

# 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.

**License** BSD\_3\_clause + file LICENSE

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, rmarkdown

**Depends** R (>= 2.10), methods, EBImage

**Imports** colorRamps, abind, BiocParallel, graphics, stats, utils, plotly, shiny

**SystemRequirements** ImageMagick

**LazyData** true

**URL** <https://github.com/federicomarini/flowcatchR>,  
<https://federicomarini.github.io/flowcatchR/>

**BugReports** <https://github.com/federicomarini/flowcatchR/issues>

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

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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

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

**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)
```

---

addParticles	<i>Combines the information from a raw Frames object and the corresponding preprocessed one</i>
--------------	---

---

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

---

channel.Frames	<i>Channel extraction for objects</i>
----------------	---------------------------------------

---

**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	<i>Calculates the Mean Squared Displacement for a trajectory</i>
------------	--

---

**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

**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**

```
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 <a href="#">display</a> (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



## 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

```
extractKinematics.traj(  
  trajectoryset,  
  trajectoryID,  
  acquisitionFrequency = 30,  
  scala = 50  
)
```

### Arguments

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

### Value

A `KinematicsFeatures` object

### Author(s)

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

---

flowcatchR-pkg

*flowcatchR: analyzing time-lapse microscopy imaging, from detection to tracking*

---

### 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

*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

*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	<i>Explore the frames of a Frames</i>
----------------	---------------------------------------

---

### 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.

### Author(s)

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

### Examples

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

---

kinematics	<i>Calculate a set of kinematics parameter from a TrajectorySet object, or a single parameter, or from a single trajectory (all possible combinations)</i>
------------	--

---

### 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

<code>trajectoryset</code>	A TrajectorySet object
<code>trajectoryIDs</code>	The ID of a single trajectory
<code>acquisitionFrequency</code>	The frame rate of acquisition for the images, in milliseconds
<code>scala</code>	The value of micro(?)meters to which each single pixel corresponds
<code>feature</code>	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

```
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 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

```
## S3 method for class 'Frames'
length(x)
```

**Arguments**

x                    A Frames object

**Value**

An integer number

**Author(s)**

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

**Examples**

```
data("MesenteriumSubset")
length(MesenteriumSubset)
```

---

link.particles	<i>Links a ParticleSet object</i>
----------------	-----------------------------------

---

**Description**

Performs linking of the particles by tracking them through the frames

**Usage**

```
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
)
```

**Arguments**

particleset    A ParticleSet object

L                Maximum number of pixels an object can move in two consecutive frames

R                Linkrange, i.e. the number of consecutive frames to search for potential candidate links



<code>epsilon1</code>	A numeric value, to be used in the formula. Jitter for allowing angular displacements
<code>epsilon2</code>	A numeric value, to be used in the formula. Jitter for allowing spatial displacements
<code>lambda1</code>	A numeric value. Multiplicative factor for the penalty function
<code>lambda2</code>	A numeric value. Multiplicative factor applied to the angular displacement
<code>penaltyFunction</code>	A function structured in such a way to be applied as penalty function in the linking
<code>verboseOutput</code>	Logical, whether the output should report additional intermediate steps. For debugging use mainly
<code>prog</code>	Logical, whether the a progress bar should be shown during the tracking phase
<code>include.intensity</code>	Logical, whether to include also intensity change of the particles in the cost function calculation
<code>include.area</code>	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**

I F Sbalzarini and P Koumoutsakos. "Feature point tracking and trajectory analysis for video imaging in cell biology." In: *Journal of structural biology* 151.2 (Aug. 2005), pp. 182-95. ISSN: 1047-8477. DOI: 10.1016/j.jsb.2005.06.002. URL: <http://www.ncbi.nlm.nih.gov/pubmed/16043363>

**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

```
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	<i>ParticleSet class</i>
-------------------	--------------------------

---

**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	<i>Generate a penalty function</i>
--------------------------	------------------------------------

---

**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**

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

---

plot.TrajectorySet     *3D representation of a TrajectorySet object*

---

**Description**

Provides a visual representation of a TrajectorySet object

**Usage**

```
## 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

```
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

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.width = 10,
  at.height = 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 <a href="#">thresh</a> . As an alternative thresholding method, see also <a href="#">otsu</a> in the EBImage package.
at.width	Width of the window for the adaptive thresholding step - see also <a href="#">thresh</a> . As an alternative thresholding method, see also <a href="#">otsu</a> in the EBImage package.



at.height	Height of the window for the adaptive thresholding step - see also <a href="#">thresh</a> . As an alternative thresholding method, see also <a href="#">otsu</a> 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 <a href="#">opening</a> , <a href="#">closing</a>
kern.shape	Shape of the kernel used for morphological operations
ws.tolerance	Tolerance allowed in performing the watershed-based segmentation (see also <a href="#">watershed</a> )
ws.radius	Radius for the watershed-based segmentation (see also <a href="#">watershed</a> )
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**

```
## 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**

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

---

select.particles	<i>Performs filtering on a ParticleSet object</i>
------------------	---

---

### Description

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

### Usage

```
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

```
data("candidate.platelets")
selected.platelets <- select.particles(candidate.platelets, min.area = 5)
selected.platelets
```

---

shinyFlow	<i>Shiny application for exploring the features and parameters provided by flowcatchR</i>
-----------	---

---

**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	<i>Display conveniently a Frames object</i>
--------------------	---

---

**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

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

---

show, KinematicsFeatures-method

*Displaying conveniently a KinematicsFeatures object*

---

### Description

Displaying conveniently a KinematicsFeatures object

### Usage

```
## 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

```
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)
```



### 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**

```

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

```

**Arguments**

<code>raw.frames</code>	A Frames object with the raw frames data
<code>binary.frames</code>	A Frames object with the preprocessed frames data
<code>particleset</code>	A ParticleSet object with the particles data
<code>trajectoryset</code>	A TrajectorySet object with the trajectories data
<code>frameID</code>	The ID of the frame to inspect
<code>infocol</code>	The color to use for plotting the contours and the information on the clicked particle
<code>infoceX</code>	The numeric character expansion value as in <code>cex</code> to be used for printing the text on the image
<code>showVelocity</code>	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**

```

## 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

---

trajectories	<i>Generate trajectories</i>
--------------	------------------------------

---

**Description**

Generates a TrajectorySet object from a (Linked)ParticleSystem

**Usage**

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

**Arguments**

particleset	A (Linked)ParticleSystem 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**

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

---

TrajectorySet-class	<i>TrajectorySet class</i>
---------------------	----------------------------

---

**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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