# Package 'cellmigRation'

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**Type** Package

**Title** Track Cells, Analyze Cell Trajectories and Compute Migration Statistics

**Version** 1.15.0

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**Description**
Import TIFF images of fluorescently labeled cells, and track cell movements over time. Parallelization is supported for image processing and for fast computation of cell trajectories. In-depth analysis of cell trajectories is enabled by 15 trajectory analysis functions.

**biocViews** CellBiology, DataRepresentation, DataImport

**License** GPL-2

**Encoding** UTF-8

**LazyData** false

**Depends** R (>= 4.1), methods, foreach

**Imports** tiff, graphics, stats, utils, reshape2, parallel, doParallel, grDevices, matrixStats, FME, SpatialTools, sp, vioplot, FactoMineR, Hmisc

**Suggests** knitr, rmarkdown, dplyr, ggplot2, RUnit, BiocGenerics, BiocManager, kableExtra, rgl

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**BugReports** https://github.com/ocbe-uio/cellmigRation/issues

**URL** https://github.com/ocbe-uio/cellmigRation/

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# Contents

## cellmigRation-package *Track And Analyze Cell Migrations*

### Description

Track Fluorescent Cells and Analyze their movements. Compute Migration Statistics and advanced metrics to understand motility and movement characteristics of a population of cells.

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>; Damiano Fantini, <damiano.fantini@gmail.com>

### See Also

Useful links:

- https://github.com/ocbe-uio/cellmigRation/
- Report bugs at https://github.com/ocbe-uio/cellmigRation/issues

## AddDimension *Add Dimension to a Molten Data Frame*

### Description

Creates a new (molten) data matrix where all elements of y are added to each row of x. Each row in x is recycled for each element in y. Elements in y are added as the first column in the returned matrix.

### Usage

```
AddDimension(x, y)
```

### Arguments

| | |
|---|---|
| x | a matrix or data.frame with at least 1 row and 1 column. |
| y | a vector with elements that will be added to x |

### Value

a matrix with an extra column as compared to x

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::AddDimension(
    x = cbind(seq(1,4,by=1), seq(4,1,by=-1)),
    y = c(9, 7))
```

---

aggregateFR *Aggregating the outcome of several experiments or conditions.*

---

## Description

Aggregate two or more CellMig-class objects together. Input objects must carry information of trajectory analyses (otherwise an error will be raised). All trajectory results form the different experiments/conditions are returned in two data frames.

## Usage

```
aggregateFR(x, ..., export = FALSE)
```

## Arguments

| | |
|---|---|
| x | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |
| ... | one or more CellMig-class object(s) where cells' trajectories have already been analyzed. |
| export | if 'TRUE' (default), exports function output to CSV file |

## Details

The visualization shows centered trajectories where the starting point of each track is located at the origin of the coordinate system (X=0,Y=0).

## Value

two data frames: The first data frame shows the average of each parameter per experiment/condition. The second data frame shows the parameters of individual cells of all experiments/conditions.

## Author(s)

Damiano Fantini and Salim Ghannoum <salim.ghannoum@medisin.uio.no> Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(WSADataset)
wasDF1 <- WSADataset[seq(1,300,by=1), ]
wsaTD1 <- CellMig(wasDF1)
wsaTD1 <- wsaPreProcessing(wsaTD1,FrameN=55)
wsaTD1 <-FMI(wsaTD1,TimeInterval=10)
wsaTD1 <-FinRes(wsaTD1,ParCor=FALSE, export=FALSE)
wasDF2 <- WSADataset[seq(500,700,by=1), ]
wsaTD2 <- CellMig(wasDF2)
wsaTD2 <- wsaPreProcessing(wsaTD2,FrameN=55)
wsaTD2 <-FMI(wsaTD2,TimeInterval=10)
wsaTD2 <-FinRes(wsaTD2,ParCor=FALSE, export=FALSE)
AGG<-aggregateFR(wsaTD1 ,wsaTD2 ,export=FALSE)
```

---

# aggregateTrackedCells *Aggregate trackedCells Objects*

---

## Description

Aggregate two or more trackedCells-class objects together. Input objects must carry information of cell tracks (otherwise an error will be raised). All tracks form the different experiments/images are returned in a large data.frame. A new unique ID is assigned to specifically identify each cell track from each image/experiment.

## Usage

```
aggregateTrackedCells(
  x,
  ...,
  meta_id_field = c("tiff_file", "experiment", "condition", "replicate")
)
```

## Arguments

| | |
|---|---|
| x | a trackedCells-class object where cells have already been tracked |
| ... | one or more trackedCells-class object(s) where cells have already been tracked |
| meta_id_field | string, can take one of the following values, c("tiff_file", "experiment", "condition", "replicate"). Indicates the meta-data column used as unique ID for the image/experiment. Can be abbreviated. Defaults to "tiff_file". |

## Details

each trackedCells-class object passed to this function requires a unique identifier (such as a unique tiff_file name). Any of the metadata columns can be used as unique ID for an image/experiment. The function will raise an error if non-unique identifiers are found across the input objects.

## Value

An aggregate data.frame including all cells that were tracked over two or more images/experiments. The data.frame includes the following columns: "new.ID", "frame.ID", "X", "Y", "cell.ID", "tiff_name", "experiment", "condition", "replicate". The "new.ID" uniquely identifies a cell in a given image/experiment.

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
# Please, see the package vignette
# for an example of how to use this function.
# A pseudo-code example is shown below
# Let x0, x1, x2, ... be trackedCells-class objects
# with a non-empty tracks slot.
x0 <- get(data(TrackCellsDataset))
x0 <- setCellsMeta(x0, experiment = "my_exp_01", condition = "CTRL")
x1 <- setCellsMeta(x0, experiment = "my_exp_01", condition = "DMSO")
x2 <- setCellsMeta(x0, experiment = "my_exp_01", condition = "DRUG")
y <- aggregateTrackedCells(x0, x1, x2, meta_id_field = "condition")
utils::head(y, 50)
```

---

# bpass *Perform a bandpass by convolving with an appropriate kernel*

---

## Description

Implements a real-space bandpass filter that suppresses pixel noise and long-wavelength image variations while retaining information of a characteristic size. First, a lowpassed image is produced by convolving the original with a gaussian. Next, a second lowpassed image is produced by convolving the original with a boxcar function. By subtracting the boxcar version from the gaussian version, we are using the boxcar version to perform a highpass. This code 'bpass.pro' is copyright 1997, John C. Crocker and David G. Grier. It should be considered 'freeware'- and may be distributed freely in its original form when properly attributed.

## Usage

```
bpass(image_array, lnoise, lobject = NULL, threshold)
```

## Arguments

| | |
|---|---|
| image_array | Numeric matrix corresponding to the image to be filtered |
| lnoise | Characteristic lengthscale of noise in pixels. |
| lobject | Integer length in pixels somewhat larger than a typical object |
| threshold | By default, after the convolution, any negative pixels are reset to 0. Threshold changes the threshhold for setting pixels to 0. Positive values may be useful for removing stray noise or small particles. |

## Value

Numeric matrix corresponding to the filtered image

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x0 <- cbind(
    c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0),
    c(0, 0, 0, 0, 0, 1, 1, 4, 2, 0, 0, 0, 0, 0, 0),
    c(0, 0, 0, 0, 1, 2, 6, 5, 3, 0, 0, 0, 1, 0, 0),
    c(0, 0, 0, 0, 5, 5, 6, 8, 6, 1, 0, 0, 6, 2, 0),
    c(0, 0, 2, 5, 8, 7, 3, 5, 1, 0, 0, 0, 6, 2, 0),
    c(0, 0, 1, 5, 8, 7, 4, 5, 2, 0, 0, 0, 0, 0, 0),
    c(0, 0, 0, 5, 8, 7, 4, 5, 2, 0, 0, 0, 0, 0, 0),
    c(0, 0, 0, 1, 4, 5, 2, 4, 0, 0, 0, 0, 0, 0, 0),
    c(0, 0, 0, 0, 2, 3, 2, 1, 0, 0, 0, 0, 0, 0, 0),
    c(0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0),
    c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 0),
    c(9, 9, 9, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 2, 1),
    c(2, 9, 9, 0, 0, 0, 0, 0, 0, 0, 0, 0, 3, 2, 1),
    c(0, 2, 3, 0, 0, 0, 0, 0, 0, 0, 0, 0, 3, 0, 0),
    c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0),
    c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0))
y0 <- cellmigRation:::bpass(x0, lnoise = 1, lobject = 5, threshold = 1)
par(mfrow = c(1, 2))
image(x0); title("original")
image(y0); title("after bpass")
```

CellMig-class *The CellMig Class.*

## Description

The CellMig class represents objects storing all information for both random migration (RM) and wound scratch assay (WSA). It comprises 14 slots.

## Usage

```
CellMig(..., ExpName = NULL)

## S4 method for signature 'CellMig'
initialize(.Object, trajdata)

CellMig(..., ExpName = NULL)
```

## Arguments

| | |
|---|---|
| ... | arguments to pass to the CellMig constructor |
| ExpName | string, experiment name (optional) |
| .Object | the CellMig object being built |
| trajdata | data frame including trajectory data |

## Value

An S4-class object

a CellMig object

## Slots

`trajdata` The raw trajectory data matrix organized into four columns: cell ID, X coordinates, Y coordinates and Track number, which is the track's path order.

`adjDS` A data frame of the trajectory data passed from the WSAprep function.

`cellpos` A binary vector showing on which side of the wound cells are located. "0" refers to a cell located above the wound whereas "1" refers to a cell located below the wound.

`parE` A numeric vector contains estimations for the imageH, woundH, upperE and lowerE.

`preprocessedDS` list object of data frames, each data frame shows the trajectories of a single cell.

`DRtable` A data frame of the results of running the DiRatio() function.

`MSDtable` A data frame of the results of running the MSD() function.

`PerAanSpeedtable` A data frame of the results of running the PerAndSpeed() function.

`DACtable` A data frame of the results of running the DiAutoCor() function.

`VACtable` A data frame of the results of running the VeAutoCor() function.

`ForMigtable` A data frame of the results of running the ForwardMigration() function.

`FMItable` A data frame of the results of running the FMI() function.

`results` A data frame of all the results.

`parCor` A data frame for Parameters Correlation.

`meta` A list including experiment name, meta data and other information.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## Examples

```
data("TrajectoryDataset")
CellMig(TrajectoryDataset)
```

---

`CellMigPCA` *PCA*

---

## Description

The CellMigPCA function automatically generates Principal Component Analysis.

## Usage

```
CellMigPCA(object, parameters = c(1, 2, 3))
```

## Arguments

| | |
|---|---|
| `object` | `CellMig` class object, which is a list of data frames resulted from the PrePro-cessing. |
| `parameters` | A numeric vector contains the parameters to be included in the Principal Compo-nent Analysis. These numbers can be obtained from the outcome of the FinRes() function. |

## Value

PCA Graph of cells and PCA Graph of variables.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(WSADataset)
wasDF=WSADataset[seq(1,300,by=1),]
wsaTD <- CellMig(wasDF)
wsaTD <- wsaPreProcessing(wsaTD,FrameN=55)
wsaTD <-FMI(wsaTD,TimeInterval=10)
wsaTD <-ForwardMigration(wsaTD,TimeInterval=10)
wsaTD <-FinRes(wsaTD,ParCor=FALSE)
PCAplot<-CellMigPCA(wsaTD,parameters=c(1,4))
```

---

`CellMigPCAclust` *PCA Clusters*

---

## Description

The CellMigPCAclust function automatically generates clusters based on the Principal Component Analysis.

## Usage

```
CellMigPCAclust(
  object,
  parameters = c(1, 2, 3),
  export = FALSE,
  interactive = TRUE
)
```

## Arguments

| | |
|---|---|
| `object` | `CellMig` class object, which is a list of data frames resulted from the PreProcessing. |
| `parameters` | A numeric vector contains the parameters to be included in the Principal Component Analysis. These numbers can be obtained from the outcome of the FinRes() function. |
| `export` | if 'TRUE' (default), exports function output to CSV file |
| `interactive` | logical, shall the PCA analysis be generated in a interactive fashion |

## Value

PCA Graph of cells and PCA Graph of variables.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
## The analysis only supports the interactive method!
## If interactive=FALSE, the function will return NULL
data(WSADataset)
wasDF <- WSADataset[seq(1, 300, by=1), ]
wsaTD <- CellMig(wasDF)
CellMigPCAclust(wsaTD, parameters=c(1,9), interactive=FALSE)
##
## A real world example is shown below (uncomment)
# data(WSADataset)
# wasDF <- WSADataset[seq(1,300,by=1),]
# wsaTD <- CellMig(wasDF)
# wsaTD <- wsaPreProcessing(wsaTD,FrameN=55)
# wsaTD <-FMI(wsaTD,TimeInterval=10)
# wsaTD <-ForwardMigration(wsaTD,TimeInterval=10)
# wsaTD <-FinRes(wsaTD,ParCor=FALSE)
# PCAclust <- CellMigPCAclust(wsaTD,parameters=c(1,9))
```

---

# CellMigPCAclustALL *PCA Clusters of different conditions*

---

## Description

The CellMigPCAclust function automatically generates clusters based on the Principal Component Analysis.

