Package 'colocr'

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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>.

Encoding UTF-8

LazyData true

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shinyBS

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Imports imager, magick, shiny, scales, magrittr

VignetteBuilder knitr

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R topics documented:

.intensity_get *Get pixel intensities*

Description

Get the pixel intensities of certain image channels

Usage

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

Arguments

img	An object of class cimg
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
fl <- system.file('extdata', 'Image0001_.jpg', package = 'colocr')
img <- image_load(fl)

# 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*: Conduct Co-localization Analysis of Microscopy Images.*

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](#)

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colocr_app | *Run the shiny App*

Description

Run the shiny App

Usage

```
colocr_app()
```

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image_load | *Load images from files*

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   *Show pixel intensities*

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*

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 [cimg](#) or a list of multiple [cimg](#) items
threshold	A numeric to be passed to [threshold](#) or a vector of values for each image in img
shrink	A numeric to be passed to [shrink](#) or a vector of values for each image in img
grow	A numeric to be passed to [grow](#) or a vector of values for each image in img
fill	A numeric to be passed to [fill](#) or a vector of values for each image in img
clean	A numeric to be passed to [clean](#) or a vector of values for each image in img
tolerance	A numeric to be passed to [label](#) or a vector of values for each image in img
n	A numeric of the number of regions of interest or a vector of values for each image in img

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

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

# 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

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.
type	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 is `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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