... 64
- `imager.combine` ............................................. 65
- `imager.replace` ............................................. 67
- `imager.subset` ............................................... 68
- `imappend` ...................................................... 69
- `imchange` ..................................................... 70
- `imcoord` ....................................................... 71
- `imdirac` ........................................................ 72
- `imdraw` ......................................................... 73
- `imeval` .......................................................... 74
- `imfill` ........................................................... 76
- `imgradient` ..................................................... 77
- `inhessian` ...................................................... 77
- `iminfo` .......................................................... 78
- `imlap` ........................................................... 79
- `imlist` ........................................................... 79
- `imnoise` ......................................................... 80
- `implot` .......................................................... 81
- `imrep` ........................................................... 82
- `imrotate` ....................................................... 82
- `imsharpen` ..................................................... 83
- `imshift` .......................................................... 84
<table>
<thead>
<tr>
<th>R topics documented:</th>
</tr>
</thead>
<tbody>
<tr>
<td>imsplit</td>
</tr>
<tr>
<td>imsub</td>
</tr>
<tr>
<td>imwarp</td>
</tr>
<tr>
<td>im_split</td>
</tr>
<tr>
<td>index.coord</td>
</tr>
<tr>
<td>inpaint</td>
</tr>
<tr>
<td>interact</td>
</tr>
<tr>
<td>interp</td>
</tr>
<tr>
<td>is.cimg</td>
</tr>
<tr>
<td>is.imlist</td>
</tr>
<tr>
<td>is.pixset</td>
</tr>
<tr>
<td>isobblur</td>
</tr>
<tr>
<td>label</td>
</tr>
<tr>
<td>lipy</td>
</tr>
<tr>
<td>load.dir</td>
</tr>
<tr>
<td>load.example</td>
</tr>
<tr>
<td>load.image</td>
</tr>
<tr>
<td>load.video</td>
</tr>
<tr>
<td>magick</td>
</tr>
<tr>
<td>make.video</td>
</tr>
<tr>
<td>map_il</td>
</tr>
<tr>
<td>medianblur</td>
</tr>
<tr>
<td>mirror</td>
</tr>
<tr>
<td>mutate_plyr</td>
</tr>
<tr>
<td>nfline</td>
</tr>
<tr>
<td>pad</td>
</tr>
<tr>
<td>patchstat</td>
</tr>
<tr>
<td>patch_summary_cimg</td>
</tr>
<tr>
<td>periodic.part</td>
</tr>
<tr>
<td>permute_axes</td>
</tr>
<tr>
<td>pixel.grid</td>
</tr>
<tr>
<td>pixset</td>
</tr>
<tr>
<td>play</td>
</tr>
<tr>
<td>plot.cimg</td>
</tr>
<tr>
<td>plot.imlist</td>
</tr>
<tr>
<td>px.flood</td>
</tr>
<tr>
<td>px.na</td>
</tr>
<tr>
<td>px.remove_outer</td>
</tr>
<tr>
<td>RasterPackage</td>
</tr>
<tr>
<td>renorm</td>
</tr>
<tr>
<td>resize</td>
</tr>
<tr>
<td>resize_doubleXY</td>
</tr>
<tr>
<td>RGBtoHSL</td>
</tr>
<tr>
<td>rm.alpha</td>
</tr>
<tr>
<td>rotate_xy</td>
</tr>
<tr>
<td>save.image</td>
</tr>
<tr>
<td>split_connected</td>
</tr>
<tr>
<td>squeeze</td>
</tr>
</tbody>
</table>
**add.colour**

Add colour channels to a grayscale image or pixel set

**Description**

Add colour channels to a grayscale image or pixel set

**Usage**

```r
add.colour(im, simple = TRUE)
add.color(im, simple = TRUE)
```

**Arguments**

- **im**: a grayscale image
- **simple**: if TRUE just stack three copies of the grayscale image, if FALSE treat the image as the L channel in an HSL representation. Default TRUE. For pixel sets this option makes no sense and is ignored.

**Value**

an image of class `cimg`

**Functions**

- add.color: Alias for add.colour

**Author(s)**

Simon Barthelme

**Examples**

```r
grayscale(boats) # No more colour channels
add.colour(grayscale(boats)) # Image has depth = 3 (but contains only grays)
```
**as.cimg**

Convert to cimg object

**Description**

Imager implements various converters that turn your data into cimg objects. If you convert from a vector (which only has a length, and no dimension), either specify dimensions explicitly or some guesswork will be involved. See examples for clarifications.

**Usage**

```r
as.cimg(obj, ...)
```

```r
## S3 method for class 'numeric'
as.cimg(obj, ...)
```

```r
## S3 method for class 'logical'
as.cimg(obj, ...)
```

```r
## S3 method for class 'double'
as.cimg(obj, ...)
```

```r
## S3 method for class 'cimg'
as.cimg(obj, ...)
```

```r
## S3 method for class 'vector'
as.cimg(obj, x = NA, y = NA, z = NA, cc = NA, dim = NULL, ...)
```

```r
## S3 method for class 'matrix'
as.cimg(obj, ...)
```

**Arguments**

- `obj` an object
- `...` optional arguments
- `x` width
- `y` height
- `z` depth
- `cc` spectrum
- `dim` a vector of dimensions (optional, use instead of xyzcc)

**Methods (by class)**

- numeric: convert numeric
- logical: convert logical
as.cimg.array

- double: convert double
- cimg: return object
- vector: convert vector
- matrix: Convert to matrix

Author(s)
Simon Barthelme

See Also
as.cimg.array, as.cimg.function, as.cimg.data.frame

Examples
as.cimg(1:100,x=10,y=10) #10x10, grayscale image
as.cimg(rep(1:100,3),x=10,y=10,cc=3) #10x10 RGB
as.cimg(1:100,dim=c(10,10,1,1))
as.cimg(1:100) #Guesses dimensions, warning is issued
as.cimg(rep(1:100,3)) #Guesses dimensions, warning is issued

as.cimg.array Turn an numeric array into a cimg object

Description
If the array has two dimensions, we assume it’s a grayscale image. If it has three dimensions we assume it’s a video, unless the third dimension has a depth of 3, in which case we assume it’s a colour image.

Usage
## S3 method for class 'array'
as.cimg(obj, ...)

Arguments
  obj an array
  ... ignored

Examples
as.cimg(array(1:9,c(3,3)))
as.cimg(array(1,c(10,10,3))) #Guesses colour image
as.cimg(array(1:9,c(10,10,4))) #Guesses video
as.cimg.data.frame Create an image from a data.frame

Description

This function is meant to be just like as.cimg.data.frame, but in reverse. Each line in the data frame must correspond to a pixel. For example, the data frame can be of the form (x, y, value) or (x, y, z, value), or (x, y, z, c, value). The coordinates must be valid image coordinates (i.e., positive integers).

Usage

## S3 method for class 'data.frame'
as.cimg(obj, v.name = "value", dims, ...)

Arguments

- obj: a data.frame
- v.name: name of the variable to extract pixel values from (default "value")
- dims: a vector of length 4 corresponding to image dimensions. If missing, a guess will be made.
- ...: ignored

Value

an object of class cimg

Author(s)

Simon Barthelme

Examples

# Create a data.frame with columns x, y and value
df <- expand.grid(x=1:10, y=1:10) %>% dplyr::mutate(value=x*y)
# Convert to cimg object (2D, grayscale image of size 10x10
as.cimg(df, dims=c(10,10,1,1)) %>% plot
Create an image by sampling a function

**Description**

Similar to as.im.function from the spatstat package, but simpler. Creates a grid of pixel coordinates x=1:width, y=1:height and (optional) z=1:depth, and evaluates the input function at these values.

**Usage**

```r
## S3 method for class `function`
as.cimg(
  obj,
  width,
  height,
  depth = 1,
  spectrum = 1,
  standardise = FALSE,
  dim = NULL,
  ...
)
```

**Arguments**

- **obj**: a function with arguments (x,y), or (x,y,cc), or (x,y,z), etc. Must be vectorised; see examples.
- **width**: width of the image (in pixels)
- **height**: height of the image (in pixels)
- **depth**: depth of the image (in pixels). Default 1.
- **spectrum**: number of colour channels. Default 1.
- **standardise**: coordinates are scaled and centered (see doc for pixel.grid)
- **dim**: a vector of image dimensions (can be used instead of width, height, etc.)
- **...**: ignored

**Value**

an object of class cimg

**Author(s)**

Simon Barthelme
Examples

```r
im = as.cimg(function(x,y) cos(sin(x*y/100)),100,100)
plot(im)

# The following is just a rectangle at the center of the image
im = as.cimg(function(x,y) (abs(x) < .1)*(abs(y) < .1) ,100,100,standardise=TRUE)
plot(im)

# Since coordinates are standardised the rectangle scales with the size of the image
im = as.cimg(function(x,y) (abs(x) < .1)*(abs(y) < .1) ,200,200,standardise=TRUE)
plot(im)

# A Gaussian mask around the center
im = as.cimg(function(x,y) dnorm(x,sd=.1)*dnorm(y,sd=.3) ,dim=dim(boats),standardise=TRUE)
im = im/max(im)
plot(im*boats)

# A Gaussian mask for just the red channel
fun = function(x,y,cc) ifelse(cc==1,dnorm(x,sd=.1)*dnorm(y,sd=.3),0)
im = as.cimg(fun,dim=dim(boats),standardise=TRUE)
plot(im*boats)
```

---

### as.cimg.raster

Convert a raster object to a cimg object

---

Description

R's native object for representing images is a "raster". This function converts raster objects to cimg objects.

Usage

```r
## S3 method for class 'raster'
as.cimg(obj, ...)
```

Arguments

- `obj` a raster object
- `...` ignored

Value

a cimg object

Author(s)

Simon Barthelme
as.data.frame.cimg

Examples

rst <- as.raster(matrix((1:4)/4, 2, 2))
as.cimg(rst) %>% plot(int=FALSE)
all.equal(rst, as.raster(as.cimg(rst)))

Convert a pixel image to a data.frame

Description

This function combines the output of pixel.grid with the actual values (stored in $value)

Usage

## S3 method for class 'cimg'
as.data.frame(x, ..., wide = c(FALSE, "c", "d"))

Arguments

x an image of class cimg
...
arguments passed to pixel.grid
wide if "c" or "d" return a data.frame that is wide along colour or depth (for example with rgb values along columns). The default is FALSE, with each pixel forming a separate entry.

Value

da.data.frame

Author(s)

Simon Barthelme

Examples

#First five pixels
as.data.frame(boats) %>% head(5)
#Wide format along colour axis
as.data.frame(boats, wide="c") %>% head(5)
as.data.frame.imlist  
*Convert image list to data.frame*

**Description**

Convert image list to data.frame

**Usage**

```r
## S3 method for class 'imlist'
as.data.frame(x, ..., index = "im")
```

**Arguments**

- `x`  
  an image list (an imlist object)
- `...`  
  Passed on to as.data.frame.cimg
- `index`  
  Name of the column containing the index (or name) of the image in the list. Default: "im"

**Examples**

```r
# Transform the image gradient into a data.frame
gr <- imgradient(boats,"xy") %>% setNames(c("dx","dy")) %>% as.data.frame
str(gr)
```

as.data.frame.pixset  
*Methods to convert pixsets to various objects*

**Description**

Methods to convert pixsets to various objects

**Usage**

```r
## S3 method for class 'pixset'
as.data.frame(x, ..., drop = FALSE)
```

**Arguments**

- `x`  
  pixset to convert
- `...`  
  ignored
- `drop`  
  drop flat dimensions

**See Also**

where
Examples

```r
px <- boats > 250
# Convert to array of logicals
as.logical(px) %>% dim
# Convert to data.frame: gives all pixel locations in the set
as.data.frame(px) %>% head
# Drop flat dimensions
as.data.frame(px, drop=TRUE) %>% head
```

Description

In this graph representation, every pixel is a vertex connected to its neighbours. The image values along edges are stored as graph attributes (see examples).

Usage

```r
## S3 method for class 'cimg'
as.igraph(x, mask = px.all(channel(im, 1)), ...)
```

Arguments

- `x`: an image (must be 2D, 3D not implemented yet)
- `mask`: optional: a pixset. if provided, pixels are only connected if they are both in the pixset.
- `...`: ignored

Value

a graph (igraph format) with attributes `value.from`, `value.to` and `dist`

Author(s)

Simon Barthelme

See Also

as.igraph.pixset
Examples

```r
library(igraph)

im <- imfill(5,5)
G <- as.igraph(im)
plot(G)

# Shortest-path distance from pixel 1 to all other pixels
d <- igraph::distances(G,1) %>% as.vector
as.cimg(d,dim=gsdim(im)) %>% plot(interpolate=FALSE)

# Notice that moving along the diagonal has the same cost
# as moving along the cardinal directions, whereas the Euclidean distance
# is actually sqrt(2) and not 1.
# Modify weight attribute, to change the way distance is computed
igraph::E(G)$weight <- G$dist
d2 <- igraph::distances(G,1) %>% as.vector
as.cimg(d2,dim=gsdim(im)) %>% plot(interpolate=FALSE)

# More interesting example
im <- grayscale(boats)
G <- as.igraph(im)

# value.from holds the value of the source pixel, value.to the sink's
# set w_ij = (|v_i - v_j|)/d_ij
igraph::E(G)$weight <- (abs(G$value.from - G$value.to))/G$dist
igraph::distances(G,5000) %>% as.vector %>% as.cimg(dim=gsdim(im)) %>% plot
```

as.igraph.pixset

Form an adjacency graph from a pixset

Description

Return a graph where nodes are pixels, and two nodes are connected if and only if both nodes are in the pixset, and the pixels are adjacent. Optionnally, add weights corresponding to distance (either 1 or sqrt(2), depending on the orientation of the edge). The graph is represented as an igraph "graph" object

Usage

```r
## S3 method for class 'pixset'
as.igraph(x, weighted = TRUE, ...)
```

Arguments

- `x`: a pixset
- `weighted`: add weight for distance (default TRUE)
- `...`: ignored

Value

an igraph "graph" object
### as.imlist.list

Convert various objects to image lists

#### Description

Convert various objects to image lists

#### Usage

```r
## S3 method for class 'list'
as.imlist(obj, ...)

as.imlist(obj, ...)

## S3 method for class 'imlist'
as.imlist(obj, ...)

## S3 method for class 'cimg'
as.imlist(obj, ...)
```
Arguments

- obj: an image list
- ...: ignored

Value

- a list

Methods (by class)

- list: convert from list
- imlist: Convert from imlist (identity)
- cimg: Convert from image

Examples

```r
list(a=boats,b=boats*2) %>% as.imlist
```

### as.pixset

Methods to convert various objects to pixsets

Description

Methods to convert various objects to pixsets

Usage

```r
as.pixset(x, ...)
```

```r
# S3 method for class 'cimg'
as.pixset(x, ...)
```

```r
# S3 method for class 'pixset'
as.cimg(obj, ...)
```

Arguments

- x: object to convert to pixset
- ...: ignored
- obj: pixset to convert

Methods (by class)

- cimg: convert cimg to pixset
- pixset: convert pixset to cimg
Examples

# When converting an image to a pixset, the default is to include all pixels with non-zero value
as.pixset(boats)
# The above is equivalent to:
boats!=0

Description

raster objects are used by R’s base graphics for plotting. R wants hexadecimal RGB values for plotting, e.g. gray(0) yields #000000, meaning black. If you want to control precisely how numerical values are turned into colours for plotting, you need to specify a colour scale using the colourscale argument (see examples). Otherwise the default is "gray" for grayscale images, "rgb" for colour. These expect values in [0..1], so the default is to rescale the data to [0..1]. If you wish to over-ride that behaviour, set rescale=FALSE.

Usage

## S3 method for class 'cimg'
as.raster(
  x,
  frames,
  rescale = TRUE,
  colourscale = NULL,
  colorscale = NULL,
  col.na = rgb(0, 0, 0, 0),
  ...
)

Arguments

x an image (of class cimg)
frames which frames to extract (in case depth > 1)
rescale rescale so that pixel values are in [0,1]? (subtract min and divide by range). default TRUE
colourscale a function that returns RGB values in hexadecimal
colorscale same as above in American spelling
col.na which colour to use for NA values, as R rgb code. The default is "rgb(0,0,0)", which corresponds to a fully transparent colour.
... ignored
Return or set pixel value at coordinates

Description

Return or set pixel value at coordinates

Usage

at(im, x, y, z = 1, cc = 1)

at(im, x, y, z = 1, cc = 1) <- value

color.at(im, x, y, z = 1)

color.at(im, x, y, z = 1) <- value

Examples

#A raster is a simple array of RGB values
as.raster(boats) %>% str
#By default as.raster rescales input values, so that:
all.equal(as.raster(boats), as.raster(boats/2)) #TRUE
#Setting rescale to FALSE changes that
as.raster(boats, rescale=FALSE) %>% plot
as.raster(boats/2, rescale=FALSE) %>% plot
#For grayscale images, a colourmap should take a single value and
#return an RGB code
#Example: mapping grayscale value to saturation
cscale <- function(v) hsv(.5, v, 1)
grayscale(boats) %>% as.raster(colourscale=cscale) %>% plot
Arguments

im  an image (cimg object)
x  x coordinate (vector)
y  y coordinate (vector)
z  z coordinate (vector, default 1)
cc  colour coordinate (vector, default 1)
value  replacement

Value

pixel values

Functions

• at<-. set value of pixel at a location
• color.at: return value of all colour channels at a location
• color.at<-: set value of all colour channels at a location

Author(s)

Simon Barthelme

Examples

im <- as.cimg(function(x,y) x+y,50,50)
at(im,10,1)
at(im,10:12,1)
at(im,10:12,1:3)
at(im,1,2) <- 10
at(im,1,2)
color.at(boats,x=10,y=10)
im <- boats
color.at(im,x=10,y=10) <- c(255,0,0)
#There should now be a red dot
imsup(im, x %inr% c(1,100), y %inr% c(1,100)) %>% plot

autocrop

Autocrop image region

Description

Autocrop image region

Usage

autocrop(im, color = color.at(im, 1, 1), axes = "zyx")
bbox

Compute the bounding box of a pixset

Arguments

px  a pixset
im  an image

Description

This function returns the bounding box of a pixset as another pixset. If the image has more than one
frame, a bounding cube is returned. If the image has several colour channels, the bounding box is
computed separately in each channel. crop.bbox crops an image using the bounding box of a pixset.