## Usage

```
CellMigPCAclustALL(
  object,
  ExpName = "PCA_Clusters",
  parameters = c(1, 2, 3),
  export = FALSE,
  interactive = TRUE
)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |
| ExpName | A character string. The ExpName will be appended to all exported tracks and statistics data. |

| | |
|---|---|
| parameters | A numeric vector contains the parameters to be included in the Principal Component Analysis. These numbers can be obtained from the outcome of the FinRes() function. |
| export | if 'TRUE' (default), exports function output to CSV file |
| interactive | logical, shall the PCA analysis be generated in a interactive fashion |

## Value

PCA Graph of cells and PCA Graph of variables.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
## The analysis only supports the interactive method!
## If interactive=FALSE, the function will return NULL
data(WSADataset)
wasDF1 <- WSADataset[seq(1,300,by=1), ]
wsaTD1 <- CellMig(wasDF1)
wsaTD1 <- wsaPreProcessing(wsaTD1,FrameN=55)
wsaTD1 <-FMI(wsaTD1,TimeInterval=10)
wsaTD1 <-FinRes(wsaTD1,ParCor=FALSE, export=FALSE)
wasDF2 <- WSADataset[seq(500,700,by=1), ]
wsaTD2 <- CellMig(wasDF2)
wsaTD2 <- wsaPreProcessing(wsaTD2,FrameN=55)
wsaTD2 <-FMI(wsaTD2, TimeInterval=10)
wsaTD2 <-FinRes(wsaTD2, ParCor=FALSE, export=FALSE)
AGG <- aggregateFR(wsaTD1, wsaTD2, export=FALSE)
CellMigPCAclustALL(AGG,ExpName="Aggregated_Conditions",
                   parameters=c(1,6), export=FALSE, interactive=FALSE)
# The previous line returns NULL
# In an interactive session, try running the following command (uncomment!)
# CellMigPCAclustALL(AGG,ExpName="Aggregated_Conditions",
#                    parameters=c(1,6), export=FALSE)
```

---

# CellTracker *Compute Cell Tracks*

---

## Description

Analyze Stacks, detect cells in each frame, and analyze cell tracks over time

## Usage

```
CellTracker(
  tc_obj,
  import_optiParam_from = NULL,
  min_frames_per_cell = 1,
  lnoise = NULL,
  diameter = NULL,
  threshold = NULL,
  maxDisp = NULL,
  memory_b = 0,
  goodenough = 0,
  threads = 1,
  show_plots = FALSE,
  verbose = FALSE,
  dryrun = FALSE
)
```

## Arguments

| | |
|---|---|
| tc_obj | a trackedCells object. |
| import_optiParam_from | a trackedCells object (optional) used to import optimized parameters; can be NULL. |
| min_frames_per_cell | numeric, minimum number of consecutive frames in which a cell shall be found in order to retain that cell in the final cell tracks data.frame. Defaults to 1. |
| lnoise | numeric, lnoise parameter; can be NULL if OptimizeParams() has already been run |
| diameter | numeric, diameter parameter; can be NULL if OptimizeParams() has already been run |
| threshold | numeric, threshold parameter; can be NULL if OptimizeParams() has already been run |
| maxDisp | numeric, maximum displacement of a cell per time interval. When many cells are detected in each frame, small maxDisp values should be used. |
| memory_b | numeric, memory_b parameter as used in the original track.m function. In the current R implementation, only the value memory_b=0 is accepted |
| goodenough | numeric, goodenough parameter as used in the original track.m function. In the current R implementation, only the value goodenough=0 is accepted |
| threads | integer, number of cores to use for parallelization |
| show_plots | logical, shall cells detected in each frame of the image stack be visualized |
| verbose | logical, shall info about the progress of the cell tracking job be printed |
| dryrun | logical, shall a dryrun be performed |

## Details

The lnoise param is used to guide a lowpass blurring operation, while the lobject param is used to guide a highpass background subtraction. The threshold param is used for a background correction following the initial image convolution

- **lnoise**: Characteristic lengthscale of noise in pixels. Additive noise averaged over this length should vanish. May assume any positive floating value. May be also set to 0, in which case only the highpass "background subtraction" operation is performed.
- **lobject** Integer length in pixels somewhat larger than a typical object. Can also be set to 0, in which case only the lowpass "blurring" operation defined by lnoise is done without the background subtraction defined by lobject
- **threshold** Numeric. By default, after the convolution, any negative pixels are reset to 0. Threshold changes the threshhold for setting pixels to 0. Positive values may be useful for removing stray noise or small particles.

## Value

a trackedCells object

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x <- get(data(TrackCellsDataset))
x <- CellTracker(x, dryrun=TRUE)
getTracks(x)[seq(1,12,by=1),]
```

---

# CellTrackerMainLoop *Cell Tracker Main Loop*

---

## Description

Tool for Cell Tracker Main Loop

### Usage

```
CellTrackerMainLoop(
  FinalImage,
  threads,
  tc_obj,
  min_frames_per_cell,
  track_params
)
```

### Arguments

| | |
|---|---|
| FinalImage | list of numeric matrices |
| threads | numeric, number of cores to use |
| tc_obj | trackingCell object |
| min_frames_per_cell | numeric, minimum number of frames per cell |
| track_params | a list of tracking parameters |

### Details

This is an internal function supporting the CellTracker function.

### Value

list of processed data

### Examples

```
cellmigRation:::CellTrackerMainLoop(list(1), 1, 1, list(1))
```

---

## CentroidArray *Build a Centroid Array*

---

### Description

Create an array containing centroid data for particles identified in each frame of the imported TIFF image stack

### Usage

```
CentroidArray(stack, lobject, threshold, dryrun = FALSE)
```

### Arguments

| | |
|---|---|
| stack | 3D matrix loaded to workspace from .tif stack |
| lobject | Integer length in pixels somewhat larger than a typical object |
| threshold | the minimum brightness of a pixel that might be local maxima |
| dryrun | logical, shall the execution be skipped |

### Value

data.frame of centroids, with 4 columns corresponding to x-position of centroid, y-postion of centroid, brightness, and square of the radius of gyration

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

### Examples

```
# by default, the dryrun argument is set to FALSE
df <- get(data(TrackCellsDataset))
x0 <- getCellImages(df)
y0 <- cellmigRation:::CentroidArray(x0, 16, 10, TRUE)
y0
```

---

## CentroidValidation *Validate Centroids*

---

### Description

Validate parameters used to identify cells in a image stack. A figure containing current image frame with identified particles labeled with circles and numerical tags is generated. This function is included for consistency and compatibility reasons with the original fastTracks software (Matlab). Also, consider using VisualizeStackCentroids() or visualizeCellTracks() instead.

### Usage

```
CentroidValidation(
  stack,
  slice,
  lobject,
  threshold,
```

```
  pnt.cex = 1.2,
  txt.cex = 0.85,
  offset = 0.18
)
```

## Arguments

| | |
|---|---|
| stack | stack of images to be evaluated |
| slice | index of the frame within the stack to be evaluated |
| lobject | integer, length in pixels somewhat larger than a typical object (cell) |
| threshold | the minimum brightness of a pixel that might be local maxima. NOTE: Make it big and the code runs faster but you might miss some particles. Make it small and you'll get everything and it'll be slow. |
| pnt.cex | cex of the circle drawn around each cell |
| txt.cex | cex of the text used for annotating cells |
| offset | offset used for annotating cells |

## Value

data.frame of centroid positions

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x <- get(data(TrackCellsDataset))
x <- getCellImages(x)
x$images[[1]] <- x$images[[1]][seq(110,160,by=1), seq(100,160,by=1)]
cellmigRation:::CentroidValidation(x, slice = 1, lobject =10, threshold = 5)
```

---

# circshift *Shift Array Circularly*

---

## Description

Circularly shift the elements in an array by a user-defined number of positions. This emulates the behavior of the corresponding Matlab Circhsift function.

### Usage

```
circshift(x, n = 1)
```

### Arguments

| | |
|---|---|
| x | a character, numeric, or logical vector with at least n + 1 elements |
| n | an integer corresponding to the number of positions for the shift |

### Value

a vector corresponding to x (same size, same class), whose elements have been shifted

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/

### Examples

```
cellmigRation:::circshift(seq(1,10,by=1), -2)
```

---

## cntrd *Calculates Centroids*

---

### Description

Calculates the centroid of bright spots to sub-pixel accuracy. Inspired by Grier & Crocker's feature for IDL, but greatly simplified and optimized for MATLAB, and then further ported to R. CREATED: Eric R. Dufresne, Yale University, Feb 4 2005.

### Usage

```
cntrd(im, mx, sz, interactive = NULL)
```

### Arguments

| | |
|---|---|
| im | numeric matrix corresponding to the image to process |
| mx | location of local maxima to pixel-levels accuracy |
| sz | diameter of the window over which to average to calculate the centroid. should be big enough. |
| interactive | numeric; if set to 1 (or any positive number), an image showing the computed centroids will be visualized |

### Value

a data.frame with 4 columns, containing, x, y, brightness, and the square of the radius of gyration for each cell.

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

### Examples

```
x0 <- getCellImages(get(data(TrackCellsDataset)))
x0 <- x0$images[[1]][seq(80,150,by=1), seq(80,150,by=1)]
b <- cellmigRation:::bpass(image_array = x0, lnoise = 2,
                           lobject = 15, threshold = 1)
pk <- cellmigRation:::pkfnd(b, th = 2, sz = 5)
cnt <- cellmigRation:::cntrd(im = b, mx = pk, sz = 5)
cnt
```

---

## ComputeTracksStats *Compute Tracks Stats*

---

### Description

Wrapper for the MigrationStats() function. It computes statistics for a trackedCells object where cells have already been tracked.

### Usage

```
ComputeTracksStats(tc_obj, time_between_frames, resolution_pixel_per_micron)
```

### Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |
| time_between_frames | integer, time interval between two successive frames were taken |
| resolution_pixel_per_micron | integer, image resolution, i.e. number of pixels per micron |

### Value

a trackedCells object, including cell track statistics

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

### Examples

```
x <- get(data(TrackCellsDataset))
x <- ComputeTracksStats(x, time_between_frames = 10,
                        resolution_pixel_per_micron = 20)
getCellsStats(x)
```

---

## DetectRadii *Detect Linear Paricle Diameters*

---

### Description

Estimates the diameters of particles in a numeric or logical vector

### Usage

```
DetectRadii(x)
```

### Arguments

| | |
|---|---|
| x | numeric or logical vector |

### Value

data.frame including two columns: MPOS indicates the centroid position of a particle, and LEN indicates the diameter size

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/

### Examples

```
cellmigRation:::DetectRadii(c(0,0,1,1,0,1,1,1,1,0,0, 1,0,0,1,1))
```

DiAutoCor *Direction AutoCorrelation*

## Description

The DiAutoCor function automatically compute the angular persistence across several sequantial time intervals.

## Usage

```
DiAutoCor(
  object,
  TimeInterval = 10,
  sLAG = 0.25,
  sPLOT = TRUE,
  aPLOT = TRUE,
  export = FALSE,
  ExpName = NULL
)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| sLAG | A numeric value to be used to get the number of lags for the slope fitting. Default is 0.25, which represents 25 percent of the steps. |
| sPLOT | A logical vector that allows generating individual plots showing the angular persistence across several sequantial time intervals. Default is TRUE. |
| aPLOT | A logical vector that allows generating a plot showing the angular persistence across several sequantial time intervals of all cells. Default is TRUE. |
| export | if 'TRUE' (default), exports function output to CSV file |
| ExpName | string, name of the experiment. Can be NULL |

## Value

An CellMig class Object with a data frame and plots. The data frame, which contains six rows: "Cell Number", "Angular Persistence", "Intercept of DA quadratic model", "Mean Direction AutoCorrelation (all lags)", "Stable Direction AutoCorrelation through the track" and "Difference between Mean DA and Intercept DA".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(TrajectoryDataset)
rmDF=TrajectoryDataset[seq(1,220,by=1),]
rmTD <- CellMig(rmDF)
rmTD <- rmPreProcessing(rmTD,FrameN=55)
rmTD <- DiAutoCor(rmTD, TimeInterval=10, sLAG=0.25, sPLOT=FALSE,
                  aPLOT=FALSE, export=FALSE)
```

---

# DiRatio *Directionality Table*

---

## Description

Directionality Ratio is the displacement divided by the total length of the total path distance, where displacement is the straight line length between the start point and the endpoint of the migration trajectory,

## Usage

```
DiRatio(object, TimeInterval = 10, export = FALSE, ExpName = NULL)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| export | if 'TRUE' (default), exports function output to CSV file |
| ExpName | string |

## Details

Directionality Ratio and Directional persistence

## Value

An CellMig class object with a data frame stored in the DRtable slot. It contains nine rows: "Cell Number", "Directionality Ratio","Mean Cumulative Directionality Ratio", "Stable Directionality Ratio", "Number of returns","Min CumDR", "Location of Min CumDR, Steps with less CumDR than DR", "Directional Persistence"

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

### References

https://www.data-pulse.com/dev_site/cellmigration/

### Examples

```
rmTD <- get(data(preProcCellMig))
rmTD <- DiRatio(rmTD, export=FALSE)
```

---

## DiRatioPlot *Directionality Ratio plots*

---

### Description

Directionality Ratio is the displacement divided by the total length of the total path distance, where displacement is the straightline length between the start point and the endpoint of the migration trajectory,

### Usage

```
DiRatioPlot(object, TimeInterval = 10, export = FALSE, ExpName = NULL)
```

### Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| export | if 'TRUE' (default), exports plot to JPG file |
| ExpName | string, name of the experiment. Can be NULL |

### Details

Directionality Ratio

### Value

Directionality Ratio plots

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
rmTD <- get(data(preProcCellMig))
DiRatioPlot(object=rmTD, export=FALSE)
```

---

EstimateDiameterRange *Detect Paricle Diameters in a Numeric matrix*

---

## Description

Estimates the diameters of particles in a numeric matrix

## Usage

```
EstimateDiameterRange(
  x,
  px.margin = 2,
  min.px.diam = 5,
  quantile.val = 0.99,
  plot = TRUE
)
```

## Arguments

| | |
|---|---|
| x | numeric matrix corresponding to a digital image |
| px.margin | integer, number of pixels used as margin while searching/filtering for neighboring particles |
| min.px.diam | integer, minimum diameter of a particle (cell). Particles with a diameter smaller than min.px.diam are discarded |
| quantile.val | numeric, must be bigger than 0 and smaller than 1. Quantile for discriminating signal and background; only pixels with intensity higher than the corresponding quantile will count as signal while estimating particle diameters |
| plot | logial, shall a histogram of the distribution of diameters be shown |

## Value

list including summary stats and data about the particles found in the image

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
a <- cbind(c(1, 1, 1, 0, 0, 0, 0, 0, 1, 1),
           c(1, 1, 0, 0, 0, 0, 0, 0, 1, 1),
           c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0),
           c(0, 0, 0, 0, 1, 1, 0, 0, 0, 0),
           c(0, 0, 0, 1, 1, 1, 0, 0, 0, 0))
graphics::image(a)
b <- EstimateDiameterRange(a, min.px.diam = 2)
print(b$estim.cell.num)
print(b$raw)
```

---

# FianlizeOptiParams *Finalize Output in Parameter Optimization*

---

## Description

Finalize Output as part of the Optimization Parameter process

## Usage

