Package ‘flowcatchR’

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Type Package

Title Tools to analyze in vivo microscopy imaging data focused on tracking flowing blood cells

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Description flowcatchR is a set of tools to analyze in vivo microscopy imaging data, focused on tracking flowing blood cells. It guides the steps from segmentation to calculation of features, filtering out particles not of interest, providing also a set of utilities to help checking the quality of the performed operations (e.g. how good the segmentation was). It allows investigating the issue of tracking flowing cells such as in blood vessels, to categorize the particles in flowing, rolling and adherent. This classification is applied in the study of phenomena such as hemostasis and study of thrombosis development. Moreover, flowcatchR presents an integrated workflow solution, based on the integration with a Shiny App and Jupyter notebooks, which is delivered alongside the package, and can enable fully reproducible bioimage analysis in the R environment.

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VignetteBuilder knitr

Suggests BiocStyle, knitr, shiny

Depends R (>= 2.10), methods, EBImage

Imports rgl, colorRamps, abind, BiocParallel

SystemRequirements ImageMagick

LazyData true

URL https://github.com/federicomarini/flowcatchR

BugReports https://github.com/federicomarini/flowcatchR/issues

biocViews Software, Visualization, CellBiology, Classification, Infrastructure, GUI

NeedsCompilation no

Author Federico Marini [aut, cre]
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add.contours

*Add object contours to a Frames object*

**Description**

Creates a Frames object containing raw information, combined with the segmented images and the relative trajectory under analysis.

**Usage**

```r
add.contours(raw.frames, binary.frames = NULL, trajectoryset = NULL, 
trajIDs = NULL, mode = "particles", col = NULL, channel = NULL)
```

**Arguments**

- `raw.frames`: A Frames object with raw images
- `binary.frames`: A Frames object with preprocessed frames
- `trajectoryset`: A TrajectorySet object
- `trajIDs`: Numeric vector, the ID(s) of the trajectory.
- `mode`: A character string, can assume the values `particles` or `trajectories`. Defaults to `particles`.
- `col`: A vector of color strings
- `channel`: A character string, to select which channel to process

**Details**

If a TrajectorySet is provided and mode is set to `trajectories`, returns a Frames with all trajectories included in the IDs vector painted accordingly. If the mode is set to `particles`, it will just plot the particles (all) on all frames. If no TrajectorySet is provided, it will be computed with default parameters. If no binary.frames is provided, it will be computed also with default parameters.

**Value**

A new Frames object with contours of the objects added

**Author(s)**

Federico Marini, <marinif@uni-mainz.de>, 2014

**Examples**

```r
data("MesenteriumSubset")
## Not run:
paintedTrajectories <- add.contours(raw.frames = MesenteriumSubset, mode = "trajectories", col = "red")
paintedParticles <- add.contours(raw.frames = MesenteriumSubset, mode = "particles", col = "red")
inspect.Frames(paintedTrajectories)
inspect.Frames(paintedParticles)

## End(Not run)
```
addParticles

*Combines the information from a raw Frames object and the corresponding preprocessed one*

**Description**

All objects are painted with a unique colour - for sake of speed

**Usage**

`addParticles(raw.frames, binary.frames, col = NULL)`

**Arguments**

- `raw.frames`: A Frames object containing the raw images
- `binary.frames`: A Frames object with the preprocessed versions of the images (e.g. segmented)
- `col`: A color character string, to select which color will be used for drawing the contours of the particles. If not specified, it will default according to the objects provided

**Value**

A Frames object, whose images are the combination of the raw images with the segmented objects drawn on them

**Author(s)**

Federico Marini, <marinif@uni-mainz.de>, 2014

---

axesInfo

*Info on the dimensions of the FOV*

**Description**

Auxiliary function to return the dimensions of the field of interest

**Usage**

`axesInfo(frames)`

**Arguments**

- `frames`: A Frames object

**Value**

A list object, containing the extremes of the field of interest (x-y-z, where z is time)

**Author(s)**

Federico Marini, <marinif@uni-mainz.de>, 2014
**candidate.platelets**  
* A sample ParticleSet object

**Description**

The sample ParticleSet object is constituted by the platelets identified from the MesenteriumSubset data.