Usage

bbox(px)
crop.bbox(im, px)

Arguments

px  a pixset
im  an image

Value

a pixset object
blur_anisotropic

Functions

- crop.bbox: crop image using the bounding box of pixset px

Author(s)

Simon Barthelme

Examples

```r
im <- grayscale(boats)
px <- im > .85
plot(im)
highlight(bbox(px))
highlight(px,col="green")
crop.bbox(im,px) %>% plot
```

---

**blur_anisotropic**  
*Blur image anisotropically, in an edge-preserving way.*

Description

Standard blurring removes noise from images, but tends to smooth away edges in the process. This anisotropic filter preserves edges better.

Usage

```r
blur_anisotropic(
im,
amplitude,
sharpness = 0.7,
anisotropy = 0.6,
alpha = 0.6,
sigma = 1.1,
dl = 0.8,
da = 30,
gauss_prec = 2,
interpolation_type = 0L,
fast_approx = TRUE
)
```

Arguments

- **im** an image
- **amplitude** Amplitude of the smoothing.
- **sharpness** Sharpness.
- **anisotropy** Anisotropy.
alpha  Standard deviation of the gradient blur.
sigma  Standard deviation of the structure tensor blur.
dl     Spatial discretization.
da     Angular discretization.
gauss_prec  Precision of the diffusion process.
interpolation_type
            Interpolation scheme. Can be 0=nearest-neighbor | 1=linear | 2=Runge-Kutta
fast_approx  If true, use fast approximation (default TRUE)

Examples

im <- load.image(system.file('extdata/Leonardo_Birds.jpg', package='imager'))
im.noisy <- (im + 80*rnorm(prod(dim(im))))
blur_anisotropic(im.noisy, ampl=1e4, sharp=1) %>% plot

boats  

Photograph of sailing boats from Kodak set

Description

This photograph was downloaded from http://r0k.us/graphics/kodak/kodim09.html. Its size was reduced by half to speed up loading and save space.

Usage

boats

Format

an image of class cimg

Source

http://r0k.us/graphics/kodak/kodim09.html
**boundary**

*Find the boundary of a shape in a pixel set*

**Description**

Find the boundary of a shape in a pixel set

**Usage**

`boundary(px, depth = 1, high_connexity = FALSE)`

**Arguments**

- `px` pixel set
- `depth` boundary depth (default 1)
- `high_connexity` if FALSE, use 4-point neighbourhood. If TRUE, use 8-point. (default FALSE)

**Examples**

- `px.diamond(10,30,30) %>% boundary %>% plot`
- `px.square(10,30,30) %>% boundary %>% plot`
- `px.square(10,30,30) %>% boundary(depth=3) %>% plot`
- `px <- (px.square(10,30,30) | px.circle(12,30,30))`
- `boundary(px,high=TRUE) %>% plot(int=TRUE,main="8-point neighbourhood")`
- `boundary(px,high=TRUE) %>% plot(int=FALSE,main="4-point neighbourhood")`

---

**boxblur**

*Blur image with a box filter (square window)*

**Description**

Blur image with a box filter (square window)

**Usage**

`boxblur(im, boxsize, neumann = TRUE)`

**Arguments**

- `im` an image
- `boxsize` Size of the box window (can be subpixel).
- `neumann` If true, use Neumann boundary conditions, Dirichlet otherwise (default true, Neumann)
See Also
deriche(), vanvliet().

Examples

boxblur(boats, 5) %>% plot(main = "Dirichlet boundary")
boxblur(boats, 5, TRUE) %>% plot(main = "Neumann boundary")

boxblur_xy(boats, 20, 5) %>% plot(main = "Anisotropic blur")
**bucketfill**

**Bucket fill**

**Description**

Bucket fill

**Usage**

bucketfill(
  im,
  x,
  y,
  z = 1,
  color,
  opacity = 1,
  sigma = 0,
  high_connexity = FALSE
)

**Arguments**

- **im**: an image
- **x**: X-coordinate of the starting point of the region to fill.
- **y**: Y-coordinate of the starting point of the region to fill.
- **z**: Z-coordinate of the starting point of the region to fill.
- **color**: a vector of values (of length spectrum(im)), or a colour name (e.g. "red"). If missing, use the colour at location (x,y,z).
- **opacity**: opacity. If the opacity is below 1, paint with transparency.
- **sigma**: Tolerance for neighborhood values: spread to neighbours if difference is less than sigma (for grayscale). If there are several channels, the sum of squared differences is used: if it below sigma^2, the colour spreads.
- **high_connexity**: Use 8-connexity (only for 2d images, default FALSE).

**See Also**

px.flood

**Examples**

#Change the colour of a sail
boats.new <- bucketfill(boats,x=169,y=179,color="pink",sigma=.2)
layout(t(1:2))
plot(boats,main="Original")
plot(boats.new,main="New sails")
# More spreading, lower opacity, colour specified as vector
ugly <- bucketfill(boats,x=169,y=179,color=c(0,1,0),sigma=.6,opacity=.5)
plot(ugly)

cannyEdges  

Canny edge detector

Description
If the threshold parameters are missing, they are determined automatically using a k-means heuristic. Use the alpha parameter to adjust the automatic thresholds up or down. The thresholds are returned as attributes. The edge detection is based on a smoothed image gradient with a degree of smoothing set by the sigma parameter.

Usage
cannyEdges(im, t1, t2, alpha = 1, sigma = 2)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>im</td>
<td>input image</td>
</tr>
<tr>
<td>t1</td>
<td>threshold for weak edges (if missing, both thresholds are determined automatically)</td>
</tr>
<tr>
<td>t2</td>
<td>threshold for strong edges</td>
</tr>
<tr>
<td>alpha</td>
<td>threshold adjustment factor (default 1)</td>
</tr>
<tr>
<td>sigma</td>
<td>smoothing</td>
</tr>
</tbody>
</table>

Author(s)
Simon Barthelme

Examples
cannyEdges(boats) %>% plot
# Make thresholds less strict
cannyEdges(boats,alpha=.4) %>% plot
# Make thresholds more strict
cannyEdges(boats,alpha=1.4) %>% plot
capture.plot  
Capture the current R plot device as a cimg image

Description
Capture the current R plot device as a cimg image

Usage
capture.plot()

Value
a cimg image corresponding to the contents of the current plotting window

Author(s)
Simon Barthelme

Examples
##interactive only:
##plot(1:10)
###Make a plot of the plot
##capture.plot() %>% plot

center.stencil  
Center stencil at a location

Description
Center stencil at a location

Usage
center.stencil(stencil, ...)

Arguments
stencil  a stencil (data.frame with coordinates dx,dy,dz,dc)
...  centering locations (e.g. x=4,y=2)

Examples
stencil <- data.frame(dx=seq(-2,2,1),dy=seq(-2,2,1))
center.stencil(stencil,x=10,y=20)
channels  
*Split a colour image into a list of separate channels*

**Description**

Split a colour image into a list of separate channels

**Usage**

```r
cierals(boats)
cierals(boats,1:2)
cierals(boats,1:2,drop=TRUE) %>% str #A list of 2D arrays
```

**Arguments**

- `im`: an image
- `index`: which channels to extract (default all)
- `drop`: if TRUE drop extra dimensions, returning normal arrays and not cimg objects

**Value**

a list of channels

**See Also**

frames

**Examples**

```r
cierals(boats)
cierals(boats,1:2)
cierals(boats,1:2,drop=TRUE) %>% str #A list of 2D arrays
```

---

ci  
*Concatenation for image lists*

**Description**

Allows you to concatenate image lists together, or images with image lists. Doesn’t quite work like R’s "c" primitive: image lists are always *flat*, not nested, meaning each element of an image list is an image.

**Usage**

```r
ci(...)
```
Arguments
...
objects to concatenate

Value
an image list

Author(s)
Simon Bartheleme

Examples

l1 <- imlist(boats,grayscale(boats))
l2 <- imgradient(boats,"xy")
ci(l1,l2) #List + list
ci(l1,imfill(3,3)) #List + image
ci(imfill(3,3),l1,l2) #Three elements, etc.

---

cimg

Create a cimg object

Description
cimg is a class for storing image or video/hyperspectral data. It is designed to provide easy inter-
action with the CImg library, but in order to use it you need to be aware of how CImg wants its
image data stored. Images have up to 4 dimensions, labelled x,y,z,c. x and y are the usual spatial
dimensions, z is a depth dimension (which would correspond to time in a movie), and c is a colour
dimension. Images are stored linearly in that order, starting from the top-left pixel and going along
*rows* (scanline order). A colour image is just three R,G,B channels in succession. A sequence of
N images is encoded as R1,R2,....RN,G1,...,GN,B1,...,BN where R_i is the red channel of frame i.
The number of pixels along the x,y,z, and c axes is called (in that order), width, height, depth and
spectrum. NB: Logical and integer values are automatically converted to type double. NAs are not
supported by CImg, so you should manage them on the R end of things.

Usage
cimg(X)

Arguments
X a four-dimensional numeric array

Value
an object of class cimg
Author(s)

Simon Barthelme

Examples

cimg(array(1,c(10,10,5,3)))

dimensions

Image dimensions

Description

Image dimensions

Usage

width(im)

height(im)

spectrum(im)

depth(im)

nPix(im)

Arguments

im an image

Functions

- width: Width of the image (in pixels)
- height: Height of the image (in pixels)
- spectrum: Number of colour channels
- depth: Depth of the image/number of frames in a video
- nPix: Total number of pixels (prod(dim(im)))
**Various shortcuts for extracting colour channels, frames, etc**

**Description**

Various shortcuts for extracting colour channels, frames, etc

Extract one frame out of a 4D image/video

**Usage**

```r
frame(im, index)
imcol(im, x)
imrow(im, y)
channel(im, ind)
R(im)
G(im)
B(im)
```

**Arguments**

- `im`: an image
- `index`: frame index
- `x`: x coordinate of the row
- `y`: y coordinate of the row
- `ind`: channel index

**Functions**

- `frame`: Extract frame
- `imcol`: Extract a particular column from an image
- `imrow`: Extract a particular row from an image
- `channel`: Extract an image channel
- `R`: Extract red channel
- `G`: Extract green channel
- `B`: Extract blue channel

**Author(s)**

Simon Barthelme
Examples

# Extract the red channel from the boats image, then the first row, plot
rw <- R(boats) %>% imrow(10)
plot(rw,type="l",xlab="x",ylab="Pixel value")
# Note that R(boats) returns an image
R(boats)
# while imrow returns a vector or a list
R(boats) %>% imrow(1) %>% str
imrow(boats,1) %>% str

---

cimg.use.openmp  

Control CImg's parallelisation

Description

On supported architectures CImg can parallelise many operations using OpenMP. Use this function to turn parallelisation on or off.

Usage

cimg.use.openmp(mode = "adaptive")

Arguments

mode  
Either "adaptive","always" or "none". The default is adaptive (parallelisation for large images only).

Value

NULL (function is used for side effects)

Author(s)

Simon Barthelme

Examples

cimg.use.openmp("never") # turn off parallelisation
cimg2im

Convert cimg to spatstat im object

Description

The spatstat library uses a different format for images, which have class "im". This utility converts a cimg object to an im object. spatstat im objects are limited to 2D grayscale images, so if the image has depth or spectrum > 1 a list is returned for the separate frames or channels (or both, in which case a list of lists is returned, with frames at the higher level and channels at the lower one).

Usage

cimg2im(img, W = NULL)

Arguments

img an image of class cimg
W a spatial window (see spatstat doc). Default NULL

Value

an object of class im, or a list of objects of class im, or a list of lists of objects of class im

Author(s)

Simon Barthelme

See Also

im, as.im

circles

Add circles to plot

Description

Base R has a function for plotting circles called "symbols". Unfortunately, the size of the circles is inconsistent across devices. This function plots circles whose radius is specified in used coordinates.

Usage

circles(x, y, radius, bg = NULL, fg = "white", ...)

Arguments

x  centers (x coordinate)
y  centers (y coordinate)
radius  radius (in user coordinates)
bg  background colour
fg  foreground colour
...  passed to polygon, e.g. lwd

Value

none, used for side effect

Author(s)

Simon Barthelme

See Also

hough_circle

clean  Clean up and fill in pixel sets (morphological opening and closing)

Description

Cleaning up a pixel set here means removing small isolated elements (speckle). Filling in means removing holes. Cleaning up can be achieved by shrinking the set (removing speckle), followed by growing it back up. Filling in can be achieved by growing the set (removing holes), and shrinking it again.

Usage

```r
clean(px, ...)
fill(px, ...)
```

Arguments

px  a pixset
...  parameters that define the structuring element to use, passed on to "grow" and "shrink"

Functions

- fill: Fill in holes using morphological closing
**Examples**

```r
im <- load.example("birds") %>% grayscale
sub <- imsub(-im,y> 380) %>% threshold("85%")
plot(sub)

# Turn into a pixel set
px <- sub==1
layout(t(1:2))
plot(px,main="Before clean-up")
clean(px,3) %>% plot(main="After clean-up")

# Now fill in the holes
px <- clean(px,3)
plot(px,main="Before filling-in")
fill(px,28) %>% plot(main="After filling-in")
```

---

**colorise**

*Fill in a colour in an area given by a pixset*

**Description**

Paint all pixels in pixset px with the same colour

**Usage**

```r
colorise(im, px, col, alpha = 1)
```

**Arguments**

- `im` an image
- `px` either a pixset or a formula, as in imeval.
- `col` colour to fill in. either a vector of numeric values or a string (e.g. "red")
- `alpha` transparency (default 1, no transparency)

**Value**

an image

**Author(s)**

Simon Barthelme
Examples

```r
im <- load.example("coins")
colorise(im,Xc(im) < 50,"blue") %>% plot
#Same thing with the formula interface
colorise(im,~ x < 50,"blue") %>% plot
#Add transparency
colorise(im,~ x < 50,"blue",alpha=.5) %>% plot
#Highlight pixels with low luminance values
colorise(im,~ . < 0.3,"blue",alpha=.2) %>% plot
```

common_pixsets

<table>
<thead>
<tr>
<th>common_pixsets</th>
<th>Various useful pixsets</th>
</tr>
</thead>
</table>

Description

These functions define some commonly used pixsets. `px.left` gives the left-most pixels of an image, `px.right` the right-most, etc. `px.circle` returns an (approximately) circular pixset of radius r, embedded in an image of width x and height y. Mathematically speaking, the set of all pixels whose L2 distance to the center equals r or less. `px.diamond` is similar but returns a diamond (L1 distance less than r) `px.square` is also similar but returns a square (Linf distance less than r).

Usage

```r
px.circle(r, x = 2 * r + 1, y = 2 * r + 1)
px.diamond(r, x = 2 * r + 1, y = 2 * r + 1)
px.square(r, x = 2 * r + 1, y = 2 * r + 1)
px.left(im, n = 1)
px.top(im, n = 1)
px.bottom(im, n = 1)
px.right(im, n = 1)
px.borders(im, n = 1)
px.all(im)
px.none(im)
```

Arguments

- `r` : radius (in pixels)
- `x` : width (default 2*r+1)
common_pixsets

\[
y \quad \text{height (default } 2r+1) \\
\text{im} \quad \text{an image} \\
n \quad \text{number of pixels to include}
\]

**Value**

a pixset

**Functions**

- `px.circle`: A circular-shaped pixset
- `px.diamond`: A diamond-shaped pixset
- `px.square`: A square-shaped pixset
- `px.left`: n left-most pixels (left-hand border)
- `px.top`: n top-most pixels
- `px.bottom`: n bottom-most pixels
- `px.right`: n right-most pixels
- `px.borders`: image borders (to depth n)
- `px.all`: all pixels in image
- `px.none`: no pixel in image

**Author(s)**

Simon Barthelme

**Examples**

```r
payne.circle(20,350,350) %>% plot(interp=FALSE)
payne.circle(3) %>% plot(interp=FALSE)
r <- 5
layout(t(1:3))
plot(px.circle(r,20,20))
plot(px.square(r,20,20))
plot(px.diamond(r,20,20))
#These pixsets are useful as structuring elements
px <- grayscale(boats) > .8
grow(px,px.circle(5)) %>% plot
#The following functions select pixels on the left, right, bottom, top of the image
im <- imfill(10,10)
px.left(im,3) %>% plot(int=FALSE)
px.right(im,1) %>% plot(int=FALSE)
px.top(im,4) %>% plot(int=FALSE)
px.bottom(im,2) %>% plot(int=FALSE)
#All of the above
px.borders(im,1) %>% plot(int=FALSE)
```
contours

Return contours of image/pixset

Description

This is just a light interface over contourLines. See help for contourLines for details. If the image has more than one colour channel, return a list with the contour lines in each channel. Does not work on 3D images.