```
FianlizeOptiParams(all_results, all_params, target_cell_num, plot)
```

## Arguments

| | |
|---|---|
| all_results | list, including all intermediates |
| all_params | data.frame, including all parameter combinations to test |
| target_cell_num | numeric, number of expected cells |
| plot | logical, shall a series of plots be generated |

## Details

This is an internal function supporting the Optimization Parameter process

## Value

a list including test results; an empty list is returned if an error is encountered.

## Examples

```
cellmigRation:::FianlizeOptiParams(list(1), data.frame(1), 10, FALSE)
```

`FilterTrackedCells` *Filter an Aggregated Table of Cell Tracks*

## Description

Filter an Aggregated Table (data.frame) of cell tracks (from multiple images/experiments) and retain cell tracks from images/experiments of interest

## Usage

```
FilterTrackedCells(x, id_list, meta_id_field)
```

## Arguments

| | |
|---|---|
| `x` | data.frame, is an aggregated Table of Cell Tracks. Must include the following columns: "new.ID", "frame.ID", "X", "Y", "cell.ID", "tiff_name", "experiment", "condition", "replicate" |
| `id_list` | character vector, indicates the IDs (such as tiff_filenames) to be retained in the output data.frame |
| `meta_id_field` | string, can take one of the following values, c("tiff_file", "experiment", "condition", "replicate"). Indicates the meta-data column used as unique ID for the image/experiment. Can be abbreviated. Defaults to "tiff_file". |

## Value

data.frame, a filtered aggregated Table of Cell Tracks

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
A <- data.frame(new.ID = seq(1,10,by=1), frame.ID = seq(10,1,by=(-1)),
                X = sample(seq(1,100,by=1), size = 10),
                Y = sample(seq(1,100,by=1), size = 10),
                cell.ID = c(rep(1, 5), rep(2, 5)),
                tiff_file= c(rep("ii", 3), rep("jj", 5), rep('kk', 2)))
FilterTrackedCells(A, id_list = c("jj", "kk"), "tiff_file")
```

FinRes *Final Results*

## Description

The FinRes function automatically generates a data frame that contains all the results.

## Usage

```
FinRes(object, ParCor = TRUE, export = FALSE, ExpName = NULL)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |
| ParCor | A logical vector that allows generating a correlation table. Default is TRUE. |
| export | if 'TRUE' (default), exports function output to CSV file |
| ExpName | string, name of the experiment. Can be NULL |

## Value

A data frame that contains all the results.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(WSADataset)
wasDF <- WSADataset[seq(1,300,by=1), ]
wsaTD <- CellMig(wasDF)
wsaTD <- wsaPreProcessing(wsaTD,FrameN=55)
wsaTD <-FMI(wsaTD,TimeInterval=10)
wsaTD <-ForwardMigration(wsaTD,TimeInterval=10,)
wsaTD <-FinRes(wsaTD,ParCor=FALSE, export=FALSE)
```

fixDA *Direction AutoCorrelation*

## Description

This function is a part of the DiAutoCor function, which computes the angular persistence across several sequantial time intervals.

## Usage

```
fixDA(Object, Step, sLAG, sPLOT, aPLOT, color, export, ExpName, new.fld)
```

## Arguments

| | |
|---|---|
| Step | A numeric value of the number of trajectory steps. |
| sLAG | A numeric value to be used to get the number of lags for the slope fitting. Default is 0.25, which represents 25 percent of the steps. |
| sPLOT | A logical vector that allows generating individual plots showing the angular persistence across several sequantial time intervals. Default is TRUE. |
| aPLOT | A logical vector that allows generating a plot showing the angular persistence across several sequantial time intervals of all cells. Default is TRUE. |
| color | A vector of colors that will be used for the plots |
| export | if 'TRUE' (default), exports function output |
| ExpName | String, name of the experiment |
| new.fld | path to the folder where to save files |
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |

## Value

A data frame named "DA.ResultsTable".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixDA(1, 1, 1, 1, 1, 1, 1, 1, 1)
```

## fixExpName *Handle non-NULL ExpName*

### Description

The fixExpName helps adjusting the name of the experiment in case it is not NULL.

### Usage

```
fixExpName(x)
```

### Arguments

| | |
|---|---|
| x | string, name of the experiment. |

### Value

A string referring to the adjusted experiment name.

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

### References

https://www.data-pulse.com/dev_site/cellmigration/

### Examples

```
cellmigRation:::fixExpName("Hello World")
```

## fixFM1 *Forward Migration First Part*

### Description

This function is a part of the ForwardMigration function, which generates data and plots for forward persistence and speed.

### Usage

```
fixFM1(Object, Step)
```

### Arguments

| | |
|---|---|
| Step | A numeric value of the number of trajectory steps. |
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |

### Value

An CellMig class Object.

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

### References

https://www.data-pulse.com/dev_site/cellmigration/

### Examples

```
cellmigRation:::fixFM1(1, 1)
```

---

## fixFM2 *Forward Migration Second Part*

---

### Description

This function is a part of the ForwardMigration function, which generates data and plots for forward persistence and speed.

### Usage

```
fixFM2(Object, Step)
```

### Arguments

| | |
|---|---|
| Step | A numeric value of the number of trajectory steps. |
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |

### Value

An CellMig class Object.

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixFM2(1, 1)
```

---

`fixFM3` *Forward Migration Third Part*

---

## Description

This function is a part of the ForwardMigration function, which generates data and plots for forward persistence and speed.

## Usage

```
fixFM3(Object, Step)
```

## Arguments

| | |
|---|---|
| `Step` | A numeric value of the number of trajectory steps. |
| `object` | `CellMig` class object, which is a list of data frames resulted from the PrePro-cessing. |

## Value

A data frame named"cosine.FP".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixFM3(1, 1)
```

fixFM4 *Forward Migration Fourth Part*

## Description

This function is a part of the ForwardMigration function, which generates data and plots for forward persistence and speed.

## Usage

```
fixFM4(Object, TimeInterval, Step)
```

## Arguments

| | |
|---|---|
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| Step | A numeric value of the number of trajectory steps. |
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |

## Value

An CellMig class Object.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixFM4(1, 1, 1)
```

`fixFM5` *Forward Migration Fifth Part*

## Description

This function is a part of the ForwardMigration function, which generates data and plots for forward persistence and speed.

## Usage

```
fixFM5(Object, TimeInterval, Step)
```

## Arguments

| | |
|---|---|
| `TimeInterval` | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| `Step` | A numeric value of the number of trajectory steps. |
| `object` | `CellMig` class object, which is a list of data frames resulted from the PreProcessing. |

## Value

A data frame named "FMResultsTable".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixFM5(1, 1, 1)
```

fixFM6 *Forward Migration Sixst Part*

## Description

This function is a part of the ForwardMigration function, which generates data and plots for forward persistence and speed.

## Usage

```
fixFM6(
  Object,
  FMResultsTable,
  Step,
  sfptPLOT,
  afptPLOT,
  export,
  color,
  TimeInterval,
  sfpPLOT,
  ExpName,
  new.fld
)
```

## Arguments

| | |
|---|---|
| FMResultsTable | A data frame resulted from the fixFM6(). |
| Step | A numeric value of the number of trajectory steps. |
| sfptPLOT | A logical vector that allows generating individual plots of persistence time vs speed per cell. Default is TRUE. |
| afptPLOT | A logical vector that allows generating a plot of persistence time vs speed for all cells. Default is TRUE. |
| export | if 'TRUE' (default), exports function output to CSV file |
| color | A vector of colors that will be used for the plots |
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| sfpPLOT | A logical vector that allows generating individual plots of angular persistence vs speed per cell. Default is TRUE. |
| ExpName | String, name of the experiment |
| new.fld | path to the folder where to save files |
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |

## Value

A data frame named "FMResultsTable".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixFM6(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
```

---

# fixID1 *Pre-processing First Part*

---

## Description

This function prepare the data in each data frame as a part of the pre-processing.

## Usage

```
fixID1(ID_split, TimeInterval)
```

## Arguments

| | |
|---|---|
| ID_split | A list of data frames. |
| TimeInterval | A numeric value of the time elapsed between |

## Value

A list of data frames.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixID1(ID_split = list(data.frame()), TimeInterval = 1)
```

## fixID2 *Pre-processing Second Part*

### Description

This function prepare the data in each data frame as a part of the pre-processing.

### Usage

```
fixID2(ID_split)
```

### Arguments

| | |
|---|---|
| ID_split | A list of data frames. |
| TimeInterval | A numeric value of the time elapsed between |

### Value

A list of data frames.

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

### References

https://www.data-pulse.com/dev_site/cellmigration/

## fixID3 *Pre-processing Third Part*

### Description

This function prepare the data in each data frame as a part of the pre-processing.

### Usage

```
fixID3(ID_split)
```

### Arguments

| | |
|---|---|
| ID_split | A list of data frames. |
| TimeInterval | A numeric value of the time elapsed between |

## Value

A list of data frames.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

---

`fixID4` *Pre-processing Fourth Part*

---

## Description

This function prepare the data in each data frame as a part of the pre-processing.

## Usage

```
fixID4(ID_split)
```

## Arguments

| | |
|---|---|
| `ID_split` | A list of data frames. |
| `TimeInterval` | A numeric value of the time elapsed between |

## Value

A list of data frames.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## fixID5 *Pre-processing Fifth Part*

### Description

This function prepare the data in each data frame as a part of the pre-processing.

### Usage

```
fixID5(ID_split, TimeInterval)
```

### Arguments

| | |
|---|---|
| ID_split | A list of data frames. |
| TimeInterval | A numeric value of the time elapsed between |

### Value

A list of data frames.

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

### References

https://www.data-pulse.com/dev_site/cellmigration/

## fixID6 *Pre-processing Sixst Part*

### Description

This function prepare the data in each data frame as a part of the pre-processing.

### Usage

```
fixID6(ID_split, TimeInterval)
```

### Arguments

| | |
|---|---|
| ID_split | A list of data frames. |
| TimeInterval | A numeric value of the time elapsed between |

## Value

A list of data frames.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

---

`fixMSD` *Mean Square Displacement*

---

## Description

This function is a part of the MSD function, which computes the mean square displacements across several sequential time intervals.

## Usage

```
fixMSD(
  Object,
  Step,
  SlopePlot,
  AllSlopesPlot,
  FurthPlot,
  AllFurthPlot,
  sLAG,
  ffLAG,
  color,
  export,
  ExpName,
  new.fld
)
```

## Arguments

| | |
|---|---|
| `Step` | A numeric value of the number of trajectory steps. |
| `SlopePlot` | A logical vector that allows generating individual plots showing the slope of the mean square displacement of the movement of individual cells. Default is TRUE. |
| `AllSlopesPlot` | A logical vector that allows generating a plot showing the slope of the mean square displacement of the movement of all cells. Default is TRUE. |
| `FurthPlot` | A logical vector that allows generating individual plots fitting the Furth formula using generalized regression by the Nelder–Mead method simplex method per cell. Default is TRUE. |

| | |
|---|---|
| AllFurthPlot | A logical vector that allows generating a plot fitting the Furth formula using generalized regression by the Nelder–Mead method simplex method for all cells. Default is TRUE. |
| sLAG | A numeric value to be used to get the number of lags for the slope fitting. Default is 0.25, which represents 25 percent of the steps. |
| ffLAG | A numeric value to be used to get the number of lags for the Furth formula fitting. Default is 0.25, which represents 25 percent of the steps. |
| color | A vector of colors that will be used for the plots |
| export | if 'TRUE' (default), exports function output |
| ExpName | String, name of the experiment |
| new.fld | path to the folder where to save files |
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |

## Value

A data frame named "MSDResultsTable".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixMSD(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
```

---

# fixPER1 *Persistence and Speed First Part*

---

## Description

This function is a part of the PerAndSpeed(), which generates data and plots for persistence and speed.

## Usage

```
fixPER1(Object, TimeInterval)
```

## Arguments

| | |
|---|---|
| TimeInterval | A numeric value of the time elapsed between |
| x | CellMig class object, which is a list of data |

## Value

A data frame named "PerResultsTable".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixPER1(1, 1)
```

---

# fixPER2 *Persistence and Speed Second Part*

---

## Description

This function is a part of the PerAndSpeed(), which generates data and plots for persistence and speed.

## Usage

```
fixPER2(
  Object,
  PerResultsTable,
  PtSplot,
  AllPtSplot,
  export,
  color,
  TimeInterval,
  ExpName,
  new.fld
)
```

## Arguments

| | |
|---|---|
| TimeInterval | A numeric value of the time elapsed between |
| ExpName | String, name of the experiment |
| new.fld | path to the folder where to save files |
| x | CellMig class object, which is a list of data |

## Value

A data frame named "PerResultsTable".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixPER2(1, 1, 1, 1, 1, 1, 1, 1, 1)
```

---

# fixPER3 *Persistence and Speed Third Part*

---

## Description

This function is a part of the PerAndSpeed(), which generates data and plots for persistence and speed.

