

Package: colocr (via r-universe)

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Type Package

Title Conduct Co-Localization Analysis of Fluorescence Microscopy Images

Version 0.1.1

License GPL-3

URL <https://docs.ropensci.org/colocr>,
<https://github.com/ropensci/colocr>

BugReports <https://github.com/ropensci/colocr/issues>

Description Automate the co-localization analysis of fluorescence microscopy images. Selecting regions of interest, extract pixel intensities from the image channels and calculate different co-localization statistics. The methods implemented in this package are based on Dunn et al. (2011) <[doi:10.1152/ajpcell.00462.2010](https://doi.org/10.1152/ajpcell.00462.2010)>.

Encoding UTF-8

LazyData true

Suggests testthat, shinytest, covr, knitr, rmarkdown, devtools, purrr, shinyBS

RoxygenNote 6.1.1

Imports imager, magick, shiny, scales, magrittr

VignetteBuilder knitr

Repository <https://ropensci.r-universe.dev>

RemoteUrl <https://github.com/ropensci/colocr>

RemoteRef master

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.intensity_get	<i>Get pixel intensities</i>
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Description

Get the pixel intensities of certain image channels

Usage

```
.intensity_get(img, ind = c(1, 2))
```

Arguments

img	An object of class <code>cimg</code>
ind	A numeric of length two for channel indexes

Value

A list of three items. The first two items are the values of the pixel intensities of the channels indicated by `ind`. The third is the labels of the individual regions of interest.

Examples

```
# load image
f1 <- system.file('extdata', 'Image0001_.jpg', package = 'colocr')
img <- image_load(f1)

# choose parameters
int <- roi_select(img, threshold = 90) %>%
  .intensity_get()
```

.labels_add *Label regions of interest*

Description

Add labels to regions of interest in an image

Usage

.labels_add(px, tolerance, n)

Arguments

px An object of class [pixset](#)
tolerance A numeric to be passed to [label](#)
n A numeric, the number of desired regions of interest

Value

An object of class [cimg](#). The labels are coded the values in the object starting from 1. The rest of the image is labeled 0.

.manders *Calculate Marnders Overlap Coefficient*

Description

Calculates the manders overlap coefficient between two numeric vectors

Usage

.manders(r, g)

Arguments

r A numeric vector
g A numeric vector

Value

A numeric of length one.

Examples

```
set.seed(123)
r <- rnorm(10)

set.seed(1234)
g <- rnorm(10)

.manders(r, g)
```

.pearson

Calculate Pearson's Correlation Coefficient

Description

Calculates the Pearson's correlation coefficient between two numeric vectors

Usage

```
.pearson(r, g)
```

Arguments

r	A numeric vector
g	A numeric vector

Value

A numeric of length one.

Examples

```
set.seed(123)
r <- rnorm(10)

set.seed(1234)
g <- rnorm(10)

.pearson(r, g)
```

colocr	colocr: <i>Conduct Co-localization Analysis of Microscopy Images.</i>
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Description

Automate the co-localization analysis of fluorescence microscopy images. Selecting regions of interest, extract pixel intensities from the image channels and calculate different co-localization statistics.

colocr functions

[roi_select](#) [roi_show](#) [roi_check](#) [roi_test](#)

colocr_app	<i>Run the shiny App</i>
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Description

Run the shiny App

Usage

```
colocr_app()
```

image_load	<i>Load images from files</i>
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Description

A wrap around [image_read](#) and [magick2cimg](#) to load one or more images from files.

Usage

```
image_load(image_file)
```

Arguments

`image_file` A character vector of one or more paths to image files

Value

A cimg object or a list of cimg objects when multiple files are passed to `image_file`.

Examples

```
# load image
fl <- system.file('extdata', 'Image0001_.jpg', package = 'colocr')
img <- image_load(fl)
```

roi_check	<i>Show pixel intensities</i>
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Description

Show the pixel intensities of certain image channels

Usage

```
roi_check(img, ind = c(1, 2))
```

Arguments

img	A cimg object or a list of multiple images such as the one returned from roi_select
ind	A numeric object of length two. For the channel indexes. or a list of similar vectors for each of img items.