Usage

contours(x, nlevels, ...)

Arguments

x an image or pixset
nlevels number of contour levels. For pixsets this can only equal two.
... extra parameters passed to contourLines

Value

a list of contours

Author(s)

Simon Bartheleme

See Also

highlight

Examples

boats.gs <- grayscale(boats)
c <- contours(boats.gs,nlevels=3)
plot(boats.gs)
# Add contour lines
purrr::walk(c,tion(v) lines(v$x,v$y,col="red"))
# Contours of a pixel set
px <- boats.gs > .8
plot(boats.gs)
c <- contours(px)
# Highlight pixset
purrr::walk(c,tion(v) lines(v$x,v$y,col="red"))
coord.index

Coordinates from pixel index

Description

Compute \((x,y,z,cc)\) coordinates from linear pixel index.

Usage

coord.index(im, index)

Arguments

- **im**: an image
- **index**: a vector of indices

Value

a data.frame of coordinate values

Author(s)

Simon Barthelme

See Also

index.coord for the reverse operation

Examples

```r
cind <- coord.index(boats,33)
#Returns \((x,y,z,cc)\) coordinates of the 33rd pixel in the array
cind
all.equal(boats[33],with(cind,at(boats,x,y,z,cc)))
all.equal(33,index.coord(boats,cind))
```

correlate

Correlation/convolution of image by filter

Description

The correlation of image \(im\) by filter \(flt\) is defined as: 
\[
res(x,y,z) = \sum_{i,j,k} im(x + i, y + j, z + k) \ast flt(i, j, k).
\]
The convolution of an image \(img\) by filter \(flt\) is defined to be: 
\[
res(x,y,z) = \sum_{i,j,k} img(x - i, y - j, z - k) \ast flt(i, j, k).
\]
**Usage**

```r
 correlate(im, filter, dirichlet = TRUE, normalise = FALSE)
 convolve(im, filter, dirichlet = TRUE, normalise = FALSE)
```

**Arguments**

- **im**: an image
- **filter**: the correlation kernel.
- **dirichlet**: boundary condition. Dirichlet if true, Neumann if false (default TRUE, Dirichlet)
- **normalise**: compute a normalised correlation (ie. local cosine similarity)

**Functions**

- convolve: convolve image with filter

**Examples**

```r
# Edge filter
filter <- as.cimg(function(x,y) sign(x-5),10,10)
layout(t(1:2))
# Convolution vs. correlation
correlate(boats,filter) %>% plot(main="Correlation")
convolve(boats,filter) %>% plot(main="Convolution")
```

---

**crop.borders**

_Crop the outer margins of an image_

**Description**

This function crops pixels on each side of an image. This function is a kind of inverse (centred) padding, and is useful e.g. when you want to get only the valid part of a convolution

**Usage**

```r
 crop.borders(im, nx = 0, ny = 0, nz = 0, nPix)
```

**Arguments**

- **im**: an image
- **nx**: number of pixels to crop along horizontal axis
- **ny**: number of pixels to crop along vertical axis
- **nz**: number of pixels to crop along depth axis
- **nPix**: optional: crop the same number of pixels along all dimensions
Value

an image

Author(s)

Simon Barzelme

Examples

# These two versions are equivalent
imfill(10,10) %>% crop.borders(nx=1,ny=1)
imfill(10,10) %>% crop.borders(nPix=1)

# Filter, keep valid part
 correlate(boats,imfill(3,3)) %>% crop.borders(nPix=2)

deriche

Description

The Deriche filter is a fast approximation to a Gaussian filter (order = 0), or Gaussian derivatives (order = 1 or 2).

Usage

deriche(im, sigma, order = 0L, axis = "x", neumann = FALSE)

Arguments

im an image
sigma Standard deviation of the filter.
order Order of the filter. 0 for a smoothing filter, 1 for first-derivative, 2 for second.
axis Axis along which the filter is computed ('x', 'y', 'z' or 'c').
neumann If true, use Neumann boundary conditions (default false, Dirichlet)

Examples

deriche(boats,sigma=2,order=0) %>% plot("Zeroth-order Deriche along x")
deriche(boats,sigma=2,order=1) %>% plot("First-order Deriche along x")
deriche(boats,sigma=2,order=1) %>% plot("Second-order Deriche along x")
deriche(boats,sigma=2,order=1,axis="y") %>% plot("Second-order Deriche along y")
**diffusion_tensors**

*Compute field of diffusion tensors for edge-preserving smoothing.*

**Description**

Compute field of diffusion tensors for edge-preserving smoothing.

**Usage**

```r
diffusion_tensors(
  im,
  sharpness = 0.7,
  anisotropy = 0.6,
  alpha = 0.6,
  sigma = 1.1,
  is_sqrt = FALSE
)
```

**Arguments**

- **im** an image
- **sharpness** Sharpness
- **anisotropy** Anisotropy
- **alpha** Standard deviation of the gradient blur.
- **sigma** Standard deviation of the structure tensor blur.
- **is_sqrt** Tells if the square root of the tensor field is computed instead.

---

**displacement**

*Estimate displacement field between two images.*

**Description**

Estimate displacement field between two images.

**Usage**

```r
displacement(
  sourceIm,
  destIm,
  smoothness = 0.1,
  precision = 5,
  nb_scales = 0L,
  iteration_max = 10000L,
  is_backward = FALSE
)
```
display

Arguments

- sourceIm: Reference image.
- destIm: Reference image.
- smoothness: Smoothness of estimated displacement field.
- precision: Precision required for algorithm convergence.
- nb_scales: Number of scales used to estimate the displacement field.
- iteration_max: Maximum number of iterations allowed for one scale.
- is_backward: If false, match I2(X + U(X)) = I1(X), else match I2(X) = I1(X - U(X)).

Description

cImg has its own functions for fast, interactive image plotting. Use this if you get frustrated with slow rendering in RStudio.

Usage

display(x, ...)

Arguments

- x: an image or a list of images
- ...: ignored

See Also

display.cimg, display.imlist

display.cimg

Description

Press escape or close the window to exit.

Usage

## S3 method for class 'cimg'
display(x, ..., rescale = TRUE)
Arguments

x an image (cimg object)
...
rescale if true pixel values are rescaled to [0-1] (default TRUE)

Examples

## Not run: interactive only
##display(boats,TRUE) #Normalisation on
##display(boats/2,TRUE) #Normalisation on, so same as above
##display(boats,FALSE) #Normalisation off
##display(boats/2,FALSE) #Normalisation off, so different from above

display.list Display image list using CImg library

Description

Click on individual images to zoom in.

Usage

## S3 method for class 'list'
display(x, ...)

Arguments

x a list of cimg objects
...

Examples

## Not run: interactive only
## imgradient(boats,"xy") %>% display
distance_transform

*Compute Euclidean distance function to a specified value.*

**Description**

The distance transform implementation has been submitted by A. Meijster, and implements the article 'W.H. Hesselink, A. Meijster, J.B.T.M. Roerdink, "A general algorithm for computing distance transforms in linear time.", In: Mathematical Morphology and its Applications to Image and Signal Processing, J. Goutsias, L. Vincent, and D.S. Bloomberg (eds.), Kluwer, 2000, pp. 331-340.' The submitted code has then been modified to fit CImg coding style and constraints.

**Usage**

```r
distance_transform(im, value, metric = 2L)
```

**Arguments**

- `im`: an image
- `value`: Reference value.
- `metric`: Type of metric. Can be `0=Chebyshev | 1=Manhattan | 2=Euclidean | 3=Squared-euclidean`.

**Examples**

```r
imd <- function(x,y) imdirac(c(100,100,1,1),x,y)
#Image is three white dots
im <- imd(20,20)+imd(40,40)+imd(80,80)
plot(im)
#How far are we from the nearest white dot?
distance_transform(im,1) %>% plot
```

---

draw_circle

*Draw circle on image*

**Description**

Add circle or circles to an image. Like other native CImg drawing functions, this is meant to be basic but fast. Use implot for flexible drawing.

**Usage**

```r
draw_circle(im, x, y, radius, color = "white", opacity = 1, filled = TRUE)
```
Arguments

- **im**: an image
- **x**: x coordinates
- **y**: y coordinates
- **radius**: radius (either a single value or a vector of length equal to length(x))
- **color**: either a string ("red"), a character vector of length equal to x, or a matrix of dimension length(x) times spectrum(im)
- **opacity**: scalar or vector of length equal to length(x). 0: transparent 1: opaque.
- **filled**: fill circle (default TRUE)

Value

an image

Author(s)

Simon Barthelme

See Also

implot

Examples

draw_circle(boats,c(50,100),c(150,200),30,"darkgreen") %>% plot
draw_circle(boats,125,60,radius=30,col=c(0,1,0),opacity=.2,filled=TRUE) %>% plot

draw_rect

Description

Add a rectangle to an image. Like other native CImg drawing functions, this is meant to be basic but fast. Use implot for flexible drawing.

Usage

draw_rect(im, x0, y0, x1, y1, color = "white", opacity = 1, filled = TRUE)
Arguments

```
im               an image
x0               x coordinate of the bottom-left corner
y0               y coordinate of the bottom-left corner
x1               x coordinate of the top-right corner
y1               y coordinate of the top-right corner
color            either a vector, or a string (e.g. "blue")
opacity          0: transparent 1: opaque.
filled            fill rectangle (default TRUE)
```

Value

an image

Author(s)

Simon Barthelme

See Also

implot, draw_circle

Examples

```
draw_rect(boats, 1, 1, 50, 50, "darkgreen") %>% plot
```

Description

Like other native CImg drawing functions, this is meant to be basic but fast. Use implot for flexible drawing.

Usage

```
draw_text(im, x, y, text, color, opacity = 1, fsize = 20)
```

Arguments

```
im               an image
x               x coord.
y               y coord.
text            text to draw (a string)
color           either a vector or a string (e.g. "red")
opacity         0: transparent 1: opaque.
fsize            font size (in pix., default 20)
```
Value

an image

Author(s)

Simon Barthelme

See Also

implot, draw_circle, draw_rect

Examples

draw_text(boats, 100, 100, "Some text", col = "black") %>% plot

---

erode 

Erode/dilate image by a structuring element.

Description

Erode/dilate image by a structuring element.

Usage

erode(im, mask, boundary_conditions = TRUE, real_mode = FALSE)
erode_rect(im, sx, sy, sz = 1L)
erode_square(im, size)
dilate(im, mask, boundary_conditions = TRUE, real_mode = FALSE)
dilate_rect(im, sx, sy, sz = 1L)
dilate_square(im, size)
mopening(im, mask, boundary_conditions = TRUE, real_mode = FALSE)
mopening_square(im, size)
mclosing_square(im, size)
mclosing(im, mask, boundary_conditions = TRUE, real_mode = FALSE)
erode

Arguments

- **im**: an image
- **mask**: Structuring element.
- **boundary_conditions**: Boundary conditions. If FALSE, pixels beyond image boundaries are considered to be 0, if TRUE one. Default: TRUE.
- **real_mode**: If TRUE, perform erosion as defined on the reals. If FALSE, perform binary erosion (default FALSE).
- **sx**: Width of the structuring element.
- **sy**: Height of the structuring element.
- **sz**: Depth of the structuring element.
- **size**: size of the structuring element.

Functions

- `erode_rect`: Erode image by a rectangular structuring element of specified size.
- `erode_square`: Erode image by a square structuring element of specified size.
- `dilate`: Dilate image by a structuring element.
- `dilate_rect`: Dilate image by a rectangular structuring element of specified size
- `dilate_square`: Dilate image by a square structuring element of specified size
- `mopening`: Morphological opening (erosion followed by dilation)
- `mopening_square`: Morphological opening by a square element (erosion followed by dilation)
- `mclosing_square`: Morphological closing by a square element (dilation followed by erosion)
- `mclosing`: Morphological closing (dilation followed by erosion)

Examples

```r
fname <- system.file('extdata/Leonardo_Birds.jpg',package='imager')
im <- load.image(fname) %>% grayscale
outline <- threshold(-im,"95%")
plot(outline)
mask <- imfill(5,10,val=1) #Rectangular mask
plot(erosion(outline,mask))
plot(erosion_rect(outline,5,10)) #Same thing
plot(erosion_square(outline,5))
plot(dilation(outline,mask))
plot(dilation_rect(outline,5,10))
plot(dilation_square(outline,5))
```
extract_patches  

Extract image patches and return a list

Description

Patches are rectangular (cubic) image regions centered at cx, cy (cz) with width wx and height wy (opt. depth wz) WARNINGS: - values outside of the image region are subject to boundary conditions. The default is to set them to 0 (Dirichlet), other boundary conditions are listed below. - widths and heights should be odd integers (they're rounded up otherwise).

Usage

extract_patches(im, cx, cy, wx, wy, boundary_conditions = 0L)

extract_patches3D(im, cx, cy, cz, wx, wy, wz, boundary_conditions = 0L)

Arguments

- **im**: an image
- **cx**: vector of x coordinates for patch centers
- **cy**: vector of y coordinates for patch centers
- **wx**: vector of patch widths (or single value)
- **wy**: vector of patch heights (or single value)
- **boundary_conditions**: integer. Can be 0 (Dirichlet, default), 1 (Neumann) 2 (Periodic) 3 (mirror).
- **cz**: vector of z coordinates for patch centers
- **wz**: vector of coordinates for patch depth

Value

a list of image patches (cimg objects)

Functions

- `extract_patches3D`: Extract 3D patches

Examples

#2 patches of size 5x5 located at (10,10) and (10,20)
extract_patches(boats,c(10,10),c(10,20),5,5)
FFT

Compute the Discrete Fourier Transform of an image

Description

This function is equivalent to R's builtin fft, up to normalisation (R's version is unnormalised, this one is). It calls CImg's implementation. Important note: FFT will compute a multidimensional Fast Fourier Transform, using as many dimensions as you have in the image, meaning that if you have a colour video, it will perform a 4D FFT. If you want to compute separate FFTs across channels, use imsplit.

Usage

FFT(im.real, im.imag, inverse = FALSE)

Arguments

im.real: The real part of the input (an image)
im.imag: The imaginary part (also an image. If missing, assume the signal is real).
inverse: If true compute the inverse FFT (default: FALSE)

Value

a list with components "real" (an image) and "imag" (an image), corresponding to the real and imaginary parts of the transform

Author(s)

Simon Barthelme

Examples

im <- as.cimg(function(x,y) sin(x/5)+cos(x/4)*sin(y/2),128,128)
ff <- FFT(im)
plot(ff$real,main="Real part of the transform")
plot(ff$imag,main="Imaginary part of the transform")
sqrt(ff$real^2+ff$imag^2) %>% plot(main="Power spectrum")
#Check that we do get our image back
check <- FFT(ff$real,ff$imag,inverse=TRUE)$real #Should be the same as original
mean((check-im)^2)
flatten.alpha

Flatten alpha channel

Description

Flatten alpha channel

Usage

flatten.alpha(im, bg = "white")

Arguments

- **im**: an image (with 4 RGBA colour channels)
- **bg**: background: either an RGB image, or a vector of colour values, or a string (e.g. "blue"). Default: white background.

Value

a blended image

Author(s)

Simon Barthelme

See Also

rm.alpha

Examples

#Add alpha channel
alpha <- Xc(grayscale(boats))/width(boats)
boats.a <- imlist(boats, alpha) %>% imappend("c")
flatten.alpha(boats.a) %>% plot
flatten.alpha(boats.a, "darkgreen") %>% plot
frames

**Split a video into separate frames**

**Description**

Split a video into separate frames

**Usage**

frames(im, index, drop = FALSE)

**Arguments**

- **im**: an image
- **index**: which channels to extract (default all)
- **drop**: if TRUE drop extra dimensions, returning normal arrays and not cimg objects

**Value**

a list of frames

**See Also**

channels

---

get.locations

**Return coordinates of subset of pixels**

**Description**

Typical use case: you want the coordinates of all pixels with a value above a certain threshold

**Usage**

get.locations(im, condition)

**Arguments**

- **im**: the image
- **condition**: a function that takes scalars and returns logicals

**Value**

coordinates of all pixels such that condition(pixel) == TRUE
get.stencil

Author(s)
Simon Barhleme

Examples

```r
im <- as.cimg(function(x,y) x+y,10,10)
get.locations(im, function(v) v < 4)
get.locations(im, function(v) v^2 + 3*v - 2 < 30)
```

get.stencil

Return pixel values in a neighbourhood defined by a stencil

Description

A stencil defines a neighbourhood in an image (for example, the four nearest neighbours in a 2d image). This function centers the stencil at a certain pixel and returns the values of the neighbouring pixels.

Usage

```r
get.stencil(im, stencil, ...)
```

Arguments

- `im`: an image
- `stencil`: a data.frame with values `dx`, `dy`, `[dz]`, `[dcc]` defining the neighbourhood
- `...`: where to center, e.g. `x=100,y=10,z=3,cc=1`

Value

pixel values in neighbourhood

Author(s)

Simon Barhleme

Examples

```r
# The following stencil defines a neighbourhood that
# includes the next pixel to the left (delta_x = -1) and the next pixel to the right (delta_x = 1)
stencil <- data.frame(dx=c(-1,1), dy=c(0,0))
im <- as.cimg(function(x,y) x+y, w=100, h=100)
get.stencil(im, stencil, x=50, y=50)

# A larger neighbourhood that includes pixels upwards and downwards of center (delta_y = -1 and +1)
stencil <- stencil.cross()
im <- as.cimg(function(x,y) x, w=100, h=100)
get.stencil(im, stencil, x=5, y=50)
```
**get_gradient**

*Compute image gradient.*

**Description**

Compute image gradient.