## Usage

```
fixPER3(
  Object,
  PerResultsTable,
  ApSplot,
  AllApSplot,
  export,
  color,
  TimeInterval,
  ExpName,
  new.fld
)
```

## Arguments

| | |
|---|---|
| Object | CellMig class object, which is a list of data. |
| PerResultsTable | A data frame. |
| ApSplot | A logical vector that allows generating individual plots of angular persistence vs speed per cell. Default is TRUE. |
| AllApSplot | A logical vector that allows generating a plot of angular persistence vs speed of all cells. Default is TRUE. |

| | |
|---|---|
| export | if 'TRUE' (default), exports function output. |
| color | A vector of colors that will be used for the plots |
| TimeInterval | A numeric value of the time elapsed between |
| ExpName | String, name of the experiment |
| new.fld | path to the folder where to save files |

## Value

A data frame named "PerResultsTable".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::fixPER3(1,1,1,1,1,1,1,1,1)
```

---

# FMI *Forward Migration Index*

---

## Description

The FMI function automatically generates data for the forward migration index

## Usage

```
FMI(object, TimeInterval = 10, export = FALSE, ExpName = NULL)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| export | if 'TRUE' (default), exports function output to CSV file |
| ExpName | string, name of the experiment. Can be NULL |

## Value

An CellMig class Object with a data frame. The data frame is stored in the FMItable slot.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(WSADataset)
wasDF=WSADataset[seq(1,300,by=1),]
wsaTD <- CellMig(wasDF)
wsaTD <- wsaPreProcessing(wsaTD,FrameN=55)
wsaTD <-FMI(wsaTD,TimeInterval=10, export=FALSE)
```

---

# ForwardMigration *Forward Migration*

---

## Description

The ForwardMigration function automatically generates data and plots for forward persistence and speed.

## Usage

```
ForwardMigration(
  object,
  TimeInterval = 10,
  sfptPLOT = TRUE,
  afptPLOT = TRUE,
  sfpPLOT = TRUE,
  afpPLOT = TRUE,
  export = FALSE,
  ExpName = NULL
)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| sfptPLOT | A logical vector that allows generating individual plots of persistence time vs speed per cell. Default is TRUE. |
| afptPLOT | A logical vector that allows generating a plot of persistence time vs speed for all cells. Default is TRUE. |

| | |
|---|---|
| sfpPLOT | A logical vector that allows generating individual plots of angular persistence vs speed per cell. Default is TRUE. |
| afpPLOT | A logical vector that allows generating a plot of angular persistence vs speed of all cells. Default is TRUE. |
| export | if 'TRUE' (default), exports function output to CSV file |
| ExpName | string, name of the experiment. Can be NULL |

## Value

An CellMig class Object with a data frame and plots. The data frame is stored in the ForMigtable slot.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(WSADataset)
wsaDF <- WSADataset[seq(1,500,by=1),]
wsaTD <- CellMig(wsaDF)
wsaTD <- wsaPreProcessing(wsaTD,FrameN=55)
wsaTD <-ForwardMigration(wsaTD, TimeInterval=10, sfptPLOT=FALSE,
                         afptPLOT= FALSE,sfpPLOT= FALSE,
                         afpPLOT= FALSE, export=FALSE)
```

---

# GenAllCombos *Generate All Combinations*

---

## Description

Generate All Combinations as part of the Optimization Parameter process

## Usage

```
GenAllCombos(...)
```

## Arguments

| | |
|---|---|
| ... | a series of arguments where each argument is a vector of values to be combined together |

## Details

This is an internal function supporting the Optimization Parameter steps

## Value

a data frame of combined parameters to be tested

## Examples

```
cellmigRation:::GenAllCombos(A=c(1,2,3), B = 10, C = c("x", "y", "z"))
```

---

`getAvailableAggrMetrics` *Get Available Aggregate Cell Metrics*

---

## Description

Retrieve a list of metrics computed for an aggregated result object. This getter function takes the output of aggregateFR() as input.

## Usage

```
getAvailableAggrMetrics(object)
```

## Arguments

| | |
|---|---|
| `object` | list of length 2, returned by the aggregateFR() function |

## Value

character vector listing all available metrics

## Author(s)

Damiano Fantini and Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(WSADataset)
wasDF1 <- WSADataset[seq(1,300,by=1), ]
wsaTD1 <- CellMig(wasDF1)
wsaTD1 <- wsaPreProcessing(wsaTD1,FrameN=65)
wsaTD1 <- FMI(wsaTD1,TimeInterval=10)
wsaTD1 <- FinRes(wsaTD1,ParCor=FALSE, export=FALSE)
wasDF2 <- WSADataset[seq(1001,1300,by=1), ]
wsaTD2 <- CellMig(wasDF2)
wsaTD2 <- wsaPreProcessing(wsaTD2,FrameN=65)
wsaTD2 <-FMI(wsaTD2,TimeInterval=10)
wsaTD2 <-FinRes(wsaTD2,ParCor=FALSE, export=FALSE)
AGG <- aggregateFR(wsaTD1 ,wsaTD2 ,export=FALSE)
getAvailableAggrMetrics(AGG)
```

---

# getCellImages *Method getCellImages*

---

## Description

Retrieve Images from a `trackedCells` object.

## Usage

```
getCellImages(x)

## S4 method for signature 'trackedCells'
getCellImages(x)
```

## Arguments

| | |
|---|---|
| x | a `trackedCells`-class object |

## Value

a list including all images

## Examples

```
data("TrackCellsDataset")
getCellImages(TrackCellsDataset)
```

## getCellMigSlot *Method getCellMigSlot*

### Description

Get Data from a slot in a CellMig object.

### Usage

```
getCellMigSlot(x, slot)

## S4 method for signature 'CellMig,character'
getCellMigSlot(x, slot)
```

### Arguments

| | |
|---|---|
| x | a CellMig-class object |
| slot | string pointing to the slot to be retrieved |

### Value

a slot from a CellMig object

### Examples

```
data("TrajectoryDataset")
x <- CellMig(TrajectoryDataset)
getCellMigSlot(x, "trajdata")
```

## getCellsMeta *Get MetaData*

### Description

Extract MetaData from a trackedCells object

### Usage

```
getCellsMeta(tc_obj)
```

### Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |

## Value

a list including four items: tiff filename, experiment name, condition label, and replicate ID.

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x0 <- get(data(TrackCellsDataset))
getCellsMeta(x0)
```

---

# getCellsStats *Get Cell migration stats*

---

## Description

Extract cell migration statistics from a trackedCells object

## Usage

```
getCellsStats(tc_obj)
```

## Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |

## Value

data.frame including cell migration stats

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x <- get(data(TrackCellsDataset))
getCellsStats(x)
```

---

`getCellTrackMeta` *Method getCellTrackMeta*

---

## Description

Retrieve Metadata from a `trackedCells` object.

## Usage

```
getCellTrackMeta(x)

## S4 method for signature 'trackedCells'
getCellTrackMeta(x)
```

## Arguments

| | |
|---|---|
| `x` | a `trackedCells`-class object |

## Value

a list including Meta Data

## Examples

```
data("TrackCellsDataset")
getCellTrackMeta(TrackCellsDataset)
```

---

`getCellTracks` *Method getCellTracks*

---

## Description

Retrieve Cell Tracks from a `trackedCells` object.

## Usage

```
getCellTracks(x)

## S4 method for signature 'trackedCells'
getCellTracks(x)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |

### Value

a data.frame including Cell Tracks

### Examples

```
data("TrackCellsDataset")
getCellTracks(TrackCellsDataset)
```

---

## getCellTrackStats *Method getCellTrackStats*

---

### Description

Retrieve Stats from a trackedCells object.

### Usage

```
getCellTrackStats(x)

## S4 method for signature 'trackedCells'
getCellTrackStats(x)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |

### Value

a list including Track statistics

### Examples

```
data("TrackCellsDataset")
getCellTrackStats(TrackCellsDataset)
```

`getDACtable` *Getting the Direction AutoCorrelation*

## Description

The DiAutoCor function automatically compute the angular persistence across several sequantial time intervals.

## Usage

```
getDACtable(object)
```

## Arguments

| | |
|---|---|
| `object` | `CellMig` class object, which is a list of data frames resulted from the PreProcessing. |

## Value

A data frame which contains six rows: "Cell Number", "Angular Persistence", "Intercept of DA quadratic model", "Mean Direction AutoCorrelation (all lags)", "Stable Direction AutoCorrelation through the track" and "Difference between Mean DA and Intercept DA".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(TrajectoryDataset)
rmDF=TrajectoryDataset[seq(1,300,by=1),]
rmTD <- CellMig(rmDF)
rmTD <- rmPreProcessing(rmTD,FrameN=55)
rmTD <- DiAutoCor(rmTD, TimeInterval=10, sLAG=0.25, sPLOT=FALSE,
                  aPLOT=FALSE, export=FALSE)
head(getDACtable(rmTD))
```

getDiRatio *Getting the Directionality Table*

## Description

Directionality Ratio is the displacement divided by the total length of the total path distance, where displacement is the straight line length between the start point and the endpoint of the migration trajectory,

## Usage

```
getDiRatio(object)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |

## Details

Directionality Ratio and Directional persistence

## Value

A data frame. It contains nine rows: "Cell Number", "Directionality Ratio","Mean Cumulative Directionality Ratio", "Stable Directionality Ratio", "Number of returns","Min CumDR", "Location of Min CumDR, Steps with less CumDR than DR", "Directional Persistence".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
rmTD <- get(data(preProcCellMig))
rmTD <- DiRatio(rmTD, export=FALSE)
head(getDiRatio(rmTD))
```

getFMItable *Getting the Forward Migration Index*

## Description

The FMI function automatically generates data for the forward migration index

## Usage

```
getFMItable(object)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |

## Value

A data frame for the FMI.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(WSADataset)
wasDF=WSADataset[seq(1,300,by=1),]
wsaTD <- CellMig(wasDF)
wsaTD <- wsaPreProcessing(wsaTD,FrameN=55)
wsaTD <-FMI(wsaTD,TimeInterval=10, export=FALSE)
head(getFMItable(wsaTD))
```

getForMigtable *Getting the Forward Migration*

## Description

The ForwardMigration function automatically generates data and plots for forward persistence and speed.

## Usage

```
getForMigtable(object)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |

## Value

A data frame inclusing values of the forward migration analysis.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(WSADataset)
wsaDF <- WSADataset[seq(1,300,by=1),]
wsaTD <- CellMig(wsaDF)
wsaTD <- wsaPreProcessing(wsaTD,FrameN=55)
wsaTD <-ForwardMigration(wsaTD, TimeInterval=10, sfptPLOT=FALSE,
                         afptPLOT= FALSE, sfpPLOT= FALSE,
                         afpPLOT= FALSE, export=FALSE)
head(getForMigtable(wsaTD))
```

## getImageCentroids *Method getImageCentroids*

### Description

Retrieve Image Centroids from a trackedCells object.

### Usage

```
getImageCentroids(x)

## S4 method for signature 'trackedCells'
getImageCentroids(x)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |

### Value

a list including all centroids

### Examples

```
data("TrackCellsDataset")
getImageCentroids(TrackCellsDataset)
```

## getImageStacks *Get Image Stacks*

### Description

Extract Images Stacks from a trackedCells object

### Usage

```
getImageStacks(tc_obj)
```

### Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |

### Value

a list including stack images (formatted as numeric matrices)

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

### Examples

```
x0 <- get(data(TrackCellsDataset))
y0 <- getImageStacks(x0)
graphics::image(y0[[1]])
```

---

## getMSDtable *Getting the Mean Square Displacement*

---

### Description

The MSD function automatically computes the mean square displacements across several sequential time intervals. MSD parameters are used to assess the area explored by cells over time.

### Usage

```
getMSDtable(object)
```

### Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |

### Value

A data frame of MSD values.

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

### References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(TrajectoryDataset)
rmDF <- TrajectoryDataset[seq(1,600,by=1), ]
rmTD <- CellMig(rmDF)
rmTD <- rmPreProcessing(rmTD,FrameN=100)
rmTD <- MSD(rmTD, sLAG=0.25, ffLAG=0.25, export=FALSE)
head(getMSDtable(rmTD))
```

---

`getOptimizedParameters` *Get Auto Optimized Parameters*

---

## Description

Extract Parameters that were automatically optimized

## Usage

```
getOptimizedParameters(tc_obj)
```

## Arguments

| | |
|---|---|
| `tc_obj` | a `trackedCells` object |

## Value

a list including optimized parameter values (lnoise, diameter, and threshold)

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x <- get(data(TrackCellsDataset))
getOptimizedParameters(x)
```

## getOptimizedParams *Method getOptimizedParams*

### Description

Retrieve Optimized Params from a trackedCells object.

### Usage

```
getOptimizedParams(x)

## S4 method for signature 'trackedCells'
getOptimizedParams(x)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |

### Value

a list including Optimized Parameters

### Examples

```
data("TrackCellsDataset")
getOptimizedParams(TrackCellsDataset)
```

## getPerAndSpeed *Getting the table of Persistence and Speed.*

### Description

The PerAndSpeed() generates data and plots for persistence and speed.

### Usage

```
getPerAndSpeed(object)
```

### Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |

### Value

A data frame of Persistence and Speed.

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

### References

https://www.data-pulse.com/dev_site/cellmigration/

### Examples

```
rmTD <- get(data(preProcCellMig))
rmTD <- PerAndSpeed(rmTD,TimeInterval=10, export=FALSE)
head(getPerAndSpeed(rmTD))
```

---

## getPopulationStats *Get Cell population stats*

---

### Description

Extract cell population statistics from a trackedCells object

### Usage

```
getPopulationStats(tc_obj)
```

### Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |

### Value

data.frame including cell population stats

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

### Examples

```
x <- get(data(TrackCellsDataset))
getPopulationStats(x)
```

## getProcessedImages *Method getProcessedImages*

### Description

Retrieve Processed Images from a `trackedCells` object.

### Usage

```
getProcessedImages(x)

## S4 method for signature 'trackedCells'
getProcessedImages(x)
```

### Arguments

| | |
|---|---|
| x | a `trackedCells`-class object |

### Value

a list including all processed images

### Examples

```
data("TrackCellsDataset")
getProcessedImages(TrackCellsDataset)
```

## getProcessingStatus *Method getProcessingStatus*

### Description

Retrieve Processing Status from a `trackedCells` object.

### Usage

```
getProcessingStatus(x)

## S4 method for signature 'trackedCells'
getProcessingStatus(x)
```

### Arguments

| | |
|---|---|
| x | a `trackedCells`-class object |

## Value

a list including Processing Status

## Examples

```
data("TrackCellsDataset")
getProcessingStatus(TrackCellsDataset)
```

---

`getResults` *Final Results*

---

## Description

The FinRes function automatically generates a data frame that contains all the results.

## Usage

```
getResults(object)
```

## Arguments

| | |
|---|---|
| `object` | `CellMig` class object, which is a list of data frames resulted from the PrePro-cessing. |

## Value

A data frame that contains all the results.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(WSADataset)
wasDF <- WSADataset[seq(1,300,by=1), ]
wsaTD <- CellMig(wasDF)
wsaTD <- wsaPreProcessing(wsaTD,FrameN=55)
wsaTD <-FMI(wsaTD,TimeInterval=10)
wsaTD <-ForwardMigration(wsaTD,TimeInterval=10,)
wsaTD <-FinRes(wsaTD,ParCor=FALSE, export=FALSE)
head(getResults(wsaTD))
```

## getTracks *Get Track Data*

### Description

Extract Track Data from a trackedCells object

### Usage

```
getTracks(tc_obj, attach_meta = FALSE)
```

### Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |
| attach_meta | logical, shall metaData be attached to tracks |

### Value

a data.frame including cell tracks data

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

### Examples

```
x <- get(data(TrackCellsDataset))
getTracks(x)[seq(1,10,by=1),]
```

## getVACtable *Getting the Velocity AutoCorrelation*

### Description

The VeAutoCor function automatically compute the changes in both speed and direction across several sequantial time intervals.