**Author(s)**

Federico Marini, <marini@uni-mainz.de>, 2014

---

**channel.Frames**  
* Channel extraction for objects

**Description**

channel

**Usage**

channel.Frames(frames, mode)

**Arguments**

- frames  
  A Frames object
- mode  
  A character value specifying the target mode for conversion.

**Value**

A Frames object with just the information on the selected channel

**Examples**

```r
data("MesenteriumSubset")
channel.Frames(MesenteriumSubset,"red")
```
computeMSD  
*Calculates the Mean Squared Displacement for a trajectory*

**Description**

Calculates the Mean Squared Displacement for a trajectory

**Usage**

```r
computeMSD(sx, sy, until = 4)
```

**Arguments**

- `sx`: x axis positions along the trajectory
- `sy`: y axis positions along the trajectory
- `until`: how many points should be included in the Mean Squared Displacement curve

**Value**

A numeric vector containing the values of the MSD

**Author(s)**

Federico Marini, <marinif@uni-mainz.de>, 2014

---

crop.Frames  
*Cuts borders of a *Frames* object*

**Description**

Performs cropping on the *Frames* object, selecting how many pixels should be cut on each side

**Usage**

```r
crop.Frames(frames, cutLeft = 5, cutRight = 5, cutUp = 5, cutDown = 5,
            cutAll = 0, testing = FALSE, ...)
```

**Arguments**

- `frames`: An input *Frames* object
- `cutLeft`: Amount of pixels to be cut at the side
- `cutRight`: Amount of pixels to be cut at the side
- `cutUp`: Amount of pixels to be cut at the side
- `cutDown`: Amount of pixels to be cut at the side
- `cutAll`: Amount of pixels to be cut at all sides. Overrides the single side values
- `testing`: Logical, whether to just test the cropping or to actually perform it. Default set to FALSE

... Arguments to be passed to `display` (e.g. setting the method argument)
**export.Frames**

### Details

Cropping can be performed with careful choice of all cutting sides, or cropping a single value from all sides.

### Value

A Frames object, with cropped frames in the image slot.

### Author(s)

Federico Marini, <marini@uni-mainz.de>, 2014

### Examples

```r
data("MesenteriumSubset")
crop.Frames(MesenteriumSubset)
```

### Description

Exports a Frames object

**Description**

Writes the images contained in the image slot of the Frames object elements. The images can be exported as single frames, or as a .gif image that is composed by the single frames.

### Usage

```r
export.Frames(frames, dir = tempdir(), nameStub = "testExport", createGif = FALSE, removeAfterCreatingGif = TRUE)
```

### Arguments

- **frames**: A Frames object
- **dir**: The path of the folder where the image should be written
- **nameStub**: The stub for the file name, that will be used as a prefix for the exported images
- **createGif**: Logical, whether to create or not an animated .gif file
- **removeAfterCreatingGif**: Logical, whether to remove the single exported .png images after creating the single .gif

### Value

Image files are written in the desired location

### Author(s)

Federico Marini, <marini@uni-mainz.de>, 2014

### Examples

```r
data("MesenteriumSubset")
## Not run: export.Frames(MesenteriumSubset,nameStub="subset_export_",createGif=TRUE,removeAfterCreatingGif=FALSE)
```
export.particles  Exports a ParticleSet object

Description

Writes the particles contained in the particles data frame slot of the ParticleSet object elements. A track of the provenience of the particles is stored as a comment line above the header.

Usage

```r
export.particles(particleset, dir = tempdir(),
                 nameStub = "testExport_particles")
```

Arguments

- `particleset`: A ParticleSet object.
- `dir`: The path of the folder where the particle sets should be written.
- `nameStub`: The stub for the file name, that will be used as a prefix for the exported particle sets.

Value

Particle sets files are written in the desired location.

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

```r
data("candidate.platelets")
## Not run: export.particles(candidate.platelets)
```

extractKinematics.traj

Calculate a set of kinematics parameters from a single trajectory

Description

The computed set of parameters include `delta.x`, `delta.t` and `delta.v` (displacements and instantaneous velocity), `totalTime`, `totalDistance`, `distStartToEnd`, `curvilinearVelocity`, `straightLineVelocity`, and `linearityForwardProgression`, Mean Squared Displacement, velocity autocorrelation, and more.

