# Package 'TrackMateR'

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Title Working with TrackMate outputs in R
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<b>Description</b> TrackMate, a plugin for ImageJ/Fiji, is a popular single-particle tracking solution. Building on the trackR package by Julien Godet, the aim is to import Track-Mate data into R for further analysis and visualization.
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R topics documented:
calculateAlpha       2         calculateJD       2         calculateMSD       3         calculateTrackDensity       4         correctTrackMateData       4         find_distances       5         find_td_A1       6         find_td_A2       6         find_td_area       7         fittingJD       7         makeSummaryReport       8         plotMSD       9

2 calculateJD

	plotNMSD	10
	plot_tm_allTracks	
	plot_tm_alpha	11
	plot_tm_cumdistOverTime	12
	plot_tm_displacementHist	13
	plot_tm_displacementOverTime	13
	plot_tm_neighbours	14
	plot_tm_speed	14
	readTrackMateXML	15
Index		16

calculateAlpha

Calculate alpha (relationship between MSD and normal diffusion)

#### Description

Normal diffusion is alpha = 1. Subdiffusion is alpha < 1 and superdiffusion is alpha > 1. Input is a data matrix of msd curves. Output is mean of log2(alpha), one value for each trace.

# Usage

```
calculateAlpha(alphaMat, tstep)
```

#### **Arguments**

 $alpha Mat \qquad \qquad matrix \ of \ msd \ curves, \ each \ col \ is \ a \ track, \ each \ row \ is \ time \ lag \ (will \ contain \ NAs)$ 

tstep variable. Time step in seconds

### Value

numeric vector

calculateJD

Calculate Jump Distance (JD)

#### **Description**

Calculation of the JD of multiple tracks. Calculation is equivalent to a single time lag point on the ensemble MSD curve, typically represented as a histogram Input is a data frame of tracks imported using readTrackMateXML() The default time step is one frame - which is the equivalent to the plot generated to show displacement versus time.

#### Usage

```
calculateJD(dataList, deltaT = 1)
```

#### **Arguments**

dataList list of data frame (must include at a minimum - trace (track ID), x, y and t (in

real coords)) and calibration

deltaT integer to represent the multiple of frames that are to be analysed

calculateMSD 3

#### Value

a list of data frame of jump distances, NAs removed; and a numeric variable (jumptime)

#### **Examples**

```
xmlPath <- "~/Desktop/FakeTracks.xml"
tmObj <- readTrackMateXML(XMLpath = xmlPath)
tmObj <- correctTrackMateData(tmObj, xyscalar = 0.04)
jdObj <- calculateJD(dataList = tmObj, deltaT = 2)</pre>
```

calculateMSD

Calculate Mean Squared Displacement (MSD)

#### **Description**

Calculation of the MSD of multiple tracks. There are two methods for everaging MSD data from multiple tracks: ensemble = for each time lag average all squared displacements from all tracks time-averaged = find MSD for each track and then generate the average MSD from these curves The MSD curves will be identical if all tracks are the same length, and diverge if not. Standard deviation will be large for ensemble and smaller for time-averaged data. Input is a data frame of tracks imported using readTrackMateXML()

#### Usage

```
calculateMSD(df, method = "timeaveraged", N = 4, short = 0)
```

## **Arguments**

df	data frame must include at a minimum - trace (track ID), $x$ , $y$ and $t$ (in real coords)
method	string. Either "ensemble" or "timeaveraged" (default)
N	numeric variable for MSD. dt should be up to 1/N of number of data points (4 recommended)
short	numeric variable for the shortest number of points we will analyse. Note, this uses the number of frames from start, not number of points in track, i.e. a track with <short and="" gaps="" many="" points="" remain<="" td="" will=""></short>

#### Value

list of a data frame and a vector

#### **Examples**

```
xmlPath <- "~/Desktop/FakeTracks.xml"
tmObj <- readTrackMateXML(XMLpath = xmlPath)
tmObj <- correctTrackMateData(tmObj, xyscalar = 0.04)
tmDF <- tmObj[[1]]
msdObj <- calculateMSD(df = tmDF, method = "ensemble", N = 3, short = 8)</pre>
```

4 correctTrackMateData

calculateTrackDensity Calculate density of tracks

#### **Description**

Calculate for each track, using its starting frame, what is the relative density of tracks. We use a search radius to find how many tracks in the starting frame are neighbours of the track. The number of neighbours is normalised to the search circle, so that a track in the corner of the image with 2 neighbours has a density of 8. Code for calculating search area (intersection between search circle and the image border) is taken from https://petrelharp.github.io/circle\_rectangle\_intersection/circle\_rectangle\_intersection

#### Usage

```
calculateTrackDensity(dataList, radius = 1)
```

#### **Arguments**

dataList list of a data frame (must include at a minimum - trace (track ID), x, y and frame

(in real coords)) and a calibration data frame

radius numeric variable for search radius (in spatial units of the data)

#### Value

data frame

#### **Examples**

```
xmlPath <- "~/Desktop/FakeTracks.xml"
tmObj <- readTrackMateXML(XMLpath = xmlPath)
tmObj <- correctTrackMateData(dataList = tmObj, xyscalar = 0.04)
tdDF <- calculateTrackDensity(dataList = tmObj, radius = 2)</pre>
```

# Description

If the TrackMate data is in pixels and/or frames, the data frame can be converted with this function.

```
correctTrackMateData(
  dataList,
  xyscalar = 1,
  tscalar = 1,
  xyunit = NULL,
  tunit = NULL
)
```

find\_distances 5

#### **Arguments**

dataList	a list of a data frame (of track data) and a calibration data frame (from TrackMate XML)
xyscalar	numeric multiplier to correct pixel size of original movie. Assumes isotropic scaling, i.e. pixel height = pixel width
tscalar	numeric multiplier to correct frame interval of original movie. Frame interval of tracked data.
xyunit	string to describe spatial units
tunit	string to describe temporal unit

#### Value

list of two data frames

# **Examples**

```
xmlPath <- "~/Desktop/FakeTracks.xml"
tmObj <- readTrackMateXML(XMLpath = xmlPath)
# in the case where pixel size is 0.