### Usage

```
getVACtable(object)
```

### Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |

### Value

A data frame, which contains six rows: "Cell Number", "Velocity AutoCorrelation (lag=1)", "2nd normalized Velocity AutoCorrelation", "Intercept of VA quadratic model", "Mean Velocity AutoCorrelation (all lags)", "Mean |Acceleration|" and "Average Speed".

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

### References

https://www.data-pulse.com/dev_site/cellmigration/

### Examples

```
data(TrajectoryDataset)
rmDF=TrajectoryDataset[seq(1,300,by=1),]
rmTD <- CellMig(rmDF)
rmTD <- rmPreProcessing(rmTD,FrameN=55)
rmTD <- VeAutoCor(rmTD, TimeInterval=10, sLAG=0.25, sPLOT=FALSE,
                  aPLOT=FALSE, export=FALSE)
head(getVACtable(rmTD))
```

---

## initializeTrackParams *Initialize Tracking parameters*

---

### Description

Initialize parameter variables used for the tracking

### Usage

```
initializeTrackParams(dd = 0, params)
```

### Arguments

| | |
|---|---|
| dd | numeric, value of the dd param |
| params | a list containing a few tracking parameters that are needed for the analysis |

### Value

a list including parsed arguments

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### Examples

```
cellmigRation:::initializeTrackParams(0, NULL)
```

---

## innerBondRaster *Inner Bond Raster*

---

### Description

Perform Inner Bond Raster as part of the Cell Tracking Processing

### Usage

```
innerBondRaster(xyzs, maxdisp, j = 1, env)
```

### Arguments

| | |
|---|---|
| xyzs | data.frame, including input cell centroid positions |
| maxdisp | numeric, value of maximum cell dispersion in pixels |
| env | environment, including all objects used for the tracking |
| i | numeric, index of the iteration cycle |

### Details

a message is printed if an issue (typically arising by a non-suitable environment being passed as the env argument) is detected. See the example below.

### Value

FALSE is returned; objects in env are updated

### Examples

```
cellmigRation:::innerBondRaster(data.frame(1), 1, 1, new.env())
```

## internalPermutation *Internal Permutation*

### Description

Perform Internal Permutation as part of the Cell Tracking Processing

### Usage

```
internalPermutation(xyzs, maxdisp, env)
```

### Arguments

| | |
|---|---|
| xyzs | data.frame, including input cell centroid positions |
| maxdisp | numeric, value of maximum cell dispersion in pixels |
| env | environment, including all objects used for the tracking |

### Details

a message is printed if an issue (typically arising by a non-suitable environment being passed as the env argument) is detected. See the example below.

### Value

FALSE is returned while objects in env are updated

### Examples

```
cellmigRation:::internalPermutation(data.frame(1), 1, new.env())
```

## LinearConv2 *Linear Convolution of a Numeric Matrix*

### Description

Performs a linear convolution of a Numeric Matrix, using a user-supplied linear kernel. The convolution can be executed in a column-wise fashion by setting the col.wise argument to TRUE. Alternatively, the convolution is performed in a row-wise fashion.

### Usage

```
LinearConv2(x, krnl, col.wise = TRUE)
```

### Arguments

| | |
|---|---|
| x | numeric matrix that will be used as input for the convolution; this matrix typically corresponds to an image where signal (high values) indicates the presence of a cell or a cell-like particle |
| krnl | numeric vector corresponding to the kernel that will be used for the convolution. Briefly, the kernel includes the weights that will be used to compute a weighted sum at each position of the input numeric matrix |
| col.wise | logical; shall the linear convolution be performed in a column-wise or row-wise fashion? |

### Value

Linearly convoluted numeric matrix. The resulting matrix has the same dimensions of the inut matrix

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/

### Examples

```
graphics::par(mfrow = c(1, 2))
tmp <- vapply(
    seq_len(12),
    function(i) {(6 + abs(i - 6)) * c(seq(1,10,by=1), seq(10,1,by=-1))},
    FUN.VALUE = numeric(20)
)
cnv.tmp <- cellmigRation:::LinearConv2(tmp, c(-3, 0, 3))
graphics::image(tmp); graphics::image(cnv.tmp)
```

---

## LoadTiff *Import Image from TIFF*

---

### Description

Import a .tif stack containing fluorescently labeled point particles to be tracked

### Usage

```
LoadTiff(tiff_file, experiment = NULL, condition = NULL, replicate = NULL)
```

### Arguments

| | |
|---|---|
| tiff_file | path to a TIFF file to be read in |
| experiment | string, a label to describe the experiment (optional) |
| condition | string, a label to describe the experimental condition |
| replicate | string, a label to identify the replicate (optional) |

### Value

a trackedCells object

### Note

'experiment', 'condition' and 'replicate' are optional arguments and can be NULL.

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

### Examples

```
# Let `path/to/tiff_file.tiff` be the path to tiff file we want to
# import. If an error is thrown, NULL is returned.
x <- LoadTiff(tiff_file = "path/to/tiff_file.tiff")
```

---

## MakeHypercube *Make Hypercube*

---

### Description

Creates a Molten Hypercube with a user-defined number of dimensions. The values supplied by the user are used to fill each dimension. All possible combination of values are included in the resulting hyper cube.

### Usage

```
MakeHypercube(vals, dims)
```

### Arguments

| | |
|---|---|
| vals | vector of values used to fill the hyper cube |
| dims | integer indicating the number of dimensions. The resulting molden data frame will have a number of columns equal to dims |

## Value

Matrix corresponding to a molten hyper cube. The number of columns is equal to dims; the number of rows is equal to length(vals) ^ dims

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::MakeHypercube(seq(1,3,by=1), 3)
```

---

`matfix` *Clean And Reformat a Numeric Matrix*

---

## Description

Convert any matrix-lie object to a numeric Matrix, and coerces all the elements to integer. Row names and column names are removed.

## Usage

```
matfix(x)
```

## Arguments

| | |
|---|---|
| `x` | matrix or data.frame including numeric data (or data that can be coerced to integer) |

## Value

numeric matrix with all its elements coerced to integer

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
tmp <- data.frame(A = c(1,2,3,4), B=c(3.1, 2.8, 3.3, 9.1), C = FALSE)
cellmigRation:::matfix(tmp)
```

---

`MigrationStats` *Compute Cell Migration Statistics*

---

## Description

Calculate the statistics from X/Y positional data obtained from cell tracks

## Usage

```
MigrationStats(tracks, interval_time, pixel_micron)
```

## Arguments

| | |
|---|---|
| `tracks` | data.frame with cell tracks information |
| `interval_time` | integer, time interval between two successive frames were taken |
| `pixel_micron` | integer, image resolution, i.e. number of pixels per micron |

## Value

list of stats calculated for the cell tracks. Info include variables of speed, distance, euclidean displacement, persistence, angular displacement, yFMI, xFMI, y-displacement, x-displacement and frames

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x0 <- cbind(c(30, 35, 1, 5, 6, 7, 50, 55, 56, 58),
            c(29, 37, 2, 7, 4, 9, 40, 50, 59, 49),
            c( 1,  2, 1, 2, 3, 4,  1,  2,  3,  4),
            c( 1,  1, 2, 2, 2, 2,  3,  3,  3,  3))
cellmigRation:::MigrationStats(x0, 10, 10)
```

MSD *Mean Square Displacement*

## Description

The MSD function automatically computes the mean square displacements across several sequential time intervals. MSD parameters are used to assess the area explored by cells over time.

## Usage

```
MSD(
  object,
  TimeInterval = 10,
  sLAG = 0.25,
  ffLAG = 0.25,
  SlopePlot = TRUE,
  AllSlopesPlot = TRUE,
  FurthPlot = TRUE,
  AllFurthPlot = TRUE,
  export = FALSE,
  ExpName = NULL
)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| sLAG | A numeric value to be used to get the number of lags for the slope fitting. Default is 0.25, which represents 25 percent of the steps. |
| ffLAG | A numeric value to be used to get the number of lags for the Furth formula fitting. Default is 0.25, which represents 25 percent of the steps. |
| SlopePlot | A logical vector that allows generating individual plots showing the slope of the mean square displacement of the movement of individual cells. Default is TRUE. |
| AllSlopesPlot | A logical vector that allows generating a plot showing the slope of the mean square displacement of the movement of all cells. Default is TRUE. |
| FurthPlot | A logical vector that allows generating individual plots fitting the Furth formula using generalized regression by the Nelder–Mead method simplex method per cell. Default is TRUE. |
| AllFurthPlot | A logical vector that allows generating a plot fitting the Furth formula using generalized regression by the Nelder–Mead method simplex method for all cells. Default is TRUE. |
| export | if 'TRUE' (default), exports function output |
| ExpName | string, anem of the Experiment. Can be NULL |

## Value

An CellMig class object with a data frame and plots. The data frame is stored in the MSDtable slot.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(TrajectoryDataset)
rmDF <- TrajectoryDataset[seq(1,220,by=1), ]
rmTD <- CellMig(rmDF)
rmTD <- rmPreProcessing(rmTD,FrameN=100)
rmTD <- MSD(rmTD, sLAG=0.25, ffLAG=0.25, export=FALSE)
```

---

# NextOdd *Return the Next Odd Integer*

---

## Description

Returns the smallest odd number bigger than the number(s) provided as the argument

## Usage

```
NextOdd(x)
```

## Arguments

| | |
|---|---|
| x | a vector of class numeric |

## Value

a vector of class integer

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
cellmigRation:::NextOdd(seq(2,5,by=1))
```

---

`NonParallel4OptimizeParams` *Non Paralle Parameter Optimization*

---

## Description

Non Parallel Optimization as part of the Optimization Parameter process

## Usage

```
NonParallel4OptimizeParams(
  tmp_img = tmp_img,
  all_params = all_params,
  verbose = verbose
)
```

## Arguments

| | |
|---|---|
| `tmp_img` | numeric matrix, corresponding to the |
| `all_params` | data.frame, including all parameter combinations to test |
| `verbose` | logical, shall info be printed to console |

## Details

This is an internal function supporting the Optimization Parameter process

## Value

a list including test results; an empty list is returned if an error is encountered.

## Examples

```
cellmigRation:::NonParallel4OptimizeParams(matrix(1), data.frame(1), TRUE)
```

## NonParallelTrackLoop *Single Core Tracking Loop*

### Description

Tool for Single Core Tracking Loop

### Usage

```
NonParallelTrackLoop(FinalImage, min_frames_per_cell, track_params)
```

### Arguments

| | |
|---|---|
| FinalImage | a list of numeric matrices (images) |
| min_frames_per_cell | numeric, minimum number of frames |
| track_params | a list of tracking parameters |

### Details

This is an internal function supporting the CellTracker function.

### Value

list of processed data

### Examples

```
cellmigRation:::NonParallelTrackLoop(list(), 1, list())
```

## nontrivialBondTracking *Non-Trivial Bond Tracking*

### Description

Perform Non-Trivial Bond Tracking as part of the Cell Tracking Processing

### Usage

```
nontrivialBondTracking(xyzs, maxdisp, i, env)
```

### Arguments

| | |
|---|---|
| xyzs | data.frame, including input cell centroid positions |
| maxdisp | numeric, value of maximum cell dispersion in pixels |
| i | integer, index of the current cycle |
| env | environment, including all objects used for the tracking |

### Details

a message is printed if an issue (typically arising by a non-suitable environment being passed as the env argument) is detected. See the example below.

### Value

FALSE is returned; objects in env are updated

### Examples

```
cellmigRation:::nontrivialBondTracking(data.frame(1), 1, 1, new.env())
```

---

## OptimizeParams *Optimize Detection Params*

---

### Description

Optimize Detection Parameters for running a cell tracking job

### Usage

```
OptimizeParams(
  tc_obj,
  lnoise_range = NULL,
  min.px.diam = 5,
  diameter_range = NULL,
  threshold_range = NULL,
  target_cell_num = NULL,
  threads = 1,
  quantile.val = NULL,
  px.margin = NULL,
  plot = FALSE,
  verbose = FALSE,
  dryrun = FALSE
)
```

## Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |
| lnoise_range | numeric vector of lnoise values to be used in the optimization step. Can be NULL |
| min.px.diam | integer, minimum diameter of a particle (cell). Particles with a diameter smaller than min.px.diam are discarded |
| diameter_range | numeric vector of diameter values to be used in the optimization step. Can be NULL |
| threshold_range | numeric vector of threshold values to be used in the optimization step. Can be NULL |
| target_cell_num | integer, the expected (optimal) number of cells to be detected in each frame |
| threads | integer, number of cores to use for parallelization |
| quantile.val | numeric, argument passed to EstimateDiameterRange(). If NULL, it is defaulted to 0.99 |
| px.margin | numeric, argument passed to EstimateDiameterRange(). If NULL, it ia defaulted to 2 |
| plot | if 'TRUE', plots results in the end |
| verbose | shall information about the progress of the operation be printed to screen/console |
| dryrun | shall a dryrun be performed |

## Details

The lnoise param is used to guide a lowpass blurring operation, while the lobject param is used to guide a highpass background subtraction. The threshold param is used for a background correction following the initial image convolution

- **lnoise**: Characteristic lengthscale of noise in pixels. Additive noise averaged over this length should vanish. May assume any positive floating value. May be also set to 0, in which case only the highpass "background subtraction" operation is performed.
- **lobject** Integer length in pixels somewhat larger than a typical object. Can also be set to 0, in which case only the lowpass "blurring" operation defined by lnoise is done without the background subtraction defined by lobject
- **threshold** Numeric. By default, after the convolution, any negative pixels are reset to 0. Threshold changes the threshhold for setting pixels to 0. Positive values may be useful for removing stray noise or small particles.