Usage

```r
extractKinematics.traj(trajcetoryset, trajectoryID, acquisitionFrequency = 30,
                        scala = 50)
```
flowcatchR

Arguments

- trajectoryset: A TrajectorySet object
- trajectoryID: The ID of a single trajectory
- acquisitionFrequency: The frame rate of acquisition for the images, in milliseconds
- scala: The value of micro(?)_meters to which each single pixel corresponds

Value

A KinematicsFeatures object

Author(s)

Federico Marini, marinif@uni-mainz.de, 2014

Description

A toolset to analyze in vivo microscopy imaging data focused on tracking flowing blood cells.

Details

flowcatchR is a set of tools to analyze in vivo microscopy imaging data, focused on tracking flowing blood cells. It guides the steps from segmentation to calculation of features, filtering out particles not of interest, providing also a set of utilities to help checking the quality of the performed operations (e.g. how good the segmentation was). The main novel contribution investigates the issue of tracking flowing cells such as in blood vessels, to categorize the particles in flowing, rolling and adherent. This classification is applied in the study of phenomena such as hemostasis and study of thrombosis development.

Author(s)

Federico Marini marinif@uni-mainz.de, Johanna Mazur mazur@uni-mainz.de, Harald Binder binderh@uni-mainz.de, 2015

Maintainer: Federico Marini marinif@uni-mainz.de
Frames-class

Frames

Constructor for a Frames object

Description

Constructor for a Frames object

Usage

Frames(x, channel)

Arguments

x A multi-dimensional Image object
channel A character vector, can be ‘red’, ‘green’, ‘blue’ or ‘all’ (if in color mode)

Value

The created Frames object.

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

data("MesenteriumSubset")
inputImg <- Image(MesenteriumSubset)
Frames(inputImg,"red")

Frames-class

Description

S4 class for storing information on multiple images belonging to the same time-lapse experiment. It is designed as a subclass of the existing Image class from the EBImage package

Slots

channel A character vector, can be ‘red’, ‘green’, ‘blue’ or ‘all’ (if in color mode)
initialize.LinkedParticleSet

*Initialize a ParticleSet object for subsequent linking/tracking*

**Description**

Initialize a ParticleSet object for subsequent linking/tracking

**Usage**

initialize.LinkedParticleSet(particleSet, linkrange = 1)

**Arguments**

- **particleSet**: A ParticleSet object
- **linkrange**: The number of frames to look for candidate particles potentially belonging to the same track

**Value**

A ParticleSet object with slots dedicated for the tracking pre-filled

**Author(s)**

Federico Marini, <marinif@uni-mainz.de>, 2014

---

inspect.Frames

*Explore the frames of a Frames*

**Description**

The first frames of a Frames are displayed in the browser, and are interactively navigable.

**Usage**

inspect.Frames(frames, nframes = NULL, display.method = "browser", verbose = FALSE)

**Arguments**

- **frames**: A Frames object
- **nframes**: The number of frames to display (default value: NULL, all are displayed )
- **display.method**: Method for displaying, can be either raster or browser. Defaults to browser, by opening a window in the browser
- **verbose**: Logical, whether to provide additional output on the command line alongside with the images themselves

**Value**

inspect.Frames returns an invisible NULL.
kinematics

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014

Examples
data("MesenteriumSubset")
## Not run: inspect.Frames(MesenteriumSubset)

kinematics
Calculate a set of kinematics parameter from a TrajectorySet object, or a single parameter, or from a single trajectory (all possible combinations)

Description
The computed set of parameters include delta.x, delta.t and delta.v (displacements and instantaneous velocity), totalTime, totalDistance, distStartToEnd, curvilinearVelocity, straightLineVelocity and linearityForwardProgression, Mean Squared Displacement, velocity autocorrelation, and more. If a single trajectory is specified, the computation is performed for that trajectory alone. If a parameter is specified, only that parameter is reported, either for one or all trajectories

Usage
kinematics(trajectoryset, trajectoryIDs = NULL, acquisitionFrequency = 30, scala = 50, feature = NULL)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
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<tr>
<td>trajectoryset</td>
<td>A TrajectorySet object</td>
</tr>
<tr>
<td>trajectoryIDs</td>
<td>The ID of a single trajectory</td>
</tr>
<tr>
<td>acquisitionFrequency</td>
<td>The frame rate of acquisition for the images, in milliseconds</td>
</tr>
<tr>
<td>scala</td>
<td>The value of micro(?)meters to which each single pixel corresponds</td>
</tr>
<tr>
<td>feature</td>
<td>Character string, the name of the feature to be computed</td>
</tr>
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Value
A KinematicsFeaturesSet object, or a KinematicsFeatures object, or an atomic value, or a list(eventually coerced to a vector)

