Package ‘colocr’

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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>.

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`.intensity_get`  

*Get pixel intensities*

**Description**

Get the pixel intensities of certain image channels

**Usage**

```r
.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**

```r
# 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**
```r
.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**
```r
.manders(r, g)
```

**Arguments**
- `r`: A numeric vector
- `g`: A numeric vector

**Value**
A numeric of length one.
Examples

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

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

.pearson(r, g)
```

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

```r
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

---

**colocr_app**

**Run the shiny App**

**Description**

Run the shiny App

**Usage**

colocr_app()

---

**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)

# 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

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

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

```r
# 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

```r
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

```r
# 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()
```
### Description
Perform co-localization test statistics.

### Usage
```r
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 `img` is a list a list of such `data.frame`s is returned.

### Value
A `data.frame` or a list of `data.frame`s.

### Examples
```r
# 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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