**Usage**

```r
get_gradient(im, axes = "", scheme = 3L)
```

**Arguments**

- `im`: an image
- `axes`: Axes considered for the gradient computation, as a C-string (e.g. "xy").
- `scheme`: Numerical scheme used for the gradient computation: 1 = Backward finite differences 0 = Centered finite differences 1 = Forward finite differences 2 = Using Sobel masks 3 = Using rotation invariant masks 4 = Using Deriche recursive filter. 5 = Using Van Vliet recursive filter.

**Value**

A list of images (corresponding to the different directions)

**See Also**

`imgradient`

---

**get_hessian**

*Return image hessian.*

**Description**

Return image hessian.

**Usage**

```r
get_hessian(im, axes = "")
```

**Arguments**

- `im`: an image
- `axes`: Axes considered for the hessian computation, as a character string (e.g. "xy").
grab

Select image regions interactively

Description

These functions let you select a shape in an image (a point, a line, or a rectangle). They either return the coordinates of the shape (default), or the contents. In case of lines contents are interpolated. Note that grabLine does not support the "pixset" return type.

Usage

```r
grabLine(im, output = "coord")
grabRect(im, output = "coord")
grabPoint(im, output = "coord")
```

Arguments

- `im` an image
- `output` one of "im","pixset","coord","value". Default "coord"

Value

Depending on the value of the output parameter. Either a vector of coordinates (output = "coord"), an image (output = "im"), a pixset (output = "pixset"), or a vector of values (output = "value").

grabLine and grabPoint support the "value" output mode and not the "im" output.

Author(s)

Simon Barthelme

See Also

display

Examples

```r
##Not run: interactive only
##grabRect(boats)
##grabRect(boats,TRUE)
```
grayscale

Convert an RGB image to grayscale

Description

This function converts from RGB images to grayscale

Usage

grayscale(im, method = "Luma", drop = TRUE)

Arguments

im an RGB image
method either "Luma", in which case a linear approximation to luminance is used, or "XYZ", in which case the image is assumed to be in sRGB color space and CIE luminance is used.
drop if TRUE returns an image with a single channel, otherwise keep the three channels (default TRUE)

Value

a grayscale image (spectrum == 1)

Examples

grayscale(boats) %>% plot
#In many pictures, the difference between Luma and XYZ conversion is subtle
grayscale(boats, method="XYZ") %>% plot
grayscale(boats, method="XYZ", drop=FALSE) %>% dim

grow

Grow/shrink a pixel set

Description

Grow/shrink a pixel set through morphological dilation/erosion. The default is to use square or rectangular structuring elements, but an arbitrary structuring element can be given as input. A structuring element is a pattern to be moved over the image: for example a 3x3 square. In "shrink" mode, a element of the pixset is retained only if and only the structuring element fits entirely within the pixset. In "grow" mode, the structuring element acts like a neighbourhood: all pixels that are in the original pixset *or* in the neighbourhood defined by the structuring element belong the new pixset.
Usage

\[
grow(px, x, y = x, z = x, \text{boundary} = \text{TRUE})
\]

\[
\text{shrink}(px, x, y = x, z = x, \text{boundary} = \text{TRUE})
\]

Arguments

- **px**: a pixset
- **x**: either an integer value, or an image/pixel set.
- **y**: width of the rectangular structuring element (if x is an integer value)
- **z**: depth of the rectangular structuring element (if x is an integer value)
- **boundary**: are pixels beyond the boundary considered to have value TRUE or FALSE (default TRUE)

Functions

- **shrink**: shrink pixset using erosion

Examples

```r
# A pixel set:
a <- grayscale(boats) > .8
plot(a)
# Grow by a 8x8 square
grow(a, 8) %>% plot
# Grow by a 8x2 rectangle
grow(a, 8, 2) %>% plot
# Custom structuring element
e1 <- matrix(1, 2, 2) %>% as.cimg
all.equal(grow(a, e1), grow(a, 2))
# Circular structuring element
px.circ(5) %>% grow(a, .) %>% plot
# Sometimes boundary conditions matter
im <- imfill(10, 10)
px <- px.all(im)
shrink(px, 3, bound = TRUE) %>% plot(main = "Boundary conditions: TRUE")
shrink(px, 3, bound = FALSE) %>% plot(main = "Boundary conditions: FALSE")
```

gsdim

**Grayscale dimensions of image**

Description

Shortcut, returns the dimensions of an image if it had only one colour channel

Usage

```
gsdim(im)
```
**Arguments**

im an image

**Value**

returns c(dim(im)[1:3],1)

**Author(s)**

Simon Barthelme

**Examples**

imnoise(dim=gsdim(boats))

---

**haar**

*Compute Haar multiscale wavelet transform.*

**Description**

Compute Haar multiscale wavelet transform.

**Usage**

haar(im, inverse = FALSE, nb_scales = 1L)

**Arguments**

im an image

inverse Compute inverse transform (default FALSE)

nb_scales Number of scales used for the transform.

**Examples**

#Image compression: set small Haar coefficients to 0
hr <- haar(boats,nb=3)
mask.low <- threshold(abs(hr),"75%")
mask.high <- threshold(abs(hr),"95%")
haar(hr*mask.low,inverse=TRUE,nb=3) %>% plot(main="75% compression")
haar(hr*mask.high,inverse=TRUE,nb=3) %>% plot(main="95% compression")
**highlight**

*Highlight pixel set on image*

**Description**

Overlay an image plot with the contours of a pixel set. Note that this function doesn’t do the image plotting, just the highlighting.

**Usage**

highlight(px, col = "red", ...)

**Arguments**

- **px**: a pixel set
- **col**: color of the contours
- **...**: passed to the "lines" function

**Author(s)**

Simon Barthelme

**See Also**

colorise, another way of highlighting stuff

**Examples**

#Select similar pixels around point (180,200)
px <- px.flood(boats,180,200,sigma=.08)
plot(boats)
#Highlight selected set
highlight(px)
px.flood(boats,18,50,sigma=.08) %>% highlight(col="white",lwd=3)

---

**hough_circle**

*Circle detection using Hough transform*

**Description**

Detects circles of known radius in a pixset. The output is an image where the pixel value at (x,y) represents the amount of evidence for the presence of a circle of radius r at position (x,y). NB: in the current implementation, does not detect circles centred outside the limits of the pixset.

**Usage**

hough_circle(px, radius)
**hough_line**

**Arguments**

- `px`: a pixset (e.g., the output of a Canny detector)
- `radius`: radius of circle

**Value**

a histogram of Hough scores, with the same dimension as the original image.

**Author(s)**

Simon Barthelme

**Examples**

```r
im <- load.example('coins')
px <- cannyEdges(im)
#Find circles of radius 20
hc <- hough_circle(px, 20)
plot(hc)
#Clean up, run non-maxima suppression
nms <- function(im,sigma) { im[dilate_square(im,sigma) != im] <- 0; im}
hc.clean <- isoblur(hc, 3) %>% nms(50)
#Top ten matches
df <- as.data.frame(hc.clean) %>%
dplyr::arrange(desc(value)) %>%
head(10)
with(df, circles(x, y, 20, fg="red", lwd=3))
```

**Description**

Two algorithms are used, depending on the input: if the input is a pixset then the classical Hough transform is used. If the input is an image, then a faster gradient-based heuristic is used. The method returns either an image (the votes), or a data.frame. In both cases the parameterisation used is the Hesse normal form (theta, rho), where a line is represented as the set of values such that cos(theta)*x + sin(theta)*y = rho. Here theta is an angle and rho is a distance. The image form returns a histogram of scores in (rho, theta) space, where good candidates for lines have high scores. The data.frame form may be more convenient for further processing in R: each line represents a pair (rho, theta) along with its score. If the 'shift' argument is true, then the image is assumed to start at x=1, y=1 (more convenient for plotting in R). If false, the image begins at x=0, y=0 and in both cases the origin is at the top left.

**Usage**

```r
hough_line(im, ntheta = 100, data.frame = FALSE, shift = TRUE)
```
Arguments

- im: an image or pixset
- ntheta: number of bins along theta (default 100)
- data.frame: return a data.frame? (default FALSE)
- shift: if TRUE, image is considered to begin at (x=1,y=1).

Value

either an image or a data.frame

Author(s)

Simon Barthelme

Examples

```r
# Find the lines along the boundary of a square
px <- px.square(30, 80, 80) %>% boundary
plot(px)
# Hough transform
hough_line(px, ntheta=200) %>% plot

df <- hough_line(px, ntheta=800, data.frame=TRUE)
# Plot lines with the highest score
plot(px)
with(subset(df, score > quantile(score,.9995)), nfline(theta, rho, col="red"))

plot(boats)
df <- hough_line(boats, ntheta=800, data=TRUE)
```

Description

Shorthand for imsplit followed by purrr::map_df

Usage

```r
idply(im, axis, fun, ...)
```

Arguments

- im: image
- axis: axis for the split (e.g. "c")
- fun: function to apply
- ...: extra arguments to function fun
Examples

idply(boats,"c",mean) #mean luminance per colour channel

iiply

Split an image, apply function, recombine the results as an image

Description

This is just imsplit followed by purrr::map followed by imappend

Usage

iiply(im, axis, fun, ...)

Arguments

im image
axis axis for the split (e.g "c")
fun function to apply
... extra arguments to function fun

Examples

##' #Normalise colour channels separately, recombine
iiply(boats,"c",function(v) (v-mean(v))/sd(v)) %>% plot

ilply

Split an image along axis, apply function, return a list

Description

Shorthand for imsplit followed by purrr::map

Usage

ilply(im, axis, fun, ...)

Arguments

im image
axis axis for the split (e.g "c")
fun function to apply
... extra arguments for function fun
Examples

    parrots <- load.example("parrots")
    ilply(parrots,"c",mean) # mean luminance per colour channel

---

**im2cimg**  
*Convert an image in spatstat format to an image in cimg format*

---

**Description**

as.cimg.im is an alias for the same function

**Usage**

    im2cimg(img)

**Arguments**

    img  
    a spatstat image

**Value**

    a cimg image

**Author(s)**

Simon Barthelme

---

**imager**  
*imager: an R library for image processing, based on CImg*

---

**Description**

CImg by David Tschumperle is a C++ library for image processing. It provides most common functions for image manipulation and filtering, as well as some advanced algorithms. imager makes these functions accessible from R and adds many utilities for accessing and working with image data from R. You should install ImageMagick if you want support for image formats beyond PNG and JPEG, and ffmpeg if you need to work with videos (in which case you probably also want to take a look at experimental package imagerstreams on github). Package documentation is available at http://dahtah.github.io/imager/.
imager.combine

Combining images

Description

These functions take a list of images and combine them by adding, multiplying, taking the parallel min or max, etc. The max. in absolute value of (x1,x2) is defined as x1 if (|x1| > |x2|), x2 otherwise. It’s useful for example in getting the most extreme value while keeping the sign. "parsort","parrank" and "parorder" aren’t really reductions because they return a list of the same size. They perform a pixel-wise sort (resp. order and rank) across the list. parvar returns an unbiased estimate of the variance (as in the base var function). parsd returns the square root of parvar.

Usage

add(x, na.rm = FALSE)

wsum(x, w, na.rm = FALSE)

average(x, na.rm = FALSE)

mult(x, na.rm = FALSE)

parmax(x, na.rm = FALSE)

parmax.abs(x)

parmin.abs(x)

parmin(x, na.rm = FALSE)

enorm(x)

parmed(x, na.rm = FALSE)

parvar(x, na.rm = FALSE)

parsd(x, na.rm = FALSE)

parall(x)

parany(x)

equal(x)

which.parmax(x)

which.parmin(x)
parsort(x, increasing = TRUE)
parorder(x, increasing = TRUE)
parrank(x, increasing = TRUE)

Arguments

x a list of images
na.rm ignore NAs (default FALSE)
w weights (must be the same length as the list)
increasing if TRUE, sort in increasing order (default TRUE)

Functions

- add: Add images
- wsum: Weighted sum of images
- average: Average images
- mult: Multiply images (pointwise)
- parmax: Parallel max over images
- parmax.abs: Parallel max in absolute value over images,
- parmin.abs: Parallel min in absolute value over images,
- parmin: Parallel min over images
- enorm: Euclidean norm (i.e. \( \sqrt{A^2 + B^2 + \ldots} \))
- parmed: Median
- parvar: Variance
- parsd: Std. deviation
- parall: Parallel all (for pixsets)
- parany: Parallel any (for pixsets)
- equal: Test equality
- which.parmax: index of parallel maxima
- which.parmin: index of parallel minima
- parsort: pixel-wise sort
- parorder: pixel-wise order
- parrank: pixel-wise rank

Author(s)

Simon Barthelme
See Also

imsplit, Reduce

Examples

```r
im1 <- as.cimg(function(x,y) x,50,50)
im2 <- as.cimg(function(x,y) y,50,50)
im3 <- as.cimg(function(x,y) cos(x/10),50,50)
l <- imlist(im1,im2,im3)
add(l) %>% plot #Add the images
average(l) %>% plot #Average the images
mult(l) %>% plot #Multiply
wsum(l,c(.1,8,.1)) %>% plot #Weighted sum
parmax(l) %>% plot #Parallel max
parmin(l) %>% plot #Parallel min
parmed(l) %>% plot #Parallel median
parsd(l) %>% plot #Parallel std. dev
#parsort can also be used to produce parallel max. and min
(par(sort(l))[[1]]) %>% plot("Parallel min")
(par(sort(l))[[length(l)]])) %>% plot("Parallel max")
#Resize boats so the next examples run faster
im <- imresize(boats,.5)
#Edge detection (Euclidean norm of gradient)
imgradient(im,"xy") %>% enorm %>% plot
#Pseudo-artistic effects
l <- map_il(seq(1,35,5),~ boxblur(im,.))
parmin(l) %>% plot
average(l) %>% plot
mult(l) %>% plot
#At each pixel, which colour channel has the maximum value?
imsplit(im,"c") %>% which.parmax %>% table
#Same thing using parorder (ties are broken differently)!!!
imsplit(im,"c") %>% { parorder(.)[[length(.)]] } %>% table
```

**Description**

These replacement functions let you modify part of an image (for example, only the red channel). Note that cimg objects can also be treated as regular arrays and modified using the usual \[\] operator.

**Usage**

```r
channel(x, ind) <- value
R(x) <- value
G(x) <- value
```
\[ B(x) \leftarrow \text{value} \]
\[ \text{frame}(x, \text{ind}) \leftarrow \text{value} \]

**Arguments**

- **x**: an image to be modified
- **ind**: an index
- **value**: the image to insert

**Functions**

- `channel<-`: Replace image channel
- `R<-`: Replace red channel
- `G<-`: Replace green channel
- `B<-`: Replace blue channel
- `frame<-`: Replace image frame

**See Also**

`imdraw`

**Examples**

```r
boats.cp <- boats
# Set the green channel in the boats image to 0
G(boats.cp) <- 0
# Same thing, more verbose
channel(boats.cp, 2) <- 0
# Replace the red channel with noise
R(boats.cp) <- imnoise(width(boats), height(boats))
# A new image with 5 frames
tmp <- imfill(10, 10, 5)
# Fill the third frame with noise
frame(tmp, 3) <- imnoise(10, 10)
```

---

**imager.subset**

*Array subset operator for cimg objects*

**Description**

Internally, cimg objects are 4D arrays (stored in x,y,z,c mode) but often one doesn’t need all dimensions. This is the case for instance when working on grayscale images, which use only two. The array subset operator works like the regular array [] operator, but it won’t force you to use all dimensions. There are easier ways of accessing image data, for example `imsub`, `channels`, `R`, `G`, `B`, and the like.
Arguments

- `x` an image (cimg object)
- `drop` if true return an array, otherwise return an image object (default FALSE)
- `...` subsetting arguments

See Also

imsub, which provides a more convenient interface, autocrop, imdraw

Examples

```r
im <- imfill(4,4)
dim(im) #4 dimensional, but the last two ones are singletons
im[,1,,] <- 1:4 #Assignment the standard way
im[,1] <- 1:4 #Shortcut
as.matrix(im)
im[1:2,]
dim(boats)
#Arguments will be recycled, as in normal array operations
boats[1:2,1:3,] <- imnoise(2,3) #The same noise array is replicated over the three channels
```
Examples

```r
imappend(list(boats,boats),"x") %>% plot
imappend(list(boats,boats),"y") %>% plot
purrr::map(1:3, ~imnoise(100,100)) %>% imappend("c") %>% plot
boats.gs <- grayscale(boats)
purrr::map(seq(1,5,l=3),function(v) isoblur(boats.gs,v)) %>% imappend("c") %>% plot
#imappend also works on pixsets
imsplit(boats > .5,"c") %>% imappend("x") %>% plot
```

---

**imchange**

Modify parts of an image

Description

A shortcut for modifying parts of an image, using imeval syntax. See doc for imeval first. As part of a pipe, avoids the creating of intermediate variables.