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014
data("candidate.platelets")
platelets.trajectories <- trajectories(candidate.platelets)
# for all trajectories, all features
alltrajs.features <- kinematics(platelets.trajectories)
# for one trajectory, all features
traj11features <- kinematics(platelets.trajectories,trajectoryIDs = 11)
# for all trajectories, one feature
alltrajs.curvVel <- kinematics(platelets.trajectories,feature = "curvilinearVelocity")

---

**KinematicsFeatures-class**

*KinematicsFeatures class*

**Description**

S4 class for storing information on all kinematics features identified for a single trajectory

**Slots**

.Data A list storing the information for the kinematics features

---

**KinematicsFeaturesSet-class**

*KinematicsFeaturesSet*

**Description**

S4 class for storing information on all kinematics features identified for all trajectories. Single `KinematicsFeatures` objects are the element of the main list

**Slots**

.Data A list storing the information for the sets of kinematics features

---

**length.Frames**

*Compute the length of render frames in a Frames object*

**Description**

Compute the length of render frames in a `Frames` object

**Usage**

```r
## S3 method for class 'Frames'
length(x)
```
link.particles

Arguments

\textit{x} \hspace{1cm} A Frames object

Value

An integer number

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

data("MesenteriumSubset")
length(MesenteriumSubset)

\begin{verbatim}
link.particles  \hspace{1cm} \textit{Links a ParticleSet object}
\end{verbatim}

Description

Performs linking of the particles by tracking them through the frames

Usage

\begin{verbatim}
link.particles(particleset, L, R = 2, epsilon1 = 0.1, epsilon2 = 2, 
lambda1 = 1, lambda2 = 1, penaltyFunction = penaltyFunctionGenerator(), 
verboseOutput = FALSE, prog = FALSE, include.intensity = TRUE, 
include.area = TRUE)
\end{verbatim}

Arguments

\begin{verbatim}
particleset \hspace{1cm} A ParticleSet object  
L \hspace{1cm} Maximum number of pixels an object can move in two consecutive frames  
R \hspace{1cm} Linkrange, i.e. the number of consecutive frames to search for potential candidate links  
epsilon1 \hspace{1cm} A numeric value, to be used in the formula. Jitter for allowing angular displacements  
epsilon2 \hspace{1cm} A numeric value, to be used in the formula. Jitter for allowing spatial displacements  
lambda1 \hspace{1cm} A numeric value. Multiplicative factor for the penalty function  
lambda2 \hspace{1cm} A numeric value. Multiplicative factor applied to the angular displacement  
penaltyFunction \hspace{1cm} A function structured in such a way to be applied as penalty function in the linking  
verboseOutput \hspace{1cm} Logical, whether the output should report additional intermediate steps. For debugging use mainly  
prog \hspace{1cm} Logical, whether a progress bar should be shown during the tracking phase
\end{verbatim}
include.intensity Logical, whether to include also intensity change of the particles in the cost function calculation
include.area Logical, whether to include also area change of the particles in the cost function calculation

Value
A LinkedParticleSet object

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014

References

Examples
data("candidate.platelets")
tracked.platelets <- link.particles(candidate.platelets, L = 40)

matchTrajToParticles

Description
Match trajectories to related particles. This function returns a new ParticleSet object that contains an additional column the trajectory ID that the particular particle was assigned to. Used also by other routines, such as snap

Usage
matchTrajToParticles(particleset, trajectoryset)
normalizeFrames

Arguments

particleset A ParticleSet object
trajectoryset A TrajectorySet object coupled to the particleset

Value

A ParticleSet object with an additional column with the trajectory IDs

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2015

Examples

data(candidate.platelets)
trajs <- trajectories(candidate.platelets)
matchTrajToParticles(candidate.platelets, trajs)

MesenteriumSubset A sample Frames object

Description

The sample Frames object is constituted by a subset of a time-lapse intravital microscopy imaging dataset. Green channel marks leukocytes, red channel focuses on blood platelets. 20 frames are provided in this subset. Images are kindly provided by Sven Jaeckel (<Sven.Jaeckel@unimedizin-mainz.de>).