## Value

a trackedCells object

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x <- get(data(TrackCellsDataset))
x <- OptimizeParams(tc_obj = x, lnoise_range = c(5,7,10),
                    diameter_range = c(12,14,18),
                    threshold_range = c(4,7), dryrun = TRUE)
getOptimizedParameters(x)
```

---

`OptimizeParamsMainLoop`

*Main Loop to Parameter Optimization*

---

## Description

Main Loop as part of the Optimization Parameter process

## Usage

```
OptimizeParamsMainLoop(
  tmp_img = tmp_img,
  all_params = all_params,
  threads = threads,
  verbose = verbose
)
```

## Arguments

| | |
|---|---|
| `tmp_img` | numeric matrix, corresponding to the |
| `all_params` | data.frame, including all parameter combinations to test |
| `threads` | numeric, number of cores to use for the parallelization |
| `verbose` | logical, shall info be printed to console |

## Details

This is an internal function supporting the Optimization Parameter process

## Value

a list including test results; an empty list is returned if an error is encountered.

## Examples

```
cellmigRation:::OptimizeParamsMainLoop(matrix(1), data.frame(1), 1, FALSE)
```

---

`Parallel4OptimizeParams` *Paralle Parameter Optimization*

---

## Description

Parallel Optimization as part of the Optimization Parameter process

## Usage

```
Parallel4OptimizeParams(
  tmp_img = tmp_img,
  all_params = all_params,
  use.cores = use.cores,
  verbose = verbose
)
```

## Arguments

| | |
|---|---|
| `tmp_img` | numeric matrix, corresponding to the |
| `all_params` | data.frame, including all parameter combinations to test |
| `use.cores` | numeric, number of cores to use for the parallelization |
| `verbose` | logical, shall info be printed to console |

## Details

This is an internal function supporting the Optimization Parameter process

## Value

a list including test results; an empty list is returned if an error is encountered.

## Examples

```
cellmigRation:::Parallel4OptimizeParams(matrix(1), data.frame(1), 1, TRUE)
```

## ParallelTrackLoop *Multi Core Tracking Loop*

### Description

Tool for Multi Core Tracking Loop

### Usage

```
ParallelTrackLoop(FinalImage, use.cores, min_frames_per_cell, track_params)
```

### Arguments

| | |
|---|---|
| FinalImage | a list of numeric matrices (images) |
| use.cores | numeric, number of cores to use |
| min_frames_per_cell | numeric, minimum number of frames |
| track_params | a list of tracking parameters |

### Details

This is an internal function supporting the CellTracker function.

### Value

list of processed data

### Examples

```
cellmigRation:::ParallelTrackLoop(list(), 1, 1, list())
```

## PerAndSpeed *Persistence and Speed*

### Description

The PerAndSpeed() generates data and plots for persistence and speed.

## Usage

```
PerAndSpeed(
  object,
  TimeInterval = 10,
  PtSplot = TRUE,
  AllPtSplot = TRUE,
  ApSplot = TRUE,
  AllApSplot = TRUE,
  export = FALSE,
  ExpName = NULL
)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| PtSplot | A logical vector that allows generating individual plots of persistence time vs speed per cell. Default is TRUE. |
| AllPtSplot | A logical vector that allows generating a plot of persistence time vs speed for all cells. Default is TRUE. |
| ApSplot | A logical vector that allows generating individual plots of angular persistence vs speed per cell. Default is TRUE. |
| AllApSplot | A logical vector that allows generating a plot of angular persistence vs speed of all cells. Default is TRUE. |
| export | if 'TRUE' (default), exports function output |
| ExpName | string, indicates the name of the experiment. Can be NULL |

## Value

An CellMig class object with a data frame and plots. The data frame is stored in the PerAanSpeedtable slot.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
rmTD <- get(data(preProcCellMig))
rmTD <- PerAndSpeed(rmTD,TimeInterval=10, export=FALSE)
```

pkfnd *Find Signal Peaks*

## Description

Finds local maxima in an image to pixel level accuracy. This provides a rough guess of particle centers to be used by cntrd(). Inspired by the lmx subroutine of Grier and Crocker's. CREATED: Eric R. Dufresne, Yale University, Feb 4 2005.

## Usage

```
pkfnd(im, th, sz = NULL)
```

## Arguments

| | |
|---|---|
| im | image to process, particle should be bright spots on dark background with little noise ofen an bandpass filtered brightfield image |
| th | the minimum brightness of a pixel that might be local maxima. NOTE: Make it big and the code runs faster but you might miss some particles. Make it small and you'll get everything and it'll be slow. |
| sz | if your data is noisy, (e.g. a single particle has multiple local maxima), then set this optional keyword to a value slightly larger than the diameter of your blob. If multiple peaks are found withing a radius of sz/2 then the code will keep only the brightest. Also gets rid of all peaks within sz of boundary |

## Value

a numeric data.frame with two columns, with the coordinates of local maxima

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x0 <- getCellImages(get(data(TrackCellsDataset)))
x0 <- x0$images[[1]][seq(80,150,by=1), seq(80,150,by=1)]
b <- cellmigRation:::bpass(image_array = x0, lnoise = 2,
                           lobject = 15, threshold = 1)
pk <- cellmigRation:::pkfnd(b, th = 2, sz = 5)
pk
```

`plot3DAllTracks` *A 3D rose-plot of all cells*

## Description

Plotting the trajectory data of all cells in 3D.

## Usage

```
plot3DAllTracks(object, VS = 3, size = 2, interactive = TRUE)
```

## Arguments

| | |
|---|---|
| `object` | `CellMig` class object, which is a list of data frames resulted from the PrePro-cessing. |
| `VS` | A numeric value of the vertical separator between cells. |
| `size` | A numeric value of the point's size. |
| `interactive` | logical, shall the 3D plot be generated in a interactive fashion |

## Details

The 3D visualization shows centered trajectories where the starting point of each track is located at the origin of the coordinate system (X=0,Y=0).

## Value

A 3D rose-plot showing the tracks of all cells.

## Note

This function requires the `rgl` package to be installed on your system.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
if (Sys.info()[["sysname"]] != "Darwin") {
  # interactive shall be set to TRUE (default)
  rmTD <- get(data(preProcCellMig))
  plot3DAllTracks(rmTD, VS=3, size=2, interactive = FALSE)
}
```

plot3DTracks *A 3D rose-plot*

## Description

Plotting the trajectory data of particular cells in 3D.

## Usage

```
plot3DTracks(object, VS = 3, size = 2, cells, interactive = TRUE)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |
| VS | A numeric value of the vertical separator between cells. |
| size | A numeric value of the point's size. |
| cells | A numeric vector containing the cell's numbers to be plotted. |
| interactive | logical, shall a 3D plot built in an interactive way. |

## Details

The 3D visualization shows centered trajectories where the starting point of each track is located at the origin of the coordinate system (X=0,Y=0).

## Value

A 3D rose-plot showing the tracks of particular cells.

## Note

This function requires the rgl package to be installed on your system.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
if (Sys.info()[["sysname"]] != "Darwin") {
  # interactive shall be set to TRUE (default)
  rmTD <- get(data(preProcCellMig))
  plot3DTracks(rmTD, VS=3, size=2, cells=seq(1,5,by=1), interactive = FALSE)
}
```

plotAllTracks *A 2D rose-plot*

## Description

Plotting the trajectory data of all cells.

## Usage

```
plotAllTracks(
  object,
  Type = "l",
  FixedField = TRUE,
  export = FALSE,
  ExpName = NULL
)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |
| Type | has to be one of the following: c("p", "l", "b", "o") "p": Points; "l": Lines; "b": Both; "o": Both "overplotted". |
| FixedField | logical(1) Allows generating a plot with fixed field 800um x 800um. Default is TRUE. |
| export | if 'TRUE' (default), exports plot to JPG file |
| ExpName | string, name of the experiment. Can be NULL |

## Details

The visualization shows centered trajectories where the starting point of each track is located at the origin of the coordinate system (X=0,Y=0).

## Value

A 2D rose-plot showing the tracks of all cells.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
rmTD <- get(data(preProcCellMig))
plotAllTracks(object=rmTD, Type="l", FixedField=TRUE,export=FALSE)
```

---

`plotSampleTracks` *A 2D rose-plot of sample cells*

---

## Description

Plotting the trajectory data of some cells.

## Usage

```
plotSampleTracks(
  object,
  Type = "l",
  celNum = 35,
  FixedField = TRUE,
  export = FALSE,
  ExpName = NULL
)
```

## Arguments

| | |
|---|---|
| `object` | `CellMig` class object, which is a list of data frames resulted from the PreProcessing. |
| `Type` | has to be one of the following: c("p", "l", "b", "o") |
| `celNum` | A numeric value showing the desired number of cells to be plotted. |
| `FixedField` | logical(1) Allows generating a plot with fixed field 800um x 800um. Default is TRUE. |
| `export` | if 'TRUE' (default), exports plot to JPG file "p": Points; "l": Lines; "b": Both; "o": Both "overplotted". |
| `ExpName` | string, name of the experiment. Can be NULL |

## Details

The visualization shows centered trajectories where the starting point of each track is located at the origin of the coordinate system (X=0,Y=0).

## Value

A 2D rose-plot showing the tracks of sample cells selected randomly based on the desired number of cells selected by the user.

### Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

### References

https://www.data-pulse.com/dev_site/cellmigration/

### Examples

```
preProcCellMig <- get(data(preProcCellMig))
plotSampleTracks(preProcCellMig, Type="l", FixedField=TRUE,
                 celNum=5, export=FALSE, ExpName = NULL)
```

---

## PlotTracksSeparately *A graphical display of the track of each cell.*

---

### Description

Plotting the trajectory data of each cell.

### Usage

```
PlotTracksSeparately(
  object,
  Type = "l",
  FixedField = TRUE,
  export = FALSE,
  ExpName = NULL
)
```

### Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PreProcessing. |
| Type | has to be one of the following: [p, l, b, o] "p": Points "l": Lines "b": Both "o": Both "overplotted" |
| FixedField | logical(1) Allows generating individual plots with fixed field. Default is TRUE. |
| export | if 'TRUE' (default), exports plot to JPG file |
| ExpName | string, name of the experiment. Can be NULL |

### Details

The visualization shows centered trajectories where the starting point of each track is located at the origin of the coordinate system (X=0,Y=0).

## Value

2D rose-plots of the cells' track Separately.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
rmTD <- get(data(preProcCellMig))
PlotTracksSeparately(rmTD,Type="b", FixedField=FALSE, export = FALSE)
```

---

# PostProcessTracking *Post Processing Tracking Routine*

---

## Description

Tool for Post Processing Tracking Routine

## Usage

```
PostProcessTracking(tc_obj, all_centroids, track_params)
```

## Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |
| all_centroids | list, frame by frame centroids |
| track_params | a list of tracking parameters |

## Details

This is an internal function supporting the CellTracker function.

## Value

list of processed data

## Examples

```
cellmigRation:::PostProcessTracking(list(1), list(2), list(A=3))
```

`Prep4OptimizeParams` *Prepare For Parameter Optimization*

## Description

Pre-processing as part of the Optimization Parameter process

## Usage

```
Prep4OptimizeParams(
  stack_img,
  lnoise_range = NULL,
  min.px.diam = 5,
  diameter_range = NULL,
  threshold_range = NULL,
  target_cell_num = NULL,
  quantile.val = NULL,
  px.margin = NULL,
  plot = FALSE,
  verbose = FALSE
)
```

## Arguments

| | |
|---|---|
| `stack_img` | input image |
| `lnoise_range` | numeric, lnoise values to test |
| `min.px.diam` | numeric, minimum number of pixels of a cell signal |
| `diameter_range` | numeric, numeric values for diameter |
| `threshold_range` | numeric, numeric values for threshold |
| `target_cell_num` | numeric, target number of cells, can be NULL |
| `quantile.val` | numeric, the quantile prob used to suppress noise |
| `px.margin` | numeric, the frame margin size |
| `plot` | logical, shall a plot be printed |
| `verbose` | logical, shall info be printed to console |

## Details

This is an internal function supporting the Optimization Parameter steps

## Value

a data frame of combined parameters to be tested

## Examples

```
x <- get(data(TrackCellsDataset))
x <- cellmigRation::getCellImages(x = x)
y <- cellmigRation:::Prep4OptimizeParams(stack_img = x)
y$success
```

---

preProcCellMig *Trajectories of 11 cells*

---

## Description

Intermediates and Results from Cell Tracking Analyses, used as a representative example of a S4 CellMig object

## Usage

```
data(preProcCellMig)
```

## Format

a list including 21 elements

## Details

BT549 cell trajectories were computed by using cellmigRation. Imaging experiments were performed as described by Ghannoum S et al (paper in preparation). Briefly, triple negative breast cancer BT549 cells were cultured in RPMI supplemented with 10 and 1 NucLight green lentivirus (Essen BioScience), and then sorted by fluorescence-activated cell sorting (FACS). GFP-positive cells were seeded at a 1:3 ratio with untransduced BT549 cells in 96-well image-lock plates (EssenBio) at a density of 1000 total cells per well. Once cells reached the desired density, they were scanned at ten-minute intervals over 24h using an Incucyte S3 Live-Cell microscope (EssenBio) at 10x magnification and a Basler Ace 1920-155um camera with CMOS sensor. TIFF images were imported and processed using the cellmigRation library.

## Examples

```
data(preProcCellMig)
```

`rmPreProcessing` *Data preprocessing for random migration (RM)*

## Description

This function allows preprocessing of the trajectory data from random migration (RM) experiments.

