

# Package ‘cellmigRation’

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**Type** Package

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

**Version** 1.12.0

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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

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---

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/](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 from 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 PreProcessing.
...	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/](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 from 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/](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 threshold 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.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, 0, 1, 1, 1, 0),
  c(9, 9, 9, 0, 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, 0, 3, 2, 1),
  c(0, 2, 3, 0, 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, 0),
  c(0, 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	<i>PCA</i>
------------	------------

---

### 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 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.

### 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/](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/](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/](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**

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

## Details

The noise 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

- **noise**: 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 threshold 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.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-position 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.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.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/](https://www.data-pulse.com/dev_site/cellmigration/)

**Examples**

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

---

cntrd	<i>Calculates Centroids</i>
-------	-----------------------------

---

**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.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.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 Particle 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/](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 sequential 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 sequential time intervals. Default is TRUE.
aPLOT	A logical vector that allows generating a plot showing the angular persistence across several sequential 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/](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/](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/](https://www.data-pulse.com/dev_site/cellmigration/)

## Examples

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

---

EstimateDiameterRange *Detect Particle 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	logical, 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/](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**

<code>all_results</code>	list, including all intermediates
<code>all_params</code>	data.frame, including all parameter combinations to test
<code>target_cell_num</code>	numeric, number of expected cells
<code>plot</code>	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/](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/](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 sequential 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 sequential time intervals. Default is TRUE.
aPLOT	A logical vector that allows generating a plot showing the angular persistence across several sequential 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 PreProcessing.

### 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/](https://www.data-pulse.com/dev_site/cellmigration/)

### Examples

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

---

fixExpName	<i>Handle non-NULL ExpName</i>
------------	--------------------------------

---

**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/](https://www.data-pulse.com/dev_site/cellmigration/)

**Examples**

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

---

fixFM1	<i>Forward Migration First Part</i>
--------	-------------------------------------

---

**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 PreProcessing.

**Value**

An CellMig class Object.

**Author(s)**

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

**References**

[https://www.data-pulse.com/dev\\_site/cellmigration/](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 PreProcessing.

**Value**

An CellMig class Object.

**Author(s)**

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



**References**

[https://www.data-pulse.com/dev\\_site/cellmigration/](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 PreProcessing.

**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/](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 PreProcessing.

**Value**

An CellMig class Object.

**Author(s)**

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

**References**

[https://www.data-pulse.com/dev\\_site/cellmigration/](https://www.data-pulse.com/dev_site/cellmigration/)

**Examples**

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

---

fixFM5	<i>Forward Migration Fifth Part</i>
--------	-------------------------------------

---

### 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/](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 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/](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/](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/](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/](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/](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/](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/](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 PreProcessing.

**Value**

A data frame named "MSDResultsTable".

**Author(s)**

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

**References**

[https://www.data-pulse.com/dev\\_site/cellmigration/](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/](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/](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/](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 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, 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/](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 PreProcessing.
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/](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/](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	<i>Method getCellImages</i>
---------------	-----------------------------

---

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

**Examples**

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

---

getCellsStats	<i>Get Cell migration stats</i>
---------------	---------------------------------

---

**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.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 sequential 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/](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/](https://www.data-pulse.com/dev_site/cellmigration/)

**Examples**

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

---

getFMitable	<i>Getting the Forward Migration Index</i>
-------------	--------------------------------------------

---

### 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/](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	<i>Getting the Forward Migration</i>
----------------	--------------------------------------

---

### 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 including values of the forward migration analysis.

### Author(s)

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

### References

[https://www.data-pulse.com/dev\\_site/cellmigration/](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.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/](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 (Inoise, diameter, and threshold)

**Author(s)**

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

**References**

[https://www.data-pulse.com/dev\\_site/cellmigration/](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 PreProcessing.

**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/](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.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 PreProcessing.

**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/](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	<i>Get Track Data</i>
-----------	-----------------------

---

**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.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	<i>Getting the Velocity AutoCorrelation</i>
-------------	---------------------------------------------

---

**Description**

The VeAutoCor function automatically compute the changes in both speed and direction across several sequential 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/](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	<i>Inner Bond Raster</i>
-----------------	--------------------------

---

**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 input matrix

**Author(s)**

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

**References**

[https://www.data-pulse.com/dev\\_site/cellmigration/](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.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 molten 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  $\text{length}(\text{vals})^{\text{dims}}$

**Author(s)**

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

**References**

[https://www.data-pulse.com/dev\\_site/cellmigration/](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-like 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/](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.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 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.
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/](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/](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 is 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 threshold 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.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/](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 often a 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 within 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.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 PreProcessing.
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/](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/](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 PreProcessing.
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/](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/](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/](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/](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**

<code>xyzs</code>	data.frame, including input cell centroid positions
<code>maxdisp</code>	numeric, value of maximum cell dispersion in pixels
<code>nc</code>	numeric, value of the nc parameter
<code>i</code>	integer, index of the current cycle
<code>env</code>	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	<i>Set MetaData</i>
--------------	---------------------

---

**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.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	<i>Method setCellTracks</i>
---------------	-----------------------------

---

**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	<i>Method setExpName</i>
------------	--------------------------

---

**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	<i>Method setOptimizedParams</i>
--------------------	----------------------------------

---

**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("0")
print(2)
cellmigRation:::sinkAway("0", NULL)
print(3)
```

---

subNetworkTracking	<i>Subnetwork Tracking</i>
--------------------	----------------------------

---

**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	<i>Intermediates and Results from Cell Tracking Analyses</i>
-----------------	--------------------------------------------------------------

---

**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.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	<i>Sample Stack of Fluorescent Cells</i>
-------------------	------------------------------------------

---

## 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	<i>Tracking Slide Wrap Up</i>
------------------	-------------------------------

---

**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	<i>Trajectories of 350 cells</i>
-------------------	----------------------------------

---

**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	<i>Trivial Bond Raster</i>
-------------------	----------------------------

---

**Description**

Perform Trivial Bond Raster as part of the Cell Tracking Processing

**Usage**

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

**Arguments**

<code>xyzs</code>	data.frame, including input cell centroid positions
<code>env</code>	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**

<code>xyzs</code>	data.frame, including input cell centroid positions
<code>env</code>	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 sequential 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 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 velocity across several sequential time intervals. Default is TRUE.
aPLOT	A logical vector that allows generating a plot showing the velocity across several sequential 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/](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.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, &lt;damiano.fantini@gmail.com&gt;

**References**

[https://www.data-pulse.com/dev\\_site/cellmigration/](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, &lt;damiano.fantini@gmail.com&gt;

## References

[https://www.data-pulse.com/dev\\_site/cellmigration/](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.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.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/](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)
```

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