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

normalizeFrames Normalize the values of a Frames object

Description

Applies a transformation to the Frames object in a way that the intensities throughout the acquisition are normalized overall in term of pixel values sums. It can be used to compensate for example a global change in the illumination values, e.g. due to changed acquisition conditions in experiments that span long timescales.

Usage

normalizeFrames(frames, normFun = "median")

Arguments

frames A Frames object to normalize
normFun The normalization function chosen. Can be one of mean or median
particles

Value
A Frames object with normalized pixel values.

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014

Examples
data(MesenteriumSubset)
normalizeFrames(MesenteriumSubset,normFun="median")

particles

Extracts particles from the images of a Frames object.

Description
Extracts particles from the images of a Frames object.

Usage
particles(raw.frames, binary.frames = NULL, channel = NULL,
BPPARAM = bpparam())

Arguments
raw.frames A Frames object with the raw images (mandatory)
binary.frames A Frames object with preprocessed images (optional, if not provided gets produced with standard default parameters)
channel Character string. The channel to perform the operations on. Can be red, green or blue
BPPARAM a MulticoreParam object, used to control the performances inside the BiocParallel call to process frames in parallel by taking advantage of the computing infrastructure available

Value
A ParticleSet object, containing all detected particles for each frame

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2015

Examples
data("MesenteriumSubset")
**ParticleSet-class**  
*ParticleSet class*

**Description**

S4 class for storing information on particles detected in distinct frames.

**Slots**

- **.Data**  
  A list storing the information for the particles

- **channel**  
  A character vector, can be 'red', 'green', or 'blue'. It refers to which channel the particles were detected

---

**penaltyFunctionGenerator**

*Generate a penalty function*

**Description**

A function to generate penalty functions to use while linking particles

**Usage**

```r
penaltyFunctionGenerator(epsilon1 = 0.1, epsilon2 = 2, lambda1 = 1, lambda2 = 1)
```

**Arguments**

- **epsilon1**  
  A numeric value, to be used in the formula. Jitter for allowing angular displacements

- **epsilon2**  
  A numeric value, to be used in the formula. Jitter for allowing spatial displacements

- **lambda1**  
  A numeric value. Multiplicative factor for the penalty function

- **lambda2**  
  A numeric value. Multiplicative factor applied to the angular displacement

**Value**

A function object, to be used as penalty function

**Author(s)**

Federico Marini, <marinif@uni-mainz.de>, 2014

**Examples**

```r
custom.function <- penaltyFunctionGenerator(epsilon1=0.1,epsilon2=6,lambda1=1.5,lambda2=0)
```
Description

Provides a visual representation of a TrajectorySet object

Usage

```r
## S3 method for class 'TrajectorySet'
plot(x, frames, verbose = FALSE, ...)
```

Arguments

- `x`: A TrajectorySet object
- `frames`: A Frames object, used here to identify the limits of the region of interest
- `verbose`: Logical, whether to provide additional output on the command line
- `...`: Arguments to be passed to methods

Details

Based on the rgl library, the function extracts the region of interests from the dimensions of an image of the Frames object, and afterwards plots the x-y-time representation of the identified trajectories

Value

`plot.TrajectorySet` returns an invisible `NULL`.

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

```r
data("MesenteriumSubset")
data("candidate.platelets")
platelets.trajectories <- trajectories(candidate.platelets)
## Not run:
plot(platelets.trajectories, MesenteriumSubset)
## End(Not run)
```
plot2D.TrajectorySet 2D projection of a TrajectorySet object

Description

Provides a bird’s eye view of a TrajectorySet object on a bidimensional space

Usage

plot2D.TrajectorySet(trajectoryset, frames, trajIDs = NULL, addGrid = FALSE, verbose = FALSE, ...)

Arguments

trajectoryset A TrajectorySet object
frames A Frames object, used here to identify the limits of the region of interest
trajIDs A vector containing the ids of the desired trajectories
addGrid Logical, add an additional grid to the 2-dimensional plot (visual aid for back-tracking trajectory point locations)
verbose Logical, whether to provide additional output on the command line
... Arguments to be passed to methods

Details

Independent from the rgl library, the function extracts the region of interests from the dimensions of an image of the Frames object, and afterwards plots the x-y-time representation of the identified trajectories on a 2d plane. It is possible to subset the TrajectorySet object with the IDs of the desired trajectories

Value

plot2D.TrajectorySet returns an invisible NULL.