## Usage

```
rmPreProcessing(
  object,
  PixelSize = 1.24,
  TimeInterval = 10,
  FrameN = NULL,
  ExpName = NULL
)
```

## Arguments

| | |
|---|---|
| `object` | `CellMig` class object. |
| `PixelSize` | A numeric value of the physical size of a pixel. Default is 1.24. |
| `TimeInterval` | A numeric value of the time elapsed between successive frames in the time-lapse stack. Default is 10 min. |
| `FrameN` | A numeric value of the number of frames. Default is NULL |
| `ExpName` | string, name of the experiment. Can be NULL |

## Value

An CellMig class object with preprocessed data.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
TrajectoryDataset <- get(data(TrajectoryDataset))
rmDF=TrajectoryDataset[seq(1,40,by=1),]
rmTD <- CellMig(rmDF)
rmTD <- rmPreProcessing(rmTD, FrameN=30)
```

runTrackingPermutation *Run Tracking Permutation*

## Description

Perform Internal Permutation as part of the Cell Tracking Processing

## Usage

```
runTrackingPermutation(xyzs, maxdisp, nc, i, env)
```

## Arguments

| | |
|---|---|
| xyzs | data.frame, including input cell centroid positions |
| maxdisp | numeric, value of maximum cell dispersion in pixels |
| nc | numeric, value of the nc parameter |
| i | integer, index of the current cycle |
| env | environment, including all objects used for the tracking |

## Details

a message is printed if an issue (typically arising by a non-suitable environment being passed as the env argument) is detected. See the example below.

## Value

FALSE is returned while objects in env are updated

## Examples

```
cellmigRation:::runTrackingPermutation(data.frame(1), 1, 1, 1, new.env())
```

## setAnalyticParams *Method setAnalyticParams*

### Description

Set Analytic Params of a trackedCells object.

### Usage

```
setAnalyticParams(x, params)

## S4 method for signature 'trackedCells,list'
setAnalyticParams(x, params)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |
| params | a list including all params |

### Value

a trackedCells object

### Examples

```
data("TrackCellsDataset")
setAnalyticParams(TrackCellsDataset, list())
```

## setCellMigSlot *Method setCellMigSlot*

### Description

Set Data of a slot in a CellMig object.

### Usage

```
setCellMigSlot(x, slot, value)

## S4 method for signature 'CellMig,character'
setCellMigSlot(x, slot, value)
```

### Arguments

| | |
|---|---|
| x | a CellMig-class object |
| slot | string pointing to the slot to be updated |
| value | ANY value to be written |

### Value

a CellMig object

### Examples

```
data("TrajectoryDataset")
x <- CellMig(TrajectoryDataset)
setCellMigSlot(x, "cellpos", c(1, 2, 3))
```

---

## setCellsMeta *Set MetaData*

---

### Description

Write/Replace MetaData of a trackedCells object

### Usage

```
setCellsMeta(tc_obj, experiment = NULL, condition = NULL, replicate = NULL)
```

### Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |
| experiment | string, a label to describe the experiment (optional). Can be NULL |
| condition | string, a label to describe the experimental condition (optional). Can be NULL |
| replicate | string, a label to identify the replicate (optional). Can be NULL |

### Value

a list including three items: experiment name, condition label, and replicate ID.

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x0 <- get(data(TrackCellsDataset))
x0 <- setCellsMeta(x0, experiment = "my_exp_01", condition = "DMSO")
getCellsMeta(x0)
```

---

`setCellTracks` *Method setCellTracks*

---

## Description

Set Tracks of a `trackedCells` object.

## Usage

```
setCellTracks(x, tracks)

## S4 method for signature 'trackedCells,matrix'
setCellTracks(x, tracks)
```

## Arguments

| | |
|---|---|
| `x` | a `trackedCells`-class object |
| `tracks` | a matrix including all cell tracks |

## Value

a trackedCells object

## Examples

```
data("TrackCellsDataset")
setCellTracks(TrackCellsDataset, matrix())
```

## setExpName *Method setExpName*

### Description

Set Experiment Name of a CellMig object.

### Usage

```
setExpName(x, ExpName)

## S4 method for signature 'CellMig,character'
setExpName(x, ExpName)
```

### Arguments

| | |
|---|---|
| x | a CellMig-class object |
| ExpName | string corresponding to the ExpName |

### Value

a CellMig object

### Examples

```
data("TrajectoryDataset")
x <- CellMig(TrajectoryDataset)
setExpName(x, "My Fav Experiment")
```

## setOptimizedParams *Method setOptimizedParams*

### Description

Set Optimized Params of a trackedCells object.

### Usage

```
setOptimizedParams(x, auto_params, results)

## S4 method for signature 'trackedCells'
setOptimizedParams(x, auto_params, results)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |
| auto_params | automatically selected parameters |
| results | optimization analysis results |

### Value

a trackedCells object

### Examples

```
data("TrackCellsDataset")
setOptimizedParams(
  TrackCellsDataset,
  auto_params = list(lnoise = 6, diameter = 20, threshold = 10),
  results = list())
```

---

## setProcessedImages *Method setProcessedImages*

---

### Description

Set Processed Images of a trackedCells object.

### Usage

```
setProcessedImages(x, procImages)

## S4 method for signature 'trackedCells,list'
setProcessedImages(x, procImages)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |
| procImages | a list including all metadata |

### Value

a trackedCells object

### Examples

```
data("TrackCellsDataset")
prc.im <- getProcessedImages(TrackCellsDataset)
setProcessedImages(TrackCellsDataset, prc.im)
```

## setProcessingStatus *Method setProcessingStatus*

### Description

Set Operation Status of a trackedCells object.

### Usage

```
setProcessingStatus(x, slot, value)

## S4 method for signature 'trackedCells,character,numeric'
setProcessingStatus(x, slot, value)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |
| slot | string pointing to the slot to be updated |
| value | numeric value to be written |

### Value

a trackedCells object

### Examples

```
data("TrackCellsDataset")
setProcessingStatus(TrackCellsDataset, slot="optimized_params", value=0)
```

## setTrackedCellsMeta *Method setTrackedCellsMeta*

### Description

Set Metadata of a trackedCells object.

### Usage

```
setTrackedCellsMeta(x, meta)

## S4 method for signature 'trackedCells,list'
setTrackedCellsMeta(x, meta)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |
| meta | a list including all metadata |

### Value

a trackedCells object

### Examples

```
data("TrackCellsDataset")
meta <- getCellTrackMeta(TrackCellsDataset)
meta[["condition"]] <- "DEMO N.2"
setTrackedCellsMeta(TrackCellsDataset, meta = meta)
```

---

## setTrackedCentroids *Method setTrackedCentroids*

---

### Description

Set Centroids of a trackedCells object.

### Usage

```
setTrackedCentroids(x, centroids)

## S4 method for signature 'trackedCells,list'
setTrackedCentroids(x, centroids)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |
| centroids | a list including all metadata |

### Value

a trackedCells object

### Examples

```
data("TrackCellsDataset")
setTrackedCentroids(TrackCellsDataset, list())
```

## setTrackedPositions *Method setTrackedPositions*

### Description

Set positions of a trackedCells object.

### Usage

```
setTrackedPositions(x, positions)

## S4 method for signature 'trackedCells,data.frame'
setTrackedPositions(x, positions)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |
| positions | a data.frame including all positions |

### Value

a trackedCells object

### Examples

```
data("TrackCellsDataset")
setTrackedPositions(TrackCellsDataset, data.frame())
```

## setTrackingStats *Method setTrackingStats*

### Description

Set Tracking Statistics of a trackedCells object.

### Usage

```
setTrackingStats(x, population, cells)

## S4 method for signature 'trackedCells'
setTrackingStats(x, population, cells)
```

### Arguments

| | |
|---|---|
| x | a trackedCells-class object |
| population | population-level statistics |
| cells | cell-level statistics |

### Value

a trackedCells object

### Examples

```
data("TrackCellsDataset")
cel.sts <- getCellsStats(TrackCellsDataset)
pop.sts <- getPopulationStats(TrackCellsDataset)
setTrackingStats(TrackCellsDataset, pop.sts, cel.sts)
```

---

## sinkAway *Sinking Output as part of Parameter Optimization*

---

### Description

Tool for Sinking Output as part of the Optimization Parameter process

### Usage

```
sinkAway(ty = "M", fl = "/dev/null")
```

### Arguments

| | |
|---|---|
| ty | character, "M" for messages, anything else for output |
| fl | filename to sink the output to |

### Details

This is an internal function supporting the Optimization Parameter process

### Value

value returned by the sink() function

### Examples

```
print(1)
cellmigRation:::sinkAway("O")
print(2)
cellmigRation:::sinkAway("O", NULL)
print(3)
```

## subNetworkTracking *Subnetwork Tracking*

### Description

Perform Internal Subnetwork Tracking as part of the Cell Tracking Processing

### Usage

```
subNetworkTracking(xyzs, maxdisp, env)
```

### Arguments

| | |
|---|---|
| xyzs | data.frame, including input cell centroid positions |
| maxdisp | numeric, value of maximum cell dispersion in pixels |
| env | environment, including all objects used for the tracking |

### Details

a message is printed if an issue (typically arising by a non-suitable environment being passed as the env argument) is detected. See the example below.

### Value

FALSE is returned while objects in env are updated

### Examples

```
cellmigRation:::subNetworkTracking(data.frame(1), 1, new.env())
```

## ThreeConditions *Intermediates and Results from Cell Tracking Analyses*

### Description

Intermediates and Results from Cell Tracking Analyses, used to build the package vignette.

### Usage

```
data(ThreeConditions)
```

### Format

a list including 3 elements

## Details

BT549 cell trajectories were computed using cellmigRation. Imaging experiments were performed as described by Ghannoum S et al (paper in preparation). Briefly, triple negative breast cancer BT549 cells were cultured in RPMI supplemented with 10 and 1 NucLight green lentivirus (Essen BioScience), and then sorted by fluorescence-activated cell sorting (FACS). GFP-positive cells were seeded at a 1:3 ratio with untransduced BT549 cells in 96-well image-lock plates (EssenBio) at a density of 1000 total cells per well. Cells were scanned at ten-minute intervals over 24h using an Incucyte S3 Live-Cell microscope (EssenBio) at 10x magnification and a Basler Ace 1920-155um camera with CMOS sensor. Cells were treated with 100 uM Rac1 Inhibitor (1177865-17-6, Calbiochem) or left untreated (controls). TIFF images were imported and processed using the cellmigRation library.

## Examples

```
data(ThreeConditions)
```

---

# track *Track cells*

---

## Description

Constructs n-dimensional trajectories from a scrambled list of particle coordinates determined at discrete times (e.g. in consecutive image frames)

## Usage

```
track(xyzs, maxdisp, params)
```

## Arguments

| | |
|---|---|
| xyzs | an array listing the xy coordinates and data of the different particles at different times |
| maxdisp | an estimate of the maximum distance that a particle would move in a single time interval |
| params | a list containing a few tracking parameters that are needed for the analysis |

## Value

data.frame including cell tracks data

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x0 <- data.frame(row = c(1, 30, 50, 5, 35, 55, 6, 56, 7, 58),
                 col = c(1, 30, 50, 5, 35, 55, 6, 56, 7, 58),
                 tau = c(1, 1, 1, 2, 2, 2, 3, 3, 4, 4))
cellmigRation:::track(x0, maxdisp = 10, params = NULL)
```

---

# TrackCellsDataset *Sample Stack of Fluorescent Cells*

---

## Description

Sample Stack of Fluorescent Cells to be used for computing cell tracks and stats

## Usage

```
data(TrackCellsDataset)
```

## Format

a `trackedCells` object including 10 stacks

## Details

This stack of Fluorescent Cell images was obtained by processing TIFF files via cellmigRation. Imaging experiments were performed as described by Ghannoum S et al (paper in preparation). Briefly, triple negative breast cancer BT549 cells were cultured in RPMI supplemented with 10 and 1 NucLight green lentivirus (Essen BioScience), and then sorted by fluorescence-activated cell sorting (FACS). GFP-positive cells were seeded at a 1:3 ratio with untransduced BT549 cells in 96-well image-lock plates (EssenBio) at a density of 1000 total cells per well. Cells were scanned at ten-minute intervals over 24h using an Incucyte S3 Live-Cell microscope (EssenBio) at 10x magnification and a Basler Ace 1920-155um camera with CMOS sensor. A small selection of cells and image stacks is included in this dataset.

## Examples

```
data(TrackCellsDataset)
```

`trackedCells-class` *The trackedCells Class.*

## Description

An S4 class to represent a set of cells whose movements were tracked over time.

## Usage

```
## S4 method for signature 'trackedCells'
initialize(.Object, x)
```

## Arguments

| | |
|---|---|
| `.Object` | the trackedCells object being built |
| `x` | imported TIFF image data |

## Value

An S4-class object

a trackedCells object

## Slots

`images` is a list of imported images

`proc_images` is a list of processed images

`ops` is a list keeping track of the operations executed on the object

`optimized` is a list including results of the params auto-optimization (optional)

`centroids` is a list of detected centroids

`positions` is a data.frame of cell positions across stacks

`tracks` is a numeric matrix of cell tracks

`params` is a list of parameters used for the analysis

`stats` is a list of stats computed for the cell tracks

`metadata` is a list including labels about the image, and the experiment

## Author(s)

Damiano Fantini <damiano.fantini@gmail.com>

## trackHypercubeBuild *Track Hypercube Build*

### Description

Build an hypercube used for the tracking step

### Usage

```
trackHypercubeBuild(xyzs, env)
```

### Arguments

| | |
|---|---|
| xyzs | data.frame, including input cell centroid positions |
| env | environment, including all objects used for the tracking |

### Details

a message is printed if an issue (typically arising by a non-suitable environment being passed as the env argument) is detected. See the example below.

### Value

NULL is returned while objects in env are updated

### Examples

```
cellmigRation:::trackHypercubeBuild(data.frame(1), new.env())
```

## trackSlideProcessing *Tracking Slide Processing*

### Description

Frame-by-frame Slide Processing as part of the Cell Tracking Processing

### Usage

```
trackSlideProcessing(xyzs, maxdisp, i, env)
```

### Arguments

| | |
|---|---|
| xyzs | data.frame, including input cell centroid positions |
| maxdisp | numeric, value of maximum cell dispersion in pixels |
| env | environment, including all objects used for the tracking |

### Details

a message is printed if an issue (typically arising by a non-suitable environment being passed as the env argument) is detected. See the example below.