Details

Calling this function returns two plots. The first is a scatter plot of the pixel intensities from two channels. The second is the density distribution of the intensities from the two channels.

Examples

```
# load images
fl <- system.file('extdata', 'Image0001_.jpg', package = 'colocr')
img <- image_load(fl)

# choose ROI and show the pixel intensities
oldpar <- par()
par(mfrow = c(1, 2))

roi_select(img, threshold = 90) %>%
  roi_check()

par(oldpar)
```

roi_select	Select regions of interest
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Description

Select regions of interest in an image using different morphological operations

Usage

```
roi_select(img, threshold, shrink = 5, grow = 5, fill = 5,
           clean = 5, tolerance = 0.1, n = 1)
```

Arguments

img	An object of class <code>cimg</code> or a list of multiple <code>cimg</code> items
threshold	A numeric to be passed to <code>threshold</code> or a vector of values for each image in <code>img</code>
shrink	A numeric to be passed to <code>shrink</code> or a vector of values for each image in <code>img</code>
grow	A numeric to be passed to <code>grow</code> or a vector of values for each image in <code>img</code>
fill	A numeric to be passed to <code>fill</code> or a vector of values for each image in <code>img</code>
clean	A numeric to be passed to <code>clean</code> or a vector of values for each image in <code>img</code>
tolerance	A numeric to be passed to <code>label</code> or a vector of values for each image in <code>img</code>
n	A numeric of the number of regions of interest or a vector of values for each image in <code>img</code>

Details

The function applies several `imager` morphological manipulations to select the regions of interest. These include `threshold` which sets all values below certain cut to 0; `shrink/grow` for pixel set dilation and erosion; `fill/clean` for removing isolated regions and holes. When `n` is provided, the individual regions (connected components) are selected where `tolerance` is used to determine if two pixels belong to the same region.

Value

A `cimg`. The original input `img` with an additional attribute `label`. `label` is a vector of integers. The labels for the selected regions of interests starts from 1 and 0 is ignored. When `img` is a list, a list is returned.

Examples

```
# load images
f1 <- system.file('extdata', 'Image0001_.jpg', package = 'colocr')
img <- image_load(f1)

# choose ROI
```

```
newimg <- roi_select(img, threshold = 90)

# check the ROI labels
unique(attr(newimg, 'label'))
```

roi_show

Show the selected regions of interest

Description

Show/highlight the selected regions of interest on different image channels

Usage

```
roi_show(img, ind = c(1, 2))
```

Arguments

img	A cimg object or a list of multiple images such as the one returned from roi_select
ind	A numeric object of length two. For the channel indexes. or a list of similar vectors for each of img items.

Details

calling this function with img object which is returned from [roi_select](#) returns four different plots. The original image, a low resolution representation of the selected regions of interest and the two channels indicated through ind highlighted.

Examples

```
# load images
f1 <- system.file('extdata', 'Image0001_.jpg', package = 'colocr')
img <- image_load(f1)

# choose and show ROI
oldpar <- par()
par(mfrow=c(2,2))

roi_select(img, threshold = 90) %>%
  roi_show()

par(oldpar)
```

`roi_test`*Test Co-localization*

Description

Perform co-localization test statistics.

Usage

```
roi_test(img, ind = c(1, 2), type = "pcc")
```

Arguments

<code>img</code>	A <code>cimg</code> object or a list of multiple images such as the one returned from <code>roi_select</code>
<code>ind</code>	A numeric object of length two. For the channel indexes. or a list of similar vectors for each of <code>img</code> items.
<code>type</code>	A character vector of the desired co-localization statistics. Default is 'pcc', other inputs are 'moc' or 'both'.

Details

The co-localization stats requested in `type` is returned as a column for each. When different labels are provided, the stats are calculated for each label individually. When `img` is a list a list of such `data.frames` is returned

Value

A `data.frame` or a list of `data.frames`.

Examples

```
# load images
fl <- system.file('extdata', 'Image0001_.jpg', package = 'colocr')
img <- image_load(fl)

# choose roi and test colocalization
roi_select(img, threshold = 90) %>%
  roi_test()
```

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