Usage

```r
imchange(obj, where, fo, env = parent.frame())
```

Arguments

- `obj`: an image or imlist
- `where`: where to modify. a pixset, or a formula (in imeval syntax) that evaluates to a pixset.
- `fo`: a formula (in imeval syntax) used to modify the image part
- `env`: evaluation environment (see imeval)

Value

a modified image

Author(s)

Simon Barthelme

See Also

imeval
Examples

# Set border to 0:
imchange(boats, px.borders(boats, 10), ~ 0) %>% plot
# Eq. to
im <- boats
im[px.borders(im, 10)] <- 0
# Using formula syntax
imchange(boats, ~ px.borders(., 10), ~ 0)
# Replace with grayscale ramp
imchange(boats, ~ px.borders(., 10), ~ xs) %>% plot
# Kill red channel in image
imchange(boats, ~ c==1, ~ 0) %>% plot
# Shit hue by an amount depending on eccentricity
load.example("parrots") %>%
  RGBtoHSL %>%
inchange(~ c==1, ~ .+80*exp(-((rho/550)^2)) ) %>%
  HSLtoRGB %>%
  plot

---

imcoord

**Coordinates as images**

Description

These functions return pixel coordinates for an image, as an image. All is made clear in the examples (hopefully)

Usage

Xc(im)

Yc(im)

Zc(im)

Cc(im)

Arguments

im an image

Value

another image of the same size, containing pixel coordinates
Functions

- $X_c$: X coordinates
- $Y_c$: Y coordinates
- $Z_c$: Z coordinates
- $C_c$: C coordinates

See Also

as.cimg.function, pixel.grid

Examples

```r
im <- imfill(5,5) #An image
Xc(im) #An image of the same size, containing the x coordinates of each pixel
Xc(im) %>% imrow(1)
Yc(im) %>% imrow(3) #y is constant along rows
Yc(im) %>% imcol(1)
#Mask bits of the boats image:
plot(boats*(Xc(boats) < 100))
plot(boats*(dnorm(Xc(boats),m=100,sd=30))) #Gaussian window
```

---

imdirac

Generates a "dirac" image, i.e. with all values set to 0 except one.

Description

This small utility is useful to examine the impulse response of a filter

Usage

```r
imdirac(dims, x, y, z = 1, cc = 1)
```

Arguments

- `dims`: a vector of image dimensions, or an image whose dimensions will be used. If `dims` has length < 4 some guesswork will be used (see examples and ?as.cimg.array)
- `x`: where to put the dirac (x coordinate)
- `y`: y coordinate
- `z`: z coordinate (default 1)
- `cc`: colour coordinate (default 1)

Value

an image
**Author(s)**

Simon Bartheleme

**Examples**

```r
# Explicit settings of all dimensions
imdirac(c(50,50,1,1),20,20)
imdirac(c(50,50),20,20) # Implicit
imdirac(c(50,50,3),20,20,cc=2) # RGB
imdirac(c(50,50,7),20,20,z=2) # 50x50 video with 7 frames

# Impulse response of the blur filter
imdirac(c(50,50),20,20) %>% isoblur(sigma=2) %>% plot

# Impulse response of the first-order Deriche filter
imdirac(c(50,50),20,20) %>% deriche(sigma=2,order=1,axis="x") %>% plot

## NOT RUN, interactive only
## Impulse response of the blur filter in space-time
## resp <- imdirac(c(50,50,100),x=25,y=25,z=50) %>% isoblur(16)
### Normalise to 0...255 and play as video
### renorm(resp) %>% play(normalise=FALSE)
```

**Description**

Draw image on another image

**Usage**

```r
imdraw(im, sprite, x = 1, y = 1, z = 1, opacity = 1)
```

**Arguments**

- **im**: background image
- **sprite**: sprite to draw on background image
- **x**, **y**, **z**: location
- **opacity**: transparency level (default 1)

**Author(s)**

Simon Bartheleme

**See Also**

imager.combine, for different ways of combining images
Examples

```r
im <- load.example("parrots")
boats.small <- imresize(boats,.5)
#I'm aware the result is somewhat ugly
imdraw(im,boats.small,x=400,y=10,opacity=.7) %>% plot
```

Description

imeval does for images what "with" does for data.frames, namely contextual evaluation. It provides various shortcuts for pixel-wise operations. imdo runs imeval, and reshapes the output as an image of the same dimensions as the input (useful for functions that return vectors). imeval takes inspiration from purrr::map in using formulas for defining anonymous functions using the "." argument. Usage is made clear (hopefully) in the examples. The old version of imeval used CImg’s internal math parser, but has been retired.

Usage

```r
imeval(obj, ..., env = parent.frame())
imdo(obj, form)
```

Arguments

- **obj**: an image, pixset or imlist
- **...**: one or more formula objects, defining anonymous functions that will be evaluated with the image as first argument (with extra contextual variables added to the evaluation context)
- **env**: additional variables (defaults to the calling environment)
- **form**: a single formula

Functions

- **imdo**: run imeval and reshape

Author(s)

Simon Barthelme

See Also

imchange, which modifies specific parts of an image
Examples

```r
## Computing mean absolute deviation
imeval(boats, ~ mean(abs(. - median(.))))
### Equivalent to:
mean(abs(boats - median(boats)))
## Two statistics
imeval(boats, mad = ~ mean(abs(. - median(.))), sd = ~ sd(.))
### imeval can precompute certain quantities, like the x or y coord. of each pixel
imeval(boats, ~ x) %>% plot
### Same as Xc(boats) %>% plot
## Other predefined quantities:
## w is width, h is height
imeval(boats, ~ x/w) %>% range
### It defines certain transformed coordinate systems:
### Scaled x, y, z
## xs = x/w
## ys = y/h
### Select upper-left quadrant (returns a pixset)
imeval(boats, ~ xs < .5 & ys < .5) %>% plot
### Fade effect
imeval(boats, ~ xs*. ) %>% plot
### xc and yc are another set of transformed coordinates
### where xc = 0, yc = 0 is the image center
imeval(boats, ~ (abs(xc)/w)*. ) %>% plot

### rho, theta: circular coordinates. rho is distance to center (in pix.), theta angle
### Gaussian mask with sd 10 pix.
blank <- imfill(30,30)
imeval(blank, ~ dnorm(rho, sd=w/3)) %>% plot(int=FALSE)
imeval(blank, ~ theta) %>% plot
### imeval is made for interactive use, meaning it
### accesses the environment it got called from, e.g. this works:
f <- function()
{
    im1 <- imfill(3,3,val=1)
im2 <- imfill(3,3,val=3)

    imeval(im1, ~ .+im2)
}
f()
### imeval accepts lists as well
map_il(1:3, ~ isoblur(boats,.)) %>%
    imeval(~ xs*. ) %>%
    plot

### imeval is useful for defining pixsets:
### here, all central pixels that have value under the median
grayscale(boats) %>%
    imeval(~ (. > median(.)) & rho < 150) %>%
    plot
### Other abbreviations are defined:
### s for imshift, b for isoblur, rot for imrotate.
```
## imfill

Create an image of custom size by filling in repeated values

**Description**

This is a convenience function for quickly creating blank images, or images filled with a specific colour. See examples. If `val` is a logical value, creates a pixset instead.

**Usage**

```r
imfill(x = 1, y = 1, z = 1, val = 0, dim = NULL)
```

**Arguments**

- `x` width (default 1)
- `y` height (default 1)
- `z` depth (default 1)
- `val` fill-in values. Either a single value (for grayscale), or RGB values for colour, or a character string for a colour (e.g. "blue")
- `dim` dimension vector (optional, alternative to specifying x,y,z)

**Value**

an image object (class cimg)

**Author(s)**

Simon Barthelme

**Examples**

```r
imfill(20,20) %>% plot #Blank image of size 20x20
imfill(20,20,val=c(1,0,0)) %>% plot #All red image
imfill(20,20,val="red") %>% plot #Same, using R colour name
imfill(3,3,val=FALSE) #Pixset
imfill(dim=dim(boats)) #Blank image of the same size as the boats image
```
imgradient  
Compute image gradient

Description
Light interface for get_gradient. Refer to get_gradient for details on the computation.

Usage
imgradient(im, axes = "xy", scheme = 3)

Arguments
- **im**: an image of class cimg
- **axes**: direction along which to compute the gradient. Either a single character (e.g. "x"), or multiple characters (e.g. "xyz"). Default: "xy"
- **scheme**: numerical scheme (default '3', rotation invariant)

Value
an image or a list of images, depending on the value of "axes"

Author(s)
Simon Barthelme

Examples
grayscale(boats) %>% imgradient("x") %>% plot
imgradient(boats,"xy") #Returns a list

imhessian  
Compute image hessian.

Description
Compute image hessian.

Usage
imhessian(im, axes = c("xx", "xy", "yy"))

Arguments
- **im**: an image
- **axes**: Axes considered for the hessian computation, as a character string (e.g "xy" corresponds to d/(dx*dy)). Can be a list of axes. Default: xx,xy,yy
Value

an image, or a list of images

Examples

imhessian(boats,"xy") %>% plot(main="Second-derivative, d/(dx\,dy)")

---

**iminfo**  
*Return information on image file*

Description

This function calls ImageMagick's "identify" utility on an image file to get some information. You need ImageMagick on your path for this to work.

Usage

iminfo(fname)

Arguments

fname  
path to a file

Value

a list with fields name, format, width (pix.), height (pix.), size (bytes)

Author(s)

Simon Barthelme

Examples

```r
## Not run:
someFiles <- dir("*.png") #Find all PNGs in directory
iminfo(someFiles[[1]])
#Get info on all files, as a data frame
info <- purrr::map_df(someFiles,function(v) iminfo(v) %>% as.data.frame)
## End(Not run)
```
imlap  

Compute image Laplacian

Description

The Laplacian is the sum of second derivatives, approximated here using finite differences.

Usage

imlap(im)

Arguments

im  
an image

Examples

imlap(boats) %>% plot

imlist  

Image list

Description

An imlist object is simply a list of images (of class cimg). For convenience, some generic functions are defined that wouldn’t work on plain lists, like plot, display and as.data.frame. DEPRECATION NOTE: in v0.30 of imager, the original behaviour of the "imlist" function was to take a list and turn it into an image list. This behaviour has now been changed to make "imlist" be more like "list". If you wish to turn a list into an image list, use as.imlist.

Usage

imlist(...)  

Arguments

...  
images to be included in the image list

See Also

plot.imlist, display.imlist, as.data.frame.imlist

Examples

imlist(a=imfill(3,3),b=imfill(10,10))  
imsplit(boats,"x",6)  
imsplit(boats,"x",6) %>% plot
imnoise

Generate (Gaussian) white-noise image

Description

A white-noise image is an image where all pixel values are drawn IID from a certain distribution. Here they are drawn from a Gaussian.

Usage

imnoise(x = 1, y = 1, z = 1, cc = 1, mean = 0, sd = 1, dim = NULL)

Arguments

x                width
y                height
z                depth
cc               spectrum
mean            mean pixel value (default 0)
sd              std. deviation of pixel values (default 1)
dim             dimension vector (optional, alternative to specifying x,y,z,cc)

Value

a cimg object

Author(s)

Simon Barthelme

Examples

imnoise(100,100,cc=3) %>% plot(main="White noise in RGB")
imnoise(100,100,cc=3) %>% isoblur(5) %>% plot(main="Filtered (non-white) noise")
imnoise(dim=dim(boats)) #Noise image of the same size as the boats image
Description
This function lets you use an image as a canvas for base graphics, meaning you can use R functions like "text" and "points" to plot things on an image. The function takes as argument an image and an expression, executes the expression with the image as canvas, and outputs the result as an image (of the same size).

Usage

`implot(im, expr, ...)`

Arguments

- `im`: an image (class cimg)
- `expr`: an expression (graphics code to execute)
- `...`: passed on to plot.cimg, to control the initial rendering of the image (for example the colorscale)

Value
an image

Author(s)
Simon Barthelme

See Also
plot, capture.plot

Examples

```r
## Not run:
b.new <- implot(boats,text(150,50,"Boats!!!",cex=3))
plot(b.new)
#Draw a line on a white background
bg <- imfill(150,150,val=1)
implot(bg,lines(c(50,50),c(50,100),col="red",lwd=4))%>%plot
#You can change the rendering of the initial image
im <- grayscale(boats)
draw.fun <- function() text(150,50,"Boats!!!",cex=3)
out <- implot(im,draw.fun(),colorscale=function(v) rgb(0,v,v),rescale=FALSE)
plot(out)
## End(Not run)
```
imrep

Replicate images

Description
Kinda like rep, for images. Copy image n times and (optionally), append.

Usage
imrep(x, n = 1, axis = NULL)

Arguments
x an image
n number of replications
axis axis to append along (one of NULL, "x", "y", "z", "c"). Default: NULL

Value
either an image or an image list

Author(s)
Simon Barthelme

Examples
# Result is a list
imrep(boats,3) %>% plot
# Result is an image
imrep(boats,3,"x") %>% plot
# Make an animation by repeating each frame 10x
# map_il(1:5,~ isoblur(boats,.)) %>% imrep(10,"z") %>%
# imappend("z") %>% play

imrotate

Rotate an image along the XY plane.

Description
If cx and cy aren’t given, the default is to centre the rotation in the middle of the image. When cx
and cy are given, the algorithm used is different, and does not change the size of the image.

Usage
imrotate(im, angle, cx, cy, interpolation = 1L, boundary = 0L)
imsharpen

Arguments

- **im**: an image
- **angle**: Rotation angle, in degrees.
- **cx**: Center of rotation along x (default, image centre)
- **cy**: Center of rotation along y (default, image centre)
- **interpolation**: Type of interpolation. One of 0=nearest,1=linear,2=cubic.
- **boundary**: Boundary conditions. One of 0=dirichlet, 1=neumann, 2=periodic

See Also

imwarp, for flexible image warping, which includes rotations as a special case

Examples

```r
imrotate(boats,30) %>% plot  
#Shift centre to (20,20)
imrotate(boats,30,cx=20,cy=20) %>% plot
```

```
layout(t(1:2))
plot(boats,main="Original")
imsharpen(boats,150) %>% plot(main="Sharpened")
```

---

**Description**

The default sharpening filter is inverse diffusion. The "shock filter" is a non-linear diffusion that has better edge-preserving properties.

**Usage**

```r
imsharpen(im, amplitude, type = "diffusion", edge = 1, alpha = 0, sigma = 0)
```

**Arguments**

- **im**: an image
- **amplitude**: Sharpening amplitude (positive scalar, 0: no filtering).
- **type**: Filtering type. "diffusion" (default) or "shock"
- **edge**: Edge threshold (shock filters only, positive scalar, default 1).
- **alpha**: Window size for initial blur (shock filters only, positive scalar, default 0).
- **sigma**: Window size for diffusion tensor blur (shock filters only, positive scalar, default 0).

**Examples**

```r
layout(t(1:2))
plot(boats,main="Original")
imsharpen(boats,150) %>% plot(main="Sharpened")
```
imshift

Shift image content.

Description
Shift image content.

Usage
imshift(
im,
delta_x = 0L,
delta_y = 0L,
delta_z = 0L,
delta_c = 0L,
boundary_conditions = 0L
)

Arguments
im an image
delta_x Amount of displacement along the X-axis.
delta_y Amount of displacement along the Y-axis.
delta_z Amount of displacement along the Z-axis.
delta_c Amount of displacement along the C-axis.
boundary_conditions can be: - 0: Zero border condition (Dirichlet). - 1: Nearest neighbors (Neumann). - 2: Repeat Pattern (Fourier style).

Examples
imshift(boats,10,50) %>% plot

imsplit

Split an image along a certain axis (producing a list)

Description
Use this if you need to process colour channels separately, or frames separately, or rows separately, etc. You can also use it to chop up an image into blocks. Returns an "imlist" object, which is essentially a souped-up list.

Usage
imsplit(im, axis, nb = -1)
**imsub**

*Select part of an image*

**Arguments**

- **im**: an image
- **axis**: the axis along which to split (for example 'c')
- **nb**: number of objects to split into. If nb=-1 (the default) the maximum number of splits is used, i.e. `split(im,"c")` produces a list containing all individual colour channels.

**See Also**

`imappend` (the reverse operation)

**Examples**

```r
im <- as.cimg(function(x,y,z) x+y+z,10,10,5)
split(im,"z") #Split along the z axis into a list with 5 elements
split(im,"z",2) #Split along the z axis into two groups
split(boats,"x",-200) %>% plot #Blocks of 200 pix. along x
split(im,"z",2) %>% imappend("z") #Split and reshape into a single image
#You can also split pixsets
split(boats > .5,"c") %>% plot
```

**Description**

imsub selects an image part based on coordinates: it allows you to select a subset of rows, columns, frames etc. Refer to the examples to see how it works.

**Usage**

```r
imsub(im, ...)
```

```r
subim(im, ...)
```

**Arguments**

- **im**: an image
- **...**: various conditions defining a rectangular image region

**Details**

subim is an alias defined for backward-compatibility.