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

data("MesenteriumSubset")
data("candidate.platelets")
platelets.trajectories <- trajectories(candidate.platelets)
plot2D.TrajectorySet(platelets.trajectories, MesenteriumSubset)
Preprocessing function for Frames objects

Description
Frames objects are processed according to the chosen set of parameters. Many of them refer directly to existing EBImage functions, please see the corresponding help for additional information.

Usage
preprocess.Frames(frames, brush.size = 3, brush.shape = "disc", at.offset = 0.15, at.wwidth = 10, at.wheight = 10, kern.size = 3, kern.shape = "disc", ws.tolerance = 1, ws.radius = 1, displayprocessing = FALSE, ...)

Arguments
frames A Frames object
brush.size Size in pixels of the brush to be used for initial smoothing (low-pass filtering)
brush.shape Shape of the brush to be used for initial smoothing (low-pass filtering)
at.offset Offset to be used in the adaptive thresholding step - see also thresh. As an alternative thresholding method, see also otsu in the EBImage package.
at.wwidth Width of the window for the adaptive thresholding step - see also thresh. As an alternative thresholding method, see also otsu in the EBImage package.
at.wheight Height of the window for the adaptive thresholding step - see also thresh. As an alternative thresholding method, see also otsu in the EBImage package.
kern.size Size in pixels of the kernel used for morphological operations - e.g., opening, which is an erosion followed by a dilation, and closing which is a dilation followed by an erosion - see also opening, closing
kern.shape Shape of the kernel used for morphological operations
ws.tolerance Tolerance allowed in performing the watershed-based segmentation (see also watershed)
ws.radius Radius for the watershed-based segmentation (see also watershed)
displayprocessing Logical, whether to display intermediate steps while performing preprocessing. Dismissed currently, it could increase runtime a lot
... Arguments to be passed to methods

Value
A Frames object, whose frame images are the preprocessed versions of the input images

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014

Examples
data("MesenteriumSubset")
preprocess.Frames(channel.Frames(MesenteriumSubset,"red"))
read.Frames  

Constructor for a Frames object

Description

This function is used to create a Frames object from a vector of image files (or a folder specifying the directory containing them). The number of frames is also specified, as just a subset of the images can be used for this.

Usage

read.Frames(image.files, nframes = NULL)

Arguments

- **image.files**: Vector of strings containing the locations where the (raw) images are to be found, or alternatively, the path to the folder.
- **nframes**: Number of frames that will constitute the Frames object.

Value

An object of the Frames class, which holds the info on a list of frames, specifying for each the following elements:

- **image**: The Image object containing the image itself.
- **location**: The complete path to the location of the original image.

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

```r
## see vignette
## Not run: fullData <- read.Frames(image.files = "/path/to/the/directory", nframes = 100)
```

read.particles  

Constructor for a ParticleSet object

Description

This function is used to create a ParticleSet object from a vector/list of tab separated text files, each of one containing one line for each particle in the related frame, alongside with its coordinates and if available, the computed features. The number of frames is also specified, as just a subset of the particle lists can be used for this.

Usage

read.particles(particle.files, nframes = NULL)
Arguments

particle.files Vector of strings containing the locations where the particle coordinates are to be found, or alternatively, the path to the folder

nframes Number of frames that will constitute the ParticleSet object

Value

An object of the ParticleSet class

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

## see vignette and export.particles

repmat Function equivalent for MATLAB’s repmat - Replicate and tile arrays

Description

A more flexible and stylish alternative to replicate the behaviour of the repmat function of MATLAB

Usage

repmat(a, n, m)

Arguments

a The matrix to copy
n The n value for the tiling
m The m value for the tiling

Value

Creates a large matrix consisting of an m-by-n tiling of copies of a.

Author(s)

Robin Hankin, 2001

References

http://cran.r-project.org/doc/contrib/R-and-octave.txt
**rotate.Frames**  
*Rotates all images in a Frames object*

**Description**

Rotation is performed exploiting the rotate function of the EBImage package. Could be automated if support for coordinate/pixel interaction is included.