### Value

FALSE is returned as long as cells are detected and tracked; TRUE is returned when no further cells to track are found; objects in env are updated

### Examples

```
cellmigRation:::trackSlideProcessing(data.frame(1), 1, 1, new.env())
```

---

## trackSlideWrapUp *Tracking Slide Wrap Up*

---

### Description

Perform Tracking Slide Wrap Up as part of the Cell Tracking Processing

### Usage

```
trackSlideWrapUp(xyzs, maxdisp, i, env)
```

### Arguments

| | |
|---|---|
| xyzs | data.frame, including input cell centroid positions |
| maxdisp | numeric, value of maximum cell dispersion in pixels |
| i | integer, index of the current cycle |
| env | environment, including all objects used for the tracking |

### Details

a message is printed if an issue (typically arising by a non-suitable environment being passed as the env argument) is detected. See the example below.

### Value

FALSE is returned; objects in env are updated

### Examples

```
cellmigRation:::trackSlideWrapUp(data.frame(1), 1, 1, new.env())
```

## TrajectoryDataset *Trajectories of 350 cells*

### Description

A dataset containing the coordinates and the ID of 350 cells from a dense random migration experiment

### Usage

```
data(TrajectoryDataset)
```

### Format

A data frame with 50216 rows and 4 columns

### Details

BT549 cell trajectories were computed using cellmigRation. Imaging experiments were performed as described by Ghannoum S et al (paper in preparation). Briefly, triple negative breast cancer BT549 cells were cultured in RPMI supplemented with 10 and 1 NucLight green lentivirus (Essen BioScience), and then sorted by fluorescence-activated cell sorting (FACS). GFP-positive cells were seeded at a 1:3 ratio with untransduced BT549 cells in 96-well image-lock plates (EssenBio) at a density of 1000 total cells per well. Once cells reached the desired density, they were scanned at ten-minute intervals over 24h using an Incucyte S3 Live-Cell microscope (EssenBio) at 10x magnification and a Basler Ace 1920-155um camera with CMOS sensor. TIFF images were imported and processed using the cellmigRation library.

### Examples

```
data(TrajectoryDataset)
```

## trivialBondRaster *Trivial Bond Raster*

### Description

Perform Trivial Bond Raster as part of the Cell Tracking Processing

### Usage

```
trivialBondRaster(xyzs, env)
```

### Arguments

| | |
|---|---|
| xyzs | data.frame, including input cell centroid positions |
| env | environment, including all objects used for the tracking |

### Details

a message is printed if an issue (typically arising by a non-suitable environment being passed as the env argument) is detected. See the example below.

### Value

FALSE is returned; objects in env are updated

### Examples

```
cellmigRation:::trivialBondRaster(data.frame(1), new.env())
```

---

## trivialBondTracking *Trivial Bond Tracking*

---

### Description

Perform Trivial Bond Tracking as part of the Cell Tracking Processing

### Usage

```
trivialBondTracking(xyzs, env)
```

### Arguments

| | |
|---|---|
| xyzs | data.frame, including input cell centroid positions |
| env | environment, including all objects used for the tracking |

### Details

a message is printed if an issue (typically arising by a non-suitable environment being passed as the env argument) is detected. See the example below.

### Value

FALSE is returned when particles are correctly tracked; TRUE is returned when no particles are found to be tracked; objects in env are updated

### Examples

```
cellmigRation:::trivialBondTracking(data.frame(1), new.env())
```

`ValidateTrackingArgs` *Validate Tracking Arguments*

## Description

Tool for Validate Tracking Arguments

## Usage

```
ValidateTrackingArgs(
  import_optiParam_from = NULL,
  lnoise = NULL,
  diameter = NULL,
  threshold = NULL,
  maxDisp = NULL,
  memory_b = 0,
  goodenough = 0,
  show_plots = FALSE,
  verbose = FALSE
)
```

## Arguments

| | |
|---|---|
| `import_optiParam_from` | a trackedCells object, defaults to NULL |
| `lnoise` | numeric, lnoise value |
| `diameter` | numeric, lnoise value |
| `threshold` | numeric, lnoise value |
| `maxDisp` | numeric, lnoise value |
| `memory_b` | numeric, should be 0 |
| `goodenough` | numeric, should be 0 |
| `show_plots` | logical, shall plots be shown |
| `verbose` | logical, shall info be printed to console |

## Details

This is an internal function supporting the CellTracker function.

## Value

list of processed data

## Examples

```
cellmigRation:::ValidateTrackingArgs()
```

---

VeAutoCor *Velocity AutoCorrelation*

---

## Description

The VeAutoCor function automatically compute the changes in both speed and direction across several sequantial time intervals.

## Usage

```
VeAutoCor(
  object,
  TimeInterval = 10,
  sLAG = 0.25,
  sPLOT = TRUE,
  aPLOT = TRUE,
  export = FALSE,
  ExpName = NULL
)
```

## Arguments

| | |
|---|---|
| object | CellMig class object, which is a list of data frames resulted from the PrePro-cessing. |
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| sLAG | A numeric value to be used to get the number of lags for the slope fitting. Default is 0.25, which represents 25 percent of the steps. |
| sPLOT | A logical vector that allows generating individual plots showing the velocity across several sequantial time intervals. Default is TRUE. |
| aPLOT | A logical vector that allows generating a plot showing the velocity across several sequantial time intervals of all cells. Default is TRUE. |
| export | if 'TRUE' (default), exports function output to CSV file |
| ExpName | string, name of the experiment. Can be NULL |

## Value

Plots and a data frame, which contains six rows: "Cell Number", "Velocity AutoCorrelation (lag=1)", "2nd normalized Velocity AutoCorrelation", "Intercept of VA quadratic model", "Mean Velocity AutoCorrelation (all lags)", "Mean |Acceleration|" and "Average Speed".

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
data(TrajectoryDataset)
rmDF=TrajectoryDataset[1:300,]
rmTD <- CellMig(rmDF)
rmTD <- rmPreProcessing(rmTD,FrameN=55)
rmTD <- VeAutoCor(rmTD, TimeInterval=10, sLAG=0.25, sPLOT=FALSE,
                  aPLOT=FALSE, export=FALSE)
```

---

# visualizeCellTracks *Visualize Cell Tracks originating at an Image Stack*

---

## Description

Visualize Cell Tracks that originated at an Image Stack of interest

## Usage

```
visualizeCellTracks(
  tc_obj,
  stack = 1,
  pnt.cex = 1.2,
  lwd = 1.6,
  col = "red2",
  col.untracked = "gray45",
  main = NULL
)
```

## Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |
| stack | index of the stack |
| pnt.cex | cex of the point drawn around each cell |
| lwd | width of the lines visualizing cell tracks |
| col | color of the points and the tracks, e.g.: "red2" |
| col.untracked | color of the points that were not tracked further, e.g.: "gray45" |
| main | string used as plot title, can be NULL |

## Value

None

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x <- get(data(TrackCellsDataset))
visualizeCellTracks(tc_obj = x, stack = 2)
```

---

# VisualizeCntr *Visualize Centroids*

---

## Description

Annotates centroids over an image

## Usage

```
VisualizeCntr(
  centroids,
  width_px,
  height_px,
  pnt.cex = 1.2,
  txt.cex = 0.9,
  offset = 0.18,
  col = "red2"
)
```

## Arguments

| | |
|---|---|
| centroids | centroid data.frame |
| width_px | width of the image in pixels |
| height_px | height of the image in pixels |
| pnt.cex | cex of the point (circle) drawn around each cell |
| txt.cex | cex of the text used to annotate the image |
| offset | offset for the text annotations |
| col | color of the points, e.g. "red2" |

## Value

None

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x1 <- data.frame(
    row = c(50, 80, 20, 65, 99),
    col = c(15, 25, 50, 65, 86))
plot(2, 2, xlim = c(0,1), ylim = c(0,1), xlab = "", ylab = "", las = 2)
cellmigRation:::VisualizeCntr(x1, width_px = 100, height_px = 100)
```

---

# VisualizeImg *Visualize a matrix image*

---

## Description

Shows an image representation of a numeric matrix. Typically, this is a non-negative numeric matrix, where signal (high values) corresponds to the presence of cells, or cell-like particles.

## Usage

```
VisualizeImg(img_mtx, col = NULL, ...)
```

## Arguments

| | |
|---|---|
| img_mtx | numeric matrix corresponding to a image |
| col | character vector corresponding to a valid color palette |
| ... | additional arguments will be passed to graphics::image() |

## Value

None

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x <- vapply(
    seq_len(20),
    function(i) {runif(n = 20, min = 0, max = 10)},
    FUN.VALUE = numeric(20)
)
cellmigRation:::VisualizeImg(x)
```

---

# VisualizeStackCentroids

*Visualize Cells in an Image Stack*

---

## Description

Visualize objects that were identified as cells in a given image stack

## Usage

```
VisualizeStackCentroids(
  tc_obj,
  stack = 1,
  pnt.cex = 1.2,
  txt.cex = 0.9,
  offset = 0.18,
  main = NULL
)
```

## Arguments

| | |
|---|---|
| tc_obj | a trackedCells object |
| stack | index of the image stack to use |
| pnt.cex | cex of the points drawn around cells |
| txt.cex | cex of the text used to annotate cells |
| offset | offset value for the annotation |
| main | string used for the plot title, can be NULL= NULL |

## Value

None

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
# Representative output
x <- get(data(TrackCellsDataset))
VisualizeStackCentroids(tc_obj = x, stack = 2, pnt.cex = 5, offset = 1.3)
```

---

# visualizeTrcks *Visualize Cell Tracks*

---

## Description

Annotates an image with cell centroids by adding cell ROIs and drawing cell tracks

## Usage

```
visualizeTrcks(
  tracks,
  width_px,
  height_px,
  i.slice = 1,
  pnt.cex = 1.2,
  lwd = 1.2,
  col = "red"
)
```

## Arguments

| | |
|---|---|
| tracks | cell tracks |
| width_px | width in pixels |
| height_px | height in pixels |
| i.slice | index of the stack slice to use |
| pnt.cex | cex for the points (circles) drawn around the cells |
| lwd | lwd of cell tracks |
| col | color used for the cell tracks, .g. "red" |

## Value

None

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

https://www.data-pulse.com/dev_site/cellmigration/ https://www.mathworks.com/matlabcentral/fileexchange/60349-fasttracks

## Examples

```
x1 <- data.frame(c(10, 30, 25, 55, 43, 39, 75, 72),
                 c(22, 28, 35, 24, 31, 39, 65, 73),
                 c( 1,  2,  3,  4,  5,  6,  7,  8),
                 c( 1,  1,  1,  1,  1,  1,  1,  1))
plot(2, 2, xlim = c(0,1), ylim = c(0,1), xlab = "", ylab = "", las = 2)
cellmigRation:::visualizeTrcks(x1, width_px = 100, height_px = 100)
```

---

# warnMessage *Print Warning Messages*

---

## Description

Print warning messages to the console when an issue is encountered

## Usage

```
warnMessage(warn_log, quiet = FALSE)
```

## Arguments

| | |
|---|---|
| warn_log | list, including the warning logs |
| quiet | logical, shall the warning be printed |

## Value

log of warning messages is returned

## Examples

```
cellmigRation:::warnMessage(list("Hello world"), FALSE)
```

## WSADataset *Trajectories of 147 cells*

### Description

A dataset containing the coordinates and the ID of 147 cells from wound scratch migration experiment

### Usage

```
data(WSADataset)
```

### Format

A data frame with 11970 rows and 4 columns

### Details

BT549 cell trajectories were computed using cellmigRation. Imaging experiments were performed as described by Ghannoum S et al (paper in preparation). Briefly, triple negative breast cancer BT549 cells were cultured in RPMI supplemented with 10 and 1 NucLight green lentivirus (Essen BioScience), and then sorted by fluorescence-activated cell sorting (FACS). GFP-positive cells were seeded at a 1:3 ratio with untransduced BT549 cells in 96-well image-lock plates (EssenBio) at a density of 1000 total cells per well. Once cells reached the desired density, a thin wound was introduced by scratching the cell monolayer. Next, cells were scanned at ten-minute intervals over 24h using an Incucyte S3 Live-Cell microscope (EssenBio) at 10x magnification and a Basler Ace 1920-155um camera with CMOS sensor. TIFF images were imported and processed using the cellmigRation library.

### Examples

```
data(WSADataset)
```

## wsaPreProcessing *Data preprocessing for wound scratch assay (WSA).*

### Description

This function allows filtering of cells and preprocessing of the trajectory data from wound scratch assay (WSA) experiments.

## Usage

```
wsaPreProcessing(
  object,
  PixelSize = 1.24,
  TimeInterval = 10,
  FrameN = NULL,
  imageH = 1500,
  woundH = 600,
  upperE = 400,
  lowerE = 1000,
  mar = 75,
  clearW = TRUE,
  ExpName = NULL
)
```

## Arguments

| | |
|---|---|
| object | CellMig class object. |
| PixelSize | A numeric value of the physical size of a pixel. |
| TimeInterval | A numeric value of the time elapsed between successive frames in the time-lapse stack. |
| FrameN | A numeric value of the number of frames. Default is NULL |
| imageH | A numeric value of the image height. |
| woundH | A numeric value of the image height. |
| upperE | A numeric value of the upper edge of the wound. |
| lowerE | A numeric value of the lower edge of the wound. |
| mar | A numeric value of the margin to be used to narrow the clearing zone inside the zone. |
| clearW | A logical vector that allows removing the cells within the wound. Default is TRUE. |
| ExpName | string, name of the experiment. Can be NULL |

## Value

An CellMig class object with filtered, annotated and preprocessed data.

## Author(s)

Salim Ghannoum <salim.ghannoum@medisin.uio.no>

## References

https://www.data-pulse.com/dev_site/cellmigration/

## Examples

```
WSADataset <- get(data(WSADataset))
wasDF=WSADataset[seq(1,30,by=1),]
wsaTD <- CellMig(wasDF)
wsaTD <- wsaPreProcessing(wsaTD,FrameN=20)
```

# Index