**Value**

- an image with some parts cut out
Functions

- subim: alias for imsub

Author(s)

Simon Bartheleme

Examples

```r
parrots <- load.example("parrots")
imsub(parrots, x < 30) #Only the first 30 columns
imsub(parrots, y < 30) #Only the first 30 rows
imsub(parrots, x < 30 & y < 30) #First 30 columns and rows
imsub(parrots, sqrt(x) > 8) #Can use arbitrary expressions
imsub(parrots, x > height/2, y > width/2) #Height and width are defined based on the image
all.equal(imsub(parrots, x %inr% c(1,10)),
imsub(parrots, x >= 1, x <= 10))
imsub(parrots, cc==1) #Colour axis is "cc" not "c" here because "c" is an important R function
#Not run
#imsub(parrots, x+y==1)
#can't have expressions involving interactions between variables (domain might not be square)
```

imwarp

**Image warping**

Description

Image warping consists in remapping pixels, i.e. you define a function $M(x,y,z) \rightarrow (x',y',z')$ that displaces pixel content from $(x,y,z)$ to $(x',y',z')$. Actual implementations rely on either the forward transformation $M$, or the backward (inverse) transformation $M^{-1}$. In CImg the forward implementation will go through all source $(x,y,z)$ pixels and "paint" the corresponding pixel at $(x',y',z')$. This will result in unpainted pixels in the output if $M$ is expansive (for example in the case of a scaling $M(x,y,z) = 5*(x,y,z)$). The backward implementation will go through every pixel in the destination image and look for ancestors in the source, meaning that every pixel will be painted. There are two ways of specifying the map: absolute or relative coordinates. In absolute coordinates you specify $M$ or $M^{-1}$ directly. In relative coordinates you specify an offset function $D$: $M(x,y) = (x,y) + D(x,y)$ (forward) $M^{-1}(x,y) = (x,y) - D(x,y)$ (backward)

Usage

```r
imwarp(
im, 
map, 
direction = "forward", 
coordinates = "absolute", 
boundary = "dirichlet", 
interpolation = "linear"
)
```
Arguments

- **im**: an image
- **map**: a function that takes (x,y) or (x,y,z) as arguments and returns a named list with members (x,y) or (x,y,z)
- **direction**: "forward" or "backward" (default "forward")
- **coordinates**: "absolute" or "relative" (default "relative")
- **boundary**: boundary conditions: "dirichlet", "neumann", "periodic". Default "dirichlet"
- **interpolation**: "nearest", "linear", "cubic" (default "linear")

Details

Note that 3D warps are possible as well. The mapping should be specified via the "map" argument, see examples.

Value

a warped image

Author(s)

Simon Barthelme

See Also

warp for direct access to the CImg function

Examples

```r
im <- load.example("parrots")
#Shift image
map.shift <- function(x,y) list(x=x+10,y=y+30)
imwarp(im,map=map.shift) %>% plot
#Shift image (backward transform)
imwarp(im,map=map.shift,dir="backward") %>% plot

#Shift using relative coordinates
map.rel <- function(x,y) list(x=10+0*x,y=30+0*y)
imwarp(im,map=map.rel,coordinates="relative") %>% plot

#Scaling
map.scaling <- function(x,y) list(x=1.5*x,y=1.5*y)
imwarp(im,map=map.scaling) %>% plot #Note the holes
map.scaling.inv <- function(x,y) list(x=x/1.5,y=y/1.5)
imwarp(im,map=map.scaling.inv,dir="backward") %>% plot #No holes

#Bending
map.bend.rel <- function(x,y) list(x=50*sin(y/10),y=0*y)
imwarp(im,map=map.bend.rel,coord="relative",dir="backward") %>% plot #No holes
```
**im_split**

*Split an image along a certain axis (producing a list)*

**Description**

Split an image along a certain axis (producing a list)

**Usage**

```r
im_split(im, axis, nb = -1L)
```

**Arguments**

- `im`: an image
- `axis`: the axis along which to split (for example 'c')
- `nb`: number of objects to split into. if nb=-1 (the default) the maximum number of splits is used i.e. `split(im,"c")` produces a list containing all individual colour channels

**See Also**

`imappend` (the reverse operation)

---

**index.coord**

*Linear index in internal vector from pixel coordinates*

**Description**

Pixels are stored linearly in (x,y,z,c) order. This function computes the vector index of a pixel given its coordinates

**Usage**

```r
index.coord(im, coords, outside = "stop")
```

**Arguments**

- `im`: an image
- `coords`: a data.frame with values x,y,z (optional), c (optional)
- `outside`: what to do if some coordinates are outside the image: "stop" issues error, "NA" replaces invalid coordinates with NAs. Default: "stop".

**Value**

a vector of indices (NA if the indices are invalid)
inpaint

Author(s)
Simon Barthelme

See Also
coord.index, the reverse operation

Examples

```r
im <- as.cimg(function(x,y) x+y,100,100)
px <- index.coord(im, data.frame(x=c(3,3), y=c(1,2)))
im[px] #Values should be 3+1=4, 3+2=5
```

inpaint

Fill-in NA values in an image

Description

Fill in NA values (inpainting) using a Gaussian filter, i.e. replace missing pixel values with a weighted average of the neighbours.

Usage

```r
inpaint(im, sigma)
```

Arguments

- `im` input image
- `sigma` std. deviation of the Gaussian (size of neighbourhood)

Value

an image with missing values filled-in.

Author(s)
Simon Barthelme

Examples

```r
im <- boats
im[sample(nPix(im),1e4)] <- NA
inpaint(im,1) %>% imlist(im,.) %>%
  setNames(c("before","after")) %>% plot(layout="row")
```
interact

Build simple interactive interfaces using imager

Description
To explore the effect of certain image manipulations, filter settings, etc., it’s useful to have a basic interaction mechanism. You can use shiny for that, but imager provides a lightweight alternative. The user writes a function that gets called every time a user event happens (a click, a keypress, etc.). The role of the function is to process the event and output an image, which will then be displayed. You can exit the interface at any time by pressing Esc. See examples for more. This feature is experimental!!!

Usage
interact(fun, title = "", init)

Arguments
fun a function that takes a single argument (a list of user events) and returns an image to be plotted. The image won’t be rescaled before plotting, so make sure RGB values are in \([0,1]\).
title a title for the window (default "", none)
init initial image to display (optional)

Value
an image, specifically the last image displayed

Author(s)
Simon Barthelme

Examples
#Implement a basic image gallery:
#press "right" and "left" to view each image in a list
gallery <- function(iml)
{
  ind <- 1
  f <- function(state)
  {
    if (state$key=="arrowleft")
    {
      ind <<- max(ind-1,1)
    }
    if (state$key=="arrowright")
    {
      ind <<- min(ind+1,length(iml))
    }
  }
  f
  ret
}
interp

Interpolate image values

Description
This function provides 2D and 3D (linear or cubic) interpolation for pixel values. Locations need to be provided as a data.frame with variables x,y,z, and c (the last two are optional).

Usage
interp(im, locations, cubic = FALSE, extrapolate = TRUE)

Arguments
im
the image (class cimg)
locations
a data.frame
cubic
if TRUE, use cubic interpolation. If FALSE, use linear (default FALSE)
extrapolate
allow extrapolation (to values outside the image)

Examples
loc <- data.frame(x=runif(10,1,width(boats)),y=runif(10,1,height(boats))) #Ten random locations
test <- interp(boats,loc)

is.cimg
Checks that an object is a cimg object

Description
Checks that an object is a cimg object

Usage
is.cimg(x)

Arguments
x
an object
is.pixset

Value
.logical

is.imlist

Description
Check that an object is an imlist object

Usage
is.imlist(x)

Arguments
x an object

Value
.logical

is.pixset

Description
Check that an object is a pixset object

Usage
is.pixset(x)

Arguments
x an object

Value
.logical
isoblur

Blur image isotropically.

Description
Blur image isotropically.

Usage
isoblur(im, sigma, neumann = TRUE, gaussian = TRUE, na.rm = FALSE)

Arguments
- **im**: an image
- **sigma**: Standard deviation of the blur (positive)
- **neumann**: If true, use Neumann boundary conditions, Dirichlet otherwise (default true, Neumann)
- **gaussian**: Use a Gaussian filter (actually van Vliet-Young). Default: 0th-order Deriche filter.
- **na.rm**: if TRUE, ignore NA values. Default FALSE, in which case the whole image is NA if one of the values is NA (following the definition of the Gaussian filter)

See Also
deriche, vanvliet, inpaint, medianblur

Examples
isoblur(boats, 3) %>% plot(main="Isotropic blur, sigma=3")
isoblur(boats, 10) %>% plot(main="Isotropic blur, sigma=10")

---

label

Label connected components.

Description
The algorithm of connected components computation has been primarily done by A. Meijster, according to the publication: 'W.H. Hesselink, A. Meijster, C. Bron, "Concurrent Determination of Connected Components.", In: Science of Computer Programming 41 (2001), pp. 173–194'.

Usage
label(im, high_connectivity = FALSE, tolerance = 0)
Arguments

\texttt{im} an image
\texttt{high\_connectivity} 4(false)- or 8(true)-connectivity in 2d case, and between 6(false)- or 26(true)-connectivity in 3d case. Default FALSE
\texttt{tolerance} Tolerance used to determine if two neighboring pixels belong to the same region.

Examples

\begin{verbatim}
imname <- system.file('extdata/parrots.png',package='imager')
im <- load.image(imname) %>% grayscale
#Thresholding yields different discrete regions of high intensity
regions <- isoblur(im,10) %>% threshold("97%")
labels <- label(regions)
layout(t(1:2))
plot(regions,"Regions")
plot(labels,"Labels")
\end{verbatim}

\texttt{lipy} \hspace{1cm} \textit{Apply function to each element of a list, then combine the result as an image by appending along specified axis}

Description

This is just a shortcut for purrr::map followed by imappend

Usage

\texttt{lipy(lst, fun, axis, \ldots)}

Arguments

\texttt{lst} a list
\texttt{fun} function to apply
\texttt{axis} which axis to append along (e.g. "c" for colour)
\texttt{\ldots} further arguments to be passed to fun

Examples

\begin{verbatim}
build.im <- function(size) as.cimg(function(x,y) (x+y)/size,size,size)
lipy(c(10,50,100),build.im,"y") %>% plot
\end{verbatim}
load.dir

**Load all images in a directory**

Description

Load all images in a directory and return them as an image list.

Usage

```
load.dir(path, pattern = NULL, quiet = FALSE)
```

Arguments

- **path**: directory to load from
- **pattern**: optional: file pattern (ex. *jpg). Default NULL, in which case we look for file extensions png,jpeg,jpg,tif,bmp.
- **quiet**: if TRUE, loading errors are quiet. If FALSE, they are displayed. Default FALSE

Value

an image list

Author(s)

Simon Barthelme

Examples

```
path <- system.file(package="imager") %>% paste0("/extdata")
load.dir(path)
```

load.example

**Load example image**

Description

Imager ships with five test pictures and a video. Two (parrots and boats) come from the [Kodak set](http://r0k.us/graphics/kodak/). Another (birds) is a sketch of birds by Leonardo, from Wiki-media. The "coins" image comes from scikit-image. The Hubble Deep field (hubble) is from Wikimedia. The test video ("tennis") comes from [xiph.org](https://media.xiph.org/video/derf/)'s collection.

Usage

```
load.example(name)
```
Arguments

name name of the example

Value

an image

Author(s)

Simon Barthelme

Examples

load.example("hubble") %>% plot
load.example("birds") %>% plot
load.example("parrots") %>% plot

load.image Load image from file or URL

Description

PNG, JPEG and BMP are supported via the readbitmap package. You’ll need to install ImageMagick for other formats. If the path is actually a URL, it should start with http(s) or ftp(s).

Usage

load.image(file)

Arguments

file path to file or URL

Value

an object of class 'cimg'

Examples

#Find path to example file from package
fpath <- system.file('extdata/Leonardo_Birds.jpg', package='imager')
im <- load.image(fpath)
plot(im)

#Load the R logo directly from the CRAN webpage
#load.image("https://cran.r-project.org/Rlogo.jpg") %>% plot
load.video  

Load a video using ffmpeg

Description

You need to have ffmpeg on your path for this to work. This function uses ffmpeg to split the video into individual frames, which are then loaded as images and recombined. Videos are memory-intensive, and load.video performs a safety check before loading a video that would be larger than maxSize in memory (default 1GB)

Usage

load.video(
  fname,
  maxSize = 1,
  skip.to = 0,
  frames = NULL,
  fps = NULL,
  extra.args = "",
  verbose = FALSE
)

Arguments

fname file to load
maxSize max. allowed size in memory, in GB (default max 1GB).
skip.to skip to a certain point in time (in sec., or "hh:mm:ss" format)
frames number of frames to load (default NULL, all)
fps frames per second (default NULL, determined automatically)
extra.args extra arguments to be passed to ffmpeg (default ",", none)
verbose if TRUE, show ffmpeg output (default FALSE)

Value

an image with the extracted frames along the "z" coordinates

Author(s)

Simon Barthelme

See Also

save.video, make.video
Examples

```r
fname <- system.file('extdata/tennis_sif.mpeg', package='imager')
## Not run
## load.video(fname) %>% play
## load.video(fname, fps=10) %>% play
## load.video(fname, skip=2) %>% play
```

magick

Convert a magick image to a cimg image or image list and vice versa

Description

The magick library package stores its data as "magick-image" object, which may in fact contain several images or an animation. These functions convert magick objects into imager objects or imager objects into magick objects. Note that cimg2magick function requires magick package.

Usage

```r
magick2imlist(obj, alpha = "rm", ...)
magick2cimg(obj, alpha = "rm", ...)
cimg2magick(im, rotate = TRUE)
```

Arguments

- `obj`: an object of class "magick-image"
- `alpha`: what do to with the alpha channel ("rm": remove and store as attribute, "flatten": flatten, "keep": keep). Default: "rm"
- `...`: ignored
- `im`: an image of class cimg
- `rotate`: determine if rotate image to adjust orientation of image

Value

- an object of class cimg or imlist
- an object of class "magick-image"

Author(s)

Jan Wijffels, Simon Barthelme
Shota Ochi

See Also

- flatten.alpha, rm.alpha
Description

You need to have ffmpeg on your path for this to work. This function uses ffmpeg to combine individual frames into a video. save.video can be called directly with an image or image list as input. make.video takes as argument a directory that contains a sequence of images representing individual frames to be combined into a video.

Usage

make.video(
    dname,
    fname,
    pattern = "image-%d.png",
    fps = 25,
    extra.args = "",
    verbose = FALSE
)

save.video(im, fname, ...)

Arguments

dname name of a directory containing individual files
fname name of the output file. The format is determined automatically from the name (example "a.mpeg" will have MPEG format)
pattern pattern of filename for frames (the default matches "image-1.png", "image-2.png", etc.. See ffmpeg documentation for more).
fps frames per second (default 25)
extra.args extra arguments to be passed to ffmpeg (default "", none)
verbose if TRUE, show ffmpeg output (default FALSE)
im an image or image list
...
extra arguments to save.video, passed on to make.video

Functions

- save.video: Save a video using ffmpeg

Author(s)

Simon Barthelme
## See Also

load.video

## Examples

```r
## Not run
## iml <- map_il(seq(0,20,1=60),~ isoblur(boats,.))
## f <- tempfile(fileext=".avi")
## save.video(iml,f)
## load.video(f) %>% play
## # Making a video from a directory
## dd <- tempdir()
## for (i in 1:length(iml)) {
## (png(sprintf("%s/image-%i.png",dd,i));
##  plot(iml[[i]]); dev.off() )
## make.video(dd,f)
## load.video(f) %>% play
```

### Description

Works like purrr::map, purrr::map_dbl and the like but ensures that the output is an image list.

#### Usage

```r
map_il(...)
map2_il(...)
pmap_il(...)
```

#### Arguments

... passed to map

#### Value

an image list

#### Functions

- `map2_il`: Parallel map (two values)
- `pmap_il`: Parallel map (multiple values)

#### Author(s)

Simon Barthelme
Examples

#Returns a list
imsplit(boats,"x",2) %>% purrr::map(~ isoblur(.,3))
#Returns an "imlist" object
imsplit(boats,"x",2) %>% map_il(~ isoblur(.,3))
#Fails if function returns an object that's not an image
try(imsplit(boats,"x",2) %>% map_il(~ . > 2))
#Parallel maps
map2_il(1:3,101:103,~ imshift(boats,.x,.y))
pmap_il(list(x=1:3,y=4:6,z=7:9),function(x,y,z) imfill(x,y,z))

medianblur

Blur image with the median filter. In a window of size n x n centered at pixel (x,y), compute median pixel value over the window. Optionally, ignore values that are too far from the value at current pixel.

Usage

medianblur(im, n, threshold = 0)

Arguments

im an image
n Size of the median filter.
threshold Threshold used to discard pixels too far from the current pixel value in the median computation. Can be used for edge-preserving smoothing. Default 0 (include all pixels in window).

See Also

isoblur, boxblur

Examples

medianblur(boats,5) %>% plot(main="Median blur, 5 pixels")
medianblur(boats,10) %>% plot(main="Median blur, 10 pixels")
medianblur(boats,10,8) %>% plot(main="Median blur, 10 pixels, threshold = 8")
mirror

Mirror image content along specified axis

Description

Mirror image content along specified axis

Usage

mirror(im, axis)

Arguments

im    an image
axis   Mirror axis ("x","y","z","c")

Examples

mirror(boats,"x") %>% plot
mirror(boats,"y") %>% plot

mutate_plyr

Mutate a data frame by adding new or replacing existing columns.

Description

This function copied directly from plyr, and modified to use a different name to avoid namespace collisions with dplyr/tidyverse functions.

Usage

mutate_plyr(.data, ...)

Arguments

.data    the data frame to transform
...      named parameters giving definitions of new columns.

Details

This function is very similar to transform but it executes the transformations iteratively so that later transformations can use the columns created by earlier transformations. Like transform, unnamed components are silently dropped.

Mutate seems to be considerably faster than transform for large data frames.
**nfline**

*Plot a line, Hesse normal form parameterisation*

**Description**

This is a simple interface over abline meant to be used along with the Hough transform. In the Hesse normal form \((\theta, \rho)\), a line is represented as the set of values \((x, y)\) such that \(\cos(\theta) x + \sin(\theta) y = \rho\). Here \(\theta\) is an angle and \(\rho\) is a distance. See the documentation for `hough_lines`.