**Usage**

```
rotate.Frames(frames, angle, testing = FALSE)
```

**Arguments**

- `frames`: A `Frames` object
- `angle`: The rotation angle (clockwise) specified in degrees
- `testing`: Logical, whether to just test the rotation or to actually perform it. Default set to `FALSE`

**Value**

A `Frames` object containing the rotated frames

**Author(s)**

Federico Marini, <marinif@uni-mainz.de>, 2014

**Examples**

```
data("MesenteriumSubset")
rotate.Frames(MesenteriumSubset, angle = 40)
```

---

**select.Frames**  
*Extracts subsets of frames from a Frames object*

**Description**

An input `Frames` object is subject to subsetting. This function is useful e.g. when the trajectory of interest is presenting gaps (i.e. does not actually include a frame)

**Usage**

```
select.Frames(frames, framesToKeep = 1, ...)
```

**Arguments**

- `frames`: A `Frames` object
- `framesToKeep`: A vector containing the indexes of the frames to keep in the selection
- `...`: Arguments to be passed to methods
Value
A Frames object, composed by the subset of frames of the input Frames

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014

Examples
```r
data("MesenteriumSubset")
select.Frames(MesenteriumSubset, framesToKeep = c(1:10, 14:20))
```

---

select.particles

Performs filtering on a ParticleSet object

Description
According to parameters of interests, such as size, eccentricity/shape, filters out the particles that do not satisfy the indicated requirements

Usage
```r
select.particles(particleset, min.area = 1, max.area = 1000)
```

Arguments

- **particleset**: A ParticleSet object. A LinkedParticleSet object can also be provided as input, yet the returned object will be a ParticleSet object that needs to be linked again
- **min.area**: Size in pixels of the minimum area needed to detect the object as a potential particle of interest
- **max.area**: Size in pixels of the maximum area allowed to detect the object as a potential particle of interest

Value
A ParticleSet object

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014

Examples
```r
data("candidate.platelets")
selected.platelets <- select.particles(candidate.platelets, min.area = 5)
selected.platelets
```
**shinyFlow**  
*Shiny application for exploring the features and parameters provided by flowcatchR*

**Description**
Launches a Shiny Web Application for interactive data exploration. Default data loaded are the frames from the `MesenteriumSubset` object, custom values can be inserted by typing the location of the data stored in a local folder. The Application is structured in a variety of tabs that mirror the steps in the usual workflow in time-lapse microscopy images. These can allow the user to interactively explore the parameters and their effect in the reactive framework provided by Shiny.

**Usage**
```
shinyFlow()
```

**Value**
The Shiny Application is launched in the web browser

**Author(s)**
Federico Marini, <marinif@uni-mainz.de>, 2015

**Examples**
```
## Not run: shinyFlow()
```

---

**show,Frames-method**  
*Display conveniently a Frames object*

**Description**
Display conveniently a Frames object

**Usage**
```
## S4 method for signature 'Frames'
show(object)
```

**Arguments**

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>A Frames object</td>
</tr>
<tr>
<td>...</td>
<td>Arguments to be passed to methods</td>
</tr>
</tbody>
</table>

**Value**
This returns an invisible NULL.
Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

data("MesenteriumSubset")
print(MesenteriumSubset)

---

Description

Displaying conveniently a KinematicsFeatures object

Usage

```r
## S4 method for signature 'KinematicsFeatures'
show(object)
```

Arguments

- `object`: A KinematicsFeatures object
- `...`: Arguments to be passed to methods

Value

This returns an invisible NULL.

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

data("candidate.platelets")
platelets.trajectories <- trajectories(candidate.platelets)
traj11features <- kinematics(platelets.trajectories,trajectoryIDs = 11)
print(traj11features)
show,KinematicsFeaturesSet-method

Display conveniently a KinematicsFeatureSet object

Description
Display conveniently a KinematicsFeatureSet object

Usage

## S4 method for signature 'KinematicsFeaturesSet'
show(object)

Arguments

object A KinematicsFeatureSet object
... Arguments to be passed to methods

Value
This returns an invisible NULL.

