Package ‘flowcatchR’

March 27, 2024

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, rmarkdown

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

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add.contours  

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

Description

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.

Usage

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
addParticles

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 new Frames object with contours of the objects added

Author(s)

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

Examples

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

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

---

candidate.platelets

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

Author(s)
Federico Marini, <marinif@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**  

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**  
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
**crop.Frames**

**Author(s)**

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

---

**crop.Frames**  
*Cut 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)

**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, <marinif@uni-mainz.de>, 2014

Examples

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

export.Frames

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

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, <marinif@uni-mainz.de>, 2014
export.particles

Examples

data("MesenteriumSubset")
## Not run: export.Frames(MesenteriumSubset,nameStub="subset_export_
,createGif=TRUE,removeAfterCreatingGif=FALSE)
## End(Not run)

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

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

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(
  trajectoryset, trajectoryID, acquisitionFrequency = 30, scala = 50
)
```

**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
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>

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")
initialize.LinkedParticleSet

**Frames-class**

*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
Description

The first frames of a Frames object 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.

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), \( \text{totalTime} \), \( \text{totalDistance} \), \( \text{distStartToEnd} \), \( \text{curvilinearVelocity} \), \( \text{straightLineVelocity} \) and \( \text{linearityForwardProgression} \), 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

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

Arguments

- `trajectoryset`: A TrajectorySet object
- `trajectoryIDs`: 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
- `feature`: Character string, the name of the feature to be computed

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

Examples

```r
data("candidate.platelets")
platelets.trajectories <- trajectories(candidate.platelets)
# for all trajectories, all features
alltrajs.features <- kinematics(platelets.trajectories)
```
```r
# 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 class**

**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)
```
Arguments

\texttt{x} \quad \text{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
\end{verbatim}

\begin{verbatim}
\texttt{link.particles} \quad \texttt{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 = FALSE
)
\end{verbatim}

Arguments

\begin{verbatim}
particleset \quad \text{A ParticleSet object}
L \quad \text{Maximum number of pixels an object can move in two consecutive frames}
R \quad \text{Linkrange, i.e. the number of consecutive frames to search for potential candidate links}
\end{verbatim}
**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

**penaltyFunction**  
A function structured in such a way to be applied as penalty function in the linking

**verboseOutput**  
Logical, whether the output should report additional intermediate steps. For debugging use mainly

**prog**  
Logical, whether the a progress bar should be shown during the tracking phase

**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)
**LinkedParticleSet-class**

*LinkedParticleSet class*

**Description**

S4 class for storing information of particles after they have been tracked. It inherits the slots from the ParticleSet class.

**Slots**

- tracking: A list storing all necessary information for the tracking algorithm to work, and for providing the information to the function to determine the trajectories

**matchTrajToParticles**  
*Match trajectories to related particles.*

**Description**

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

**Usage**

`matchTrajToParticles(particleset, trajectoryset)`

**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**

```r
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

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

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

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 `plotly` 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)
```

Description

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

Usage

```r
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 backtracking trajectory point locations)
- `verbose` Logical, whether to provide additional output on the command line
- `...` Arguments to be passed to methods

Details

This 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)

==preprocess.Frames==
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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>frames</td>
<td>A Frames object</td>
</tr>
<tr>
<td>brush.size</td>
<td>Size in pixels of the brush to be used for initial smoothing (low-pass filtering)</td>
</tr>
<tr>
<td>brush.shape</td>
<td>Shape of the brush to be used for initial smoothing (low-pass filtering)</td>
</tr>
<tr>
<td>at.offset</td>
<td>Offset to be used in the adaptive thresholding step - see also thresh. As an alternative thresholding method, see also otsu in the EBImage package.</td>
</tr>
<tr>
<td>at.wwidth</td>
<td>Width of the window for the adaptive thresholding step - see also thresh. As an alternative thresholding method, see also otsu in the EBImage package.</td>
</tr>
</tbody>
</table>
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

```r
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

```r
## 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
select.Frames

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)
```

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
```
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**

- `object` A Frames object

**Value**

This returns an invisible NULL.
Author(s)
Federico Marini, <marinif@uni-mainz.de>, 2014

Examples

```r
data("MesenteriumSubset")
print(MesenteriumSubset)
```

Description

Displaying conveniently a `KinematicsFeatures` object

Usage

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

Arguments

- `object`: A `KinematicsFeatures` object

Value

This returns an invisible NULL.

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

Examples

```r
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

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)
show.ParticleSet-method

Arguments

object A LinkedParticleSet object

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

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

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

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

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

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

---

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
Generating 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)
```

TrajectorySet-class

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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