**Usage**

```r
nfline(theta, rho, col, ...)
```

**Arguments**

- `theta` angle (radians)
- `rho` distance
- `col` colour
- `...` other graphical parameters, passed along to abline

**Value**

nothing

**Author(s)**

Simon Barthelme

**Examples**

```r
# Boring example, see ?hough_lines
plot(boats)
nfline(theta=0, rho=10, col="red")
```

---

**pad**

*Pad image with n pixels along specified axis*

**Description**

Pad image with \(n\) pixels along specified axis

**Usage**

```r
pad(im, nPix, axes, pos = 0, val)
```
Arguments

- **im**: the input image
- **nPix**: how many pixels to pad with
- **axes**: which axes to pad along
- **pos**: -1: prepend 0: center 1: append
- **val**: colour of the padded pixels (default 0 in all channels). Can be a string for colour images, e.g. "red", or "black".

Value

- a padded image

Author(s)

- Simon Barthelme

Examples

```r
pad(boats, 20, "xy") %>% plot
pad(boats, 20, pos = -1, "xy") %>% plot
pad(boats, 20, pos = 1, "xy") %>% plot
pad(boats, 20, pos = 1, "xy", val = "red") %>% plot
```

Description

Patches are rectangular image regions centered at cx, cy with width wx and height wy. This function provides a fast way of extracting a statistic over image patches (for example, their mean). Supported functions: sum, mean, min, max, median, var, sd, or any valid CImg expression. WARNINGS: - values outside of the image region are considered to be 0. - widths and heights should be odd integers (they’re rounded up otherwise).

Usage

```r
patchstat(im, expr, cx, cy, wx, wy)
```

Arguments

- **im**: an image
- **expr**: statistic to extract. a string, either one of the usual statistics like "mean", "median", or a CImg expression.
- **cx**: vector of x coordinates for patch centers
- **cy**: vector of y coordinates for patch centers
- **wx**: vector of patch widths (or single value)
- **wy**: vector of patch heights (or single value)
Value

a numeric vector

See Also

extract_patches

Examples

im <- grayscale(boats)
# Mean of an image patch centered at (10,10) of size 3x3
patchstat(im, 'mean', 10, 10, 3, 3)
# Mean of image patches centered at (10,10) and (20,4) of size 2x2
patchstat(im, 'mean', c(10, 20), c(10, 4), 5, 5)
# Sample 10 random positions
ptch <- pixel.grid(im) %>% dplyr::sample_n(10)
# Compute median patch value
with(ptch, patchstat(im, 'median', x, y, 3, 3))
Examples

#Example: median filtering using patch_summary.cimg
#Center a patch at each pixel
im <- grayscale(boats)
patches <- pixel.grid(im) %>% dplyr::mutate(w=3,h=3)
#Extract patch summary
out <- dplyr::mutate(patches, med=patch_summary.cimg(im,"ic",x,y,w,h))
as.cimg(out, v.name="med") %>% plot

periodic.part

Compute the periodic part of an image, using the periodic/smooth decomposition of Moisan (2011)

Description

Moisan (2011) defines an additive image decomposition im = periodic + smooth where the periodic part shouldn’t be too far from the original image. The periodic part can be used in frequency-domain analyses, to reduce the artifacts induced by non-periodicity.

Usage

periodic.part(im)

Arguments

im an image

Value

an image

Author(s)

Simon Barthelme

References


Examples

im <- load.example("parrots") %>% subim(x <= 512)
layout(t(1:3))
plot(im, main="Original image")
periodic.part(im) %>% plot(main="Periodic part")
#The smooth error is the difference between
#the original image and its periodic part
(im - periodic.part(im)) %>% plot(main="Smooth part")
permute_axes

Permute image axes

Description

By default images are stored in xyzc order. Use permute_axes to change that order.

Usage

permute_axes(im, perm)

Arguments

im an image
perm a character string, e.g., "zxyc" to have the z-axis come first

Examples

im <- array(0,c(10,30,40,3)) %>% as.cimg
permute_axes(im,"zxyc")

pixel.grid

Return the pixel grid for an image

Description

The pixel grid for image im gives the (x,y,z,c) coordinates of each successive pixel as a data.frame. The c coordinate has been renamed 'cc' to avoid conflicts with R's c function. NB: coordinates start at (x=1,y=1), corresponding to the top left corner of the image, unless standardise == TRUE, in which case we use the usual Cartesian coordinates with origin at the center of the image and scaled such that x varies between -.5 and .5, and a y arrow pointing up

Usage

pixel.grid(im, standardise = FALSE, drop.unused = TRUE, dim = NULL)

Arguments

im an image
standardise If TRUE use a centered, scaled coordinate system. If FALSE use standard image coordinates (default FALSE)
drop.unused if TRUE ignore empty dimensions, if FALSE include them anyway (default TRUE)
dim a vector of image dimensions (optional, may be used instead of "im")
Value

a data.frame

Examples

```r
im <- as.cimg(array(0,c(10,10))) # A 10x10 image
pixel.grid(im) %>% head
pixel.grid(dim=dim(im)) %>% head # Same as above
pixel.grid(dim=c(10,10,3,2)) %>% head
pixel.grid(im, standardise=TRUE) %>% head
pixel.grid(im, drop.unused=FALSE) %>% head
```

Description

Pixel sets represent sets of pixels in images (ROIs, foreground, etc.). From an implementation point of view, they're just a thin layer over arrays of logical values, just like the cimg class is a layer over arrays of numeric values. Pixsets can be turned back into logical arrays, but they come with a number of generic functions that should make your life easier. They are created automatically whenever you run a test on an image (for example `im > 0` returns a pixset).

Usage

`pixset(x)`

Arguments

- `x` an array of logical values

Examples

```r
# A test on an image returns a pixset
boats > 250
# Pixsets can be combined using the usual Boolean operators
(boats > 230) & (Xc(boats) < width(boats)/2)
# Subset an image using a pixset
boats[boats > 250]
# Turn a pixset into an image
as.cimg(boats > 250)
# Equivalently:
(boats > 250) + 0
```
Description

A very basic video player. Press the space bar to pause and ESC to close.

Usage

\[
\text{play}(\text{vid}, \text{loop} = \text{FALSE}, \text{delay} = 30L, \text{normalise} = \text{TRUE})
\]

Arguments

- **vid**: A cimg object, to be played as video
- **loop**: loop the video (default false)
- **delay**: delay between frames, in ms. Default 30.
- **normalise**: if true pixel values are rescaled to 0..255 (default TRUE). The normalisation is based on the *first frame*. If you don’t want the default behaviour you can normalise by hand. Default TRUE.

---

**plot.cimg**  
*Display an image using base graphics*

Description

If you want to control precisely how numerical values are turned into colours for plotting, you need to specify a colour scale using the colourscale argument (see examples). Otherwise the default is "gray" for grayscale images, "rgb" for colour. These expect values in [0..1], so the default is to rescale the data to [0..1]. If you wish to over-ride that behaviour, set rescale=FALSE. See examples for an explanation. If the image is one dimensional (i.e., a simple row or column image), then pixel values will be plotted as a line.

Usage

\[
\text{## S3 method for class 'cimg'}
\text{plot(}
\text{\hspace{1em}}\text{x,}
\text{\hspace{1em}}\text{frame,}
\text{\hspace{1em}}\text{xlim = c(1, width(x)),}
\text{\hspace{1em}}\text{ylim = c(height(x), 1),}
\text{\hspace{1em}}\text{xlab = "x",}
\text{\hspace{1em}}\text{ylab = "y",}
\text{\hspace{1em}}\text{rescale = TRUE,}
\text{\hspace{1em}}\text{colourscale = NULL,}
\text{\hspace{1em}}\text{...)}
\text{)}
\]

---
colors = NULL,
interpolate = TRUE,
axes = TRUE,
main = "",
xaxs = "i",
yaxs = "i",
asp = 1,
col.na = rgb(0, 0, 0, 0),
...
)

Arguments

x the image
frame which frame to display, if the image has depth > 1
xlim x plot limits (default: 1 to width)
ylim y plot limits (default: 1 to height)
xlab x axis label
ylab y axis label
rescale rescale pixel values so that their range is [0,1]
colourscale, colourscale an optional colour scale (default is gray or rgb)
interpolate should the image be plotted with anti-aliasing (default TRUE)
axes Whether to draw axes (default TRUE)
main Main title
xaxs The style of axis interval calculation to be used for the x-axis. See ?par
yaxs The style of axis interval calculation to be used for the y-axis. See ?par
asp aspect ratio. The default value (1) means that the aspect ratio of the image will be kept regardless of the dimensions of the plot. A numeric value other than one changes the aspect ratio, but it will be kept the same regardless of dimensions. Setting asp="varying" means the aspect ratio will depend on plot dimensions (this used to be the default in versions of imager < 0.40)
col.na which colour to use for NA values, as R rgb code. The default is "rgb(0,0,0)", which corresponds to a fully transparent colour.
... other parameters to be passed to plot.default (eg "main")

See Also

display, which is much faster, as.raster, which converts images to R raster objects
Examples

plot(boats, main="Boats")
plot(boats, axes=FALSE, xlab="", ylab="")

# Pixel values are rescaled to 0-1 by default, so that the following two plots are identical
plot(boats)
plot(boats/2, main="Rescaled")

# If you don't want that behaviour, you can set rescale to FALSE, but
# then you need to make sure values are in [0,1]
try(plot(boats, rescale=FALSE)) # Error!
try(plot(boats/255, rescale=FALSE)) # Works

# You can specify a colour scale if you don't want the default one.
# A colour scale is a function that takes pixels values and return an RGB code,
# like R's rgb function, e.g.
rgb(0,1,0)

# Let's switch colour channels
cc <- function(r,g,b) rgb(b,g,r)
plot(boats/255, rescale=FALSE, colourscale=cc)

# Display slice of HSV colour space
im <- imfill(255, 255, val=1)
im <- list(Xc(im)/255, Yc(im)/255, im) %>% imappend("c")
plot(im, colourscale=hsv, rescale=FALSE,
     xlab="Hue", ylab="Satturation")

# In grayscale images, the colourscale function should take in a single value
# and return an RGB code
boats.gs <- grayscale(boats)

# We use an interpolation function from package scales
cc <- scales::gradient_n_pal(c("red", "purple", "lightblue"), c(0, .5, 1))
plot(boats.gs, rescale=FALSE, colourscale=cc)

# Plot a one-dimensional image
imsub(boats, x==1) %>% plot(main="Image values along first column")

# Plotting with and without anti-aliasing:
boats.small <- imresize(boats, .3)
plot(boats.small, interp=TRUE)
plot(boats.small, interp=FALSE)

Description

Each image in the list will be plotted separately. The layout argument controls the overall layout of the plot window. The default layout is "rect", which will fit all of your images into a rectangle that's as close to a square as possible.

Usage

## S3 method for class 'imlist'
plot(x, layout = "rect", ...)
Arguments

- \texttt{x}: an image list (of type \texttt{imlist})
- \texttt{layout}: either a matrix (in the format defined by the layout command) or one of "row","col" or "rect". Default: "rect"
- ... other parameters, to be passed to the plot command

Author(s)
Simon Bartheleme

Examples

\begin{verbatim}
imsplit(boats,"c") #Returns an image list
imsplit(boats,"c") %>% plot
imsplit(boats,"c") %>% plot(layout="row")
imsplit(boats,"c") %>% plot(layout="col")
imsplit(boats,"x",5) %>% plot(layout="rect")
\end{verbatim}

Description

Select pixels that are similar to a seed pixel. The underlying algorithm is the same as the bucket fill (AKA flood fill). Unlike with the bucket fill, the image isn’t changed, the function simply returns a pixel set containing the selected pixels.

Usage

\begin{verbatim}
px.flood(im, x, y, z = 1, sigma = 0, high_connexity = FALSE)
\end{verbatim}

Arguments

- \texttt{im}: an image
- \texttt{x}: X-coordinate of the starting point of the region to flood
- \texttt{y}: Y-coordinate of the starting point of the region to flood
- \texttt{z}: Z-coordinate of the starting point of the region to flood
- \texttt{sigma}: Tolerance concerning neighborhood values.
- \texttt{high_connexity}: Use 8-connexity (only for 2d images, default FALSE).

Details

Old name: selectSimilar (deprecated)
See Also

bucketfill

Examples

#Select part of a sail
px <- px.flood(boats,x=169,y=179,sigma=.2)
plot(boats)
highlight(px)

px.na

A pixset for NA values

Description

A pixset containing all NA pixels

Usage

px.na(im)

Arguments

im an image

Value

a pixset

Examples

im <- boats
im[1] <- NA
px.na(im)
px.remove_outer

Remove all connected regions that touch image boundaries

**Description**

All pixels that belong to a connected region in contact with image boundaries are set to FALSE.

**Usage**

```r
tax.remove_outer(px)
```

**Arguments**

- `px` a pixset

**Value**

a pixset

**Author(s)**

Simon Barthelme

**Examples**

```r
im <- draw_circle(imfill(100,100),c(0,50,100),c(50,50,50),radius=10,color=1)
plot(im)
as.pixset(im) %>% px.remove_outer %>% plot
```

---

**RasterPackage**

Convert a RasterLayer/RasterBrick to a cimg image/image list

**Description**

The raster library stores its data as "RasterLayer" and "RasterBrick" objects. The raster package can store its data out-of-RAM, so in order not to load too much data the "maxpixels" argument sets a limit on how many pixels are loaded.

**Usage**

```r
## S3 method for class 'RasterLayer'
as.cimg(obj, maxpixels = 1e+07, ...)
```

```r
## S3 method for class 'RasterStackBrick'
as.imlist(obj, maxpixels = 1e+07, ...)
```
**renorm**

**Arguments**

- **obj**: an object of class "RasterLayer"
- **maxpixels**: max. number of pixels to load (default 1e7)
- **...**: ignored

**Author(s)**

Simon Barthelme, adapted from the image method for RasterLayer by Robert J Hijmans

---

<table>
<thead>
<tr>
<th>renorm</th>
<th>Renormalise image</th>
</tr>
</thead>
</table>

**Description**

Pixel data is usually expressed on a 0...255 scale for displaying. This function performs a linear renormalisation to range min...max

**Usage**

```r
cnorm(x, min = 0, max = 255)
```

**Arguments**

- **x**: numeric data
- **min**: min of the range
- **max**: max of the range

**Author(s)**

Simon Barthelme

**Examples**

```r
cnorm(0:10)
cnorm(-5:5) #Same as above
```
Description

If the dimension arguments are negative, they are interpreted as a proportion of the original image.

Usage

```resize(
  im,
  size_x = -100L,
  size_y = -100L,
  size_z = -100L,
  size_c = -100L,
  interpolation_type = 1L,
  boundary_conditions = 0L,
  centering_x = 0,
  centering_y = 0,
  centering_z = 0,
  centering_c = 0
)
```

Arguments

- `im` an image
- `size_x` Number of columns (new size along the X-axis).
- `size_y` Number of rows (new size along the Y-axis).
- `size_z` Number of slices (new size along the Z-axis).
- `size_c` Number of vector-channels (new size along the C-axis).
- `interpolation_type` Method of interpolation: -1 = no interpolation: raw memory resizing. 0 = no interpolation: additional space is filled according to boundary_conditions. 1 = nearest-neighbor interpolation. 2 = moving average interpolation. 3 = linear interpolation. 4 = grid interpolation. 5 = cubic interpolation. 6 = lanczos interpolation.
- `boundary_conditions` Border condition type.
- `centering_x` Set centering type (only if interpolation_type=0).
- `centering_y` Set centering type (only if interpolation_type=0).
- `centering_z` Set centering type (only if interpolation_type=0).
- `centering_c` Set centering type (only if interpolation_type=0).

See Also

See imresize for an easier interface.
**Description**

Resize image by a single scale factor. For non-uniform scaling and a wider range of options, see resize.

**Usage**

- `resize_doubleXY(im)`
- `resize_halfXY(im)`
- `resize_tripleXY(im)`
- `imresize(im, scale = 1, interpolation = 3)`

**Arguments**

- **im**: an image
- **scale**: a scale factor
- **interpolation**: interpolation method to use (see doc for resize). Default 3, linear. Set to 5 for cubic, 6 for Lanczos (higher quality).