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

data("candidate.platelets")
platelets.trajectories <- trajectories(candidate.platelets)
alltrajs.features <- kinematics(platelets.trajectories)
print(alltrajs.features)

show,LinkedParticleSet-method

Display conveniently a LinkedParticleSet object

Description
Display conveniently a LinkedParticleSet object

Usage

## S4 method for signature 'LinkedParticleSet'
show(object)

Arguments

object A LinkedParticleSet object
... Arguments to be passed to methods
Value

This returns an invisible NULL.

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

data("candidate.platelets")
linked.platelets <- link.particles(candidate.platelets,L=26,R=3,epsilon1=0,
epsilon2=0,lambda1=1,lambda2=0,penaltyFunction=penaltyFunctionGenerator(),
include.area=FALSE)
print(linked.platelets)

show,ParticleSet-method

Display conveniently a ParticleSet object

Description

Display conveniently a ParticleSet object

Usage

## S4 method for signature 'ParticleSet'
show(object)

Arguments

object A ParticleSet object

Value

This returns an invisible NULL.

Author(s)

Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

data("candidate.platelets")
print(candidate.platelets)
show(TrajectorySet-method)

Display conveniently a TrajectorySet object

Description
Display conveniently a TrajectorySet object

Usage
## S4 method for signature 'TrajectorySet'
show(object)

Arguments

object A TrajectorySet object
...
Arguments to be passed to methods

Value
This returns an invisible NULL.

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014

Examples
data("candidate.platelets")
platelets.trajectories <- trajectories(candidate.platelets)
print(platelets.trajectories)

snap

Snap the features of the closest particle identified

Description
This function combines all classes related to a single experiment in order to deliver a clickable feedback on one of the frames.

Usage
snap(raw.frames, binary.frames, particleset, trajectoryset, frameID = 1, infocol = "yellow", infocex = 1, showVelocity = FALSE)
toCartesianCoords

**Arguments**

- `raw.frames` A Frames object with the raw frames data
- `binary.frames` A Frames object with the preprocessed frames data
- `particleset` A ParticleSet object with the particles data
- `trajectoryset` A TrajectorySet object with the trajectories data
- `frameID` The ID of the frame to inspect
- `infocol` The color to use for plotting the contours and the information on the clicked particle
- `infocex` The numeric character expansion value as in `cex` to be used for printing the text on the image
- `showVelocity` Logical, whether to display additional information on the instantaneous velocity of the particle

**Value**

An image of the selected frame, rendered in R native graphics, and additionally a list with the coordinates as well as the trajectory ID of the particle closest to the clicked location

**Author(s)**

Federico Marini, <marinif@uni-mainz.de>, 2015

**Examples**

```R
## Not run: data(MesenteriumSubset)
binary.frames <- preprocess.Frames(channel.Frames(MesenteriumSubset,"red"))
particleset <- particles(MesenteriumSubset,binary.frames,"red")
trajectoryset <- trajectories(particleset)
snap(MesenteriumSubset,binary.frames,particleset,trajectoryset,frameID=1)
## End(Not run)
```

---

**toCartesianCoords**

Converts polar coordinates to cartesian coordinates

**Description**

Conversion from (radius,theta) to (x,y)

**Usage**

```
toCartesianCoords(Theta, Radius)
```

**Arguments**

- `Theta` The Theta angle
- `Radius` The radius value in polar coordinates
toPolarCoords

Converts cartesian coordinates to polar coordinates

Description
Conversion from (x,y) to (radius,theta)

Usage
toPolarCoords(x, y)

Arguments
x   x coordinate
y   y coordinate

Value
A list containing Theta and Radius, as in polar coordinates

Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014

trajectories
Generate trajectories

Description
Generates a TrajectorySet object from a (Linked)ParticleSet

Usage
trajectories(particleset, verbose = FALSE, ...)

Arguments
particleset    A (Linked)ParticleSet object
verbose        Logical, currently not used - could be introduced for providing additional info on the trajectories
...            Arguments to be passed to methods
**Value**

A `TrajectorySet` object

**Author(s)**

Federico Marini, <marinif@uni-mainz.de>, 2014

**Examples**

```r
data("candidate.platelets")
platelets.trajectories <- trajectories(candidate.platelets)
```

---

**Description**

S4 class for storing information on the trajectories identified, including whether there were gaps, the number of points, and more

**Slots**

- `.Data` A list storing the information for the particles
- `channel` A character vector, can be ‘red’, ‘green’, or ‘blue’. It refers to which channel the particles were detected
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