**Value**

- an image

**Functions**

- `resize_doubleXY`: Double size
- `resize_halfXY`: Half size
- `resize_tripleXY`: Triple size
- `imresize`: resize by scale factor

**Author(s)**

Simon Barthelme

**References**

For double-scale, triple-scale, etc. uses an anisotropic scaling algorithm described in: [http://scale2x.sourceforge.net/algorithm.html](http://scale2x.sourceforge.net/algorithm.html). For half-scaling uses what the CImg doc describes as an "optimised filter", see `resize_halfXY` in CImg.h.
See Also

resize

Examples

```r
im <- load.example("parrots")
imresize(im,1/4) #Quarter size
map_il(2:4,- imresize(im,1/..)) %>% imappend("x") %>% plot
```

Colour space conversions in imager

Description

All functions listed here assume the input image has three colour channels (spectrum(im) == 3)

Usage

- `RGBtoHSL(im)`
- `RGBtoXYZ(im)`
- `XYZtoRGB(im)`
- `HSLtoRGB(im)`
- `RGBtoHSV(im)`
- `HSVtoRGB(im)`
- `RGBtoHSI(im)`
- `HSItoRGB(im)`
- `RGBtosRGB(im)`
- `sRGBtoRGB(im)`
- `RGBtoYCbCr(im)`
- `YCbCrtoRGB(im)`
- `RGBtoYUV(im)`
- `YUVtoRGB(im)`
- `LabtoRGB(im)`
RGBtoHSL

RGBtoLab(im)
LabtoXYZ(im)
XYZtoLab(im)
LabtosRGB(im)
sRGBtoLab(im)

Arguments

im an image

Functions

- RGBtoHSL: RGB to HSL conversion
- RGBtoXYZ: CIE RGB to CIE XYZ (1931) conversion, D65 white point
- XYZtoRGB: CIE XYZ to CIE RGB (1931) conversion, D65 white point
- HSLtoRGB: HSL to RGB conversion
- RGBtoHSV: RGB to HSV conversion
- HSVtoRGB: HSV to RGB conversion
- RGBtoHSI: RGB to HSI conversion
- HSItoRGB: HSI to RGB conversion
- RGBtosRGB: RGB to sRGB conversion
- sRGBtoRGB: sRGB to RGB conversion
- RGBtoYcbCr: RGB to YCbCr conversion
- YCbCrtoRGB: YCbCr to RGB conversion
- RGBtoYUV: RGB to YUV conversion
- YUVtoRGB: YUV to RGB conversion
- LabtoRGB: Lab to RGB (linear)
- RGBtoLab: RGB (linear) to Lab
- LabtoXYZ: Lab to XYZ
- XYZtoLab: XYZ to Lab
- LabtosRGB: Lab to sRGB
- sRGBtoLab: sRGB to Lab
**rm.alpha**

Remove alpha channel and store as attribute

**Description**

Remove alpha channel and store as attribute

**Usage**

```r
rm.alpha(im)
```

**Arguments**

- `im` - an image with 4 RGBA colour channels

**Value**

an image with only three RGB channels and the alpha channel as attribute

**Author(s)**

Simon Barthelme

**See Also**

flatten.alpha

**Examples**

```r
#An image with 4 colour channels (RGBA)
im <- imfill(2,2,val=c(0,0,0,0))
#Remove fourth channel
rm.alpha(im)
attr(rm.alpha(im),"alpha")
```

---

**rotate_xy**

Rotate image by an arbitrary angle, around a center point.

**Description**

Rotate image by an arbitrary angle, around a center point.

**Usage**

```r
rotate_xy(im, angle, cx, cy, interpolation = 1L, boundary_conditions = 0L)
```
**Arguments**

- **im**: an image
- **angle**: Rotation angle, in degrees.
- **cx**: X-coordinate of the rotation center.
- **cy**: Y-coordinate of the rotation center.
- **interpolation**: Interpolation type. 0=nearest | 1=linear | 2=cubic
- **boundary_conditions**: Boundary conditions. 0=dirichlet | 1=neumann | 2=periodic

**Examples**

```r
rotate_xy(boats, 30, 200, 400) %>% plot
rotate_xy(boats, 30, 200, 400, boundary=2) %>% plot
```

**Description**

You’ll need ImageMagick for formats other than PNG and JPEG.

**Usage**

```r
save.image(im, file, quality = 0.7)
```

**Arguments**

- **im**: an image (of class cimg)
- **file**: path to file. The format is determined by the file’s name
- **quality**: (JPEG only) default 0.7. Higher quality means less compression.

**Value**

nothing

**See Also**

save.video

**Examples**

```r
#Create temporary file
tmpF <- tempfile(fileext=".png")
#Save boats image
save.image(boats,tmpF)
#Read back and display
load.image(tmpF) %>% plot
```
split_connected  

Split pixset into connected components

Description

Compute connected components (using "label"), then split into as many sets as there are components. Useful for segmentation.

Usage

split_connected(px, ...)

Arguments

px  
a pixset

...  
further arguments passed to label

Value

a list of pixsets

Author(s)

Simon Barthelme

See Also

label

Examples

px <- isoblur(grayscale(boats),5) > .75
plot(px)
spl <- split_connected(px)
plot(spl[[1]])
px <- isoblur(grayscale(boats),5) > .75
plot(px)
spl <- split_connected(px)
plot(spl[[1]])
squeeze

Remove empty dimensions from an array

Description

Works just like Matlab’s squeeze function: if anything in dim(x) equals one the corresponding
dimension is removed

Usage

squeeze(x)

Arguments

x an array

Examples

A <- array(1:9,c(3,1,3)) #3D array with one flat dimension
A %>% squeeze #flat dimension removed

stencil.cross

A cross-shaped stencil

Description

Returns a stencil corresponding to all nearest-neighbours of a pixel

Usage

stencil.cross(z = FALSE, cc = FALSE, origin = FALSE)

Arguments

z include neighbours along the z axis
cc include neighbours along the cc axis
origin include center pixel (default false)

Value

a data.frame defining a stencil

Author(s)

Simon Barthelme
See Also

get.stencil

threshold

Threshold grayscale image

Description

Thresholding corresponding to setting all values below a threshold to 0, all above to 1. If you call
threshold with thr="auto" a threshold will be computed automatically using \text{\texttt{kmeans}} (i.e., using a
variant of \text{\texttt{Otsu}}'s method). This works well if the pixel values have a clear bimodal distribution.
If you call threshold with a string argument of the form "XX\%" (e.g., "98\%"), the threshold will
be set at percentile XX. Computing quantiles or running \text{\texttt{kmeans}} is expensive for large images, so
if approx == TRUE threshold will skip pixels if the total number of pixels is above 10,000. Note
that thresholding a colour image will threshold all the colour channels jointly, which may not be the
desired behaviour! Use \text{\texttt{iiply}}(im,"c",threshold) to find optimal values for each channel separately.

Usage

\text{\texttt{threshold}}(im, thr = "auto", approx = TRUE, adjust = 1)

Arguments

\texttt{im} \hspace{1cm} \text{the image}
\texttt{thr} \hspace{1cm} \text{a threshold, either numeric, or "auto", or a string for quantiles}
\texttt{approx} \hspace{1cm} \text{Skip pixels when computing quantiles in large images (default TRUE)}
\texttt{adjust} \hspace{1cm} \text{use to adjust the automatic threshold: if the auto-threshold is at k, effective
threshold will be at adjust\*k (default 1)}

Value

a pixset with the selected pixels

Author(s)

Simon Barbelme

Examples

\texttt{im <- load.example("birds")}
\texttt{im.g <- grayscale(im)}
\texttt{threshold(im.g,"15\%") \%>% plot}
\texttt{threshold(im.g,"auto") \%>% plot}
\texttt{threshold(im.g,.1) \%>% plot}
\texttt{#If auto-threshold is too high, adjust downwards or upwards
#using "adjust"}
\texttt{threshold(im,adjust=.5) \%>% plot}
\texttt{threshold(im,adjust=1.3) \%>% plot}
vanvliet

Young-Van Vliet recursive Gaussian filter.

Description

The Young-van Vliet filter is a fast approximation to a Gaussian filter (order = 0), or Gaussian derivatives (order = 1 or 2).

Usage

`vanvliet(im, sigma, order = 0L, axis = "x", neumann = FALSE)`

Arguments

- `im`: an image
- `sigma`: standard deviation of the Gaussian filter
- `order`: the order of the filter 0,1,2,3
- `axis`: Axis along which the filter is computed. One of 'x', 'y', 'z', 'c'
- `neumann`: If true, use Neumann boundary conditions (default false, Dirichlet)

References


Examples

```r
vanvliet(boats,sigma=2,order=0) %>% plot("Zeroth-order Young-van Vliet along x")
vanvliet(boats,sigma=2,order=1) %>% plot("First-order Young-van Vliet along x")
vanvliet(boats,sigma=2,order=1) %>% plot("Second-order Young-van Vliet along x")
vanvliet(boats,sigma=2,order=1,axis="y") %>% plot("Second-order Young-van Vliet along y")
```

warp

Warp image

Description

Warp image

Usage

`warp(im, warpfield, mode = 0L, interpolation = 1L, boundary_conditions = 0L)`
Arguments

\begin{itemize}
\item \texttt{im} \hspace{5mm} \text{an image}
\item \texttt{warpfield} \hspace{5mm} \text{Warping field. The (x,y,z) fields should be stacked along the colour coordinate.}
\item \texttt{mode} \hspace{5mm} \text{Can be 0=backward-absolute | 1=backward-relative | 2=forward-absolute | 3=forward-relative}
\item \texttt{interpolation} \hspace{5mm} \text{Can be <tt> 0=nearest | 1=linear | 2=cubic </tt>}
\item \texttt{boundary_conditions} \hspace{5mm} \text{Boundary conditions. Can be <tt> 0=dirichlet | 1=neumann | 2=periodic </tt>}
\end{itemize}

See Also

\texttt{imwarp} for a user-friendly interface

Examples

\begin{verbatim}
#Shift image via warp
warp.x <- imfill(width(boats),height(boats),val=5)
warp.y <- imfill(width(boats),height(boats),val=20)
warpfield <- list(warp.x,warp.y) %>% imappend("c")
warp(boats,warpfield,mode=1) %>% plot
\end{verbatim}

watershed \hspace{5mm} \textit{Compute watershed transform.}

Description

The watershed transform is a label propagation algorithm. The value of non-zero pixels will get propagated to their zero-value neighbours. The propagation is controlled by a priority map. See examples.

Usage

\begin{verbatim}
watershed(im, priority, fill_lines = TRUE)
\end{verbatim}

Arguments

\begin{itemize}
\item \texttt{im} \hspace{5mm} \text{an image}
\item \texttt{priority} \hspace{5mm} \text{Priority map.}
\item \texttt{fill_lines} \hspace{5mm} \text{Sets if watershed lines must be filled or not.}
\end{itemize}
Examples

#In our initial image we'll place three seeds
#(non-zero pixels) at various locations, with values 1, 2 and 3.
#We'll use the watershed algorithm to propagate these values
imd <- function(x,y) imdirac(c(100,100,1,1),x,y)
im <- imd(20,20)+2*imd(40,40)+3*imd(80,80)
layout(t(1:3))
plot(im,main="Seed image")
#Now we build a priority map: neighbours of our seeds
#should get high priority.
#We'll use a distance map for that
p <- 1-distance_transform(sign(im),1)
plot(p,main="Priority map")
watershed(im,p) %>% plot(main="Watershed transform")

where

<table>
<thead>
<tr>
<th>where</th>
<th>Return locations in pixel set</th>
</tr>
</thead>
</table>

Description

Return locations in pixel set

Usage

where(x)

Arguments

x

da pixset

Examples

#All pixel locations with value greater than .99
where(boats > .99)

%inr%

Check that value is in a range

Description

A shortcut for x >= a | x <= b.

Usage

x %inr% range
Arguments

- \( x \): numeric values
- range: a vector of length two, of the form \( c(a,b) \)

Value

- a vector of logicals 1:10

Author(s)

- Simon Barthelme
Index

*Topic datasets
  boats, 22
  %inr%, 127

add (imager.combine), 65
add.color (add.colour), 5
add.colour, 5
as.cimg, 6
as.cimg.array, 7
as.cimg.data.frame, 8
as.cimg.function, 9
as.cimg.pixset (as.pixset), 16
as.cimg.raster, 10
as.cimg.RasterLayer (RasterPackage), 114
as.data.frame.cimg, 11
as.data.frame.imlist, 12
as.data.frame.pixset, 12
as.igraph.cimg, 13
as.igraph.pixset, 14
as.imlist (as.imlist.list), 15
as.imlist.list, 15
as.imlist.RasterStackBrick
  (RasterPackage), 114
as.pixset, 16
as.raster.cimg, 17
at, 18
at<- (at), 18
autocrop, 19
average (imager.combine), 65

B (cimg.extract), 31
B<-> (imager.replace), 67
bbox, 20
blur_anisotropic, 21
boats, 22
boundary, 23
boxblur, 23
boxblur_xy, 24
bucketfill, 25
cannyEdges, 26
capture.plot, 27
Cc (imcoord), 71
center.stencil, 27
channel (cimg.extract), 31
channel<- (imager.replace), 67
channels, 28
ci, 28
cimg, 29
cimg.dimensions, 30
cimg.extract, 31
cimg.use.openmp, 32
cimg2im, 33
cimg2magick (magick), 98
circles, 33
clean, 34
color.at (at), 18
color.at<- (at), 18
colorise, 35
common_pixsets, 36
contours, 38
crop.bbox (bbox), 20
crop.borders, 40
depth (cimg.dimensions), 30
deriche, 41
diffusion_tensors, 42
dilate (erode), 48
dilate_rect (erode), 48
dilate_square (erode), 48
displacement, 42
display, 43
display.cimg, 43
display.list, 44
distance_transform, 45
draw_circle, 45
draw_rect, 46
draw_text, 47

enorm(imager.combine), 65
equal(imager.combine), 65
erode, 48
erode_rect(erode), 48
erode_square(erode), 48
extract_patches, 50
extract_patches3D(extract_patches), 50

FFT, 51
fill(clean), 34
flatten.alpha, 52
frame(cimg.extract), 31
frame<-(imager.replace), 67
frames, 53

G(cimg.extract), 31
G<-(imager.replace), 67
get.locations, 53
get.stencil, 54
get.gradient, 55
get.hessian, 55
grab, 56
grabLine(grab), 56
grabPoint(grab), 56
grabRect(grab), 56
grayscale, 57
grow, 57
gsdim, 58

haar, 59
height(cimg.dimensions), 30
highlight, 60
hough_circle, 60
hough_line, 61
HSItoRGB(RGBtoHSL), 118
HSLtoRGB(RGBtoHSL), 118
HSVtoRGB(RGBtoHSL), 118

idply, 62
iiply, 63
ilply, 63
im2cimg, 64
im_split, 88
imager, 64
imager.colourspaces(RGBtoHSL), 118

imager.combine, 65
imager.replace, 67
imager.subset, 68
imappend, 69
imchange, 70
imcol(cimg.extract), 31
imcoord, 71
imdirac, 72
imdo(imeval), 74
imdraw, 73
imeval, 74
imfill, 76
imgradient, 77
imhessian, 77
iminfo, 78
imlap, 79
imlist, 79
imnoise, 80
implot, 81
imrep, 82
imresize(resize_doubleXY), 117
imrotate, 82
imrow(cimg.extract), 31
imsharpen, 83
imshift, 84
imsplit, 84
imsub, 85
imwarp, 86
index.coord, 88
inpaint, 89
interact, 90
interp, 91
is.cimg, 91
is.pixset, 92
isoblur, 93

label, 93
LabtoRGB(RGBtoHSL), 118
LabtosRGB(RGBtoHSL), 118
LabtoXYZ(RGBtoHSL), 118
liply, 94
load.dir, 95
load.example, 95
load.image, 96
load.video, 97

magick, 98
magick2cimg(magick), 98
INDEX

magick2imlist (magick), 98
make.video, 99
map2 il (map il), 100
map il, 100
mclosing (erode), 48
mclosing_square (erode), 48
medianblur, 101
mirror, 102
mopening (erode), 48
mopening_square (erode), 48
mult (imager.combine), 65
mutate_plyr, 102
ncline, 103
nPix (cimg.dimensions), 30
pad, 103
parall (imager.combine), 65
parany (imager.combine), 65
parmax (imager.combine), 65
parmed (imager.combine), 65
parmin (imager.combine), 65
parorder (imager.combine), 65
parrank (imager.combine), 65
parsd (imager.combine), 65
parsort (imager.combine), 65
patch_summary_cimg, 105
patchstat, 104
periodic.part, 106
permute_axes, 107
pixel.grid, 107
pixset, 108
play, 109
plot.cimg, 109
plot.imlist, 111
pmap il (map il), 100
px.all (common pixsets), 36
px.borders (common pixsets), 36
px.bottom (common pixsets), 36
px.circle (common pixsets), 36
px.diamond (common pixsets), 36
px.flood, 112
px.left (common pixsets), 36
px.na, 113
px.none (common pixsets), 36
px.remove_outer, 114
px.right (common pixsets), 36
px.square (common pixsets), 36
px.top (common pixsets), 36
R (cimg.extract), 31
R<- (imager.replace), 67
RasterPackage, 114
renorm, 115
resize, 116
resize_doubleXY, 117
resize_halfXY (resize_doubleXY), 117
resize_tripleXY (resize_doubleXY), 117
resize_uniform (resize_doubleXY), 117
RGBtoHSI (RGBtoHSL), 118
RGBtoHSL, 118
RGBtoHSV (RGBtoHSL), 118
RGBtoLab (RGBtoHSL), 118
RGBtosRGB (RGBtoHSL), 118
RGBtoXYZ (RGBtoHSL), 118
RGBtoYCbCr (RGBtoHSL), 118
RGBtoYUV (RGBtoHSL), 118
rm.alpha, 120
rotate_xy, 120
save.image, 121
save.video (make.video), 99
shrink (grow), 57
spectrum (cimg.dimensions), 30
split_connected, 122
squeeze, 123
sRGBtoLab (RGBtoHSL), 118
sRGBtoRGB (RGBtoHSL), 118
stencil.cross, 123
subim (imsub), 85
threshold, 124
transform, 102
vanvliet, 125
warp, 125
watershed, 126
where, 127
which.parax (imager.combine), 65
which.parmin (imager.combine), 65
width (cimg.dimensions), 30
wsum (imager.combine), 65
Xc (imcoord), 71
XYZtoLab (RGBtoHSL), 118
XYZtoRGB (RGBtoHSL), 118
Yc (imcoord), 71
YCbCrtoRGB (RGBtoHSL), 118
YUVtoRGB (RGBtoHSL), 118
Zc (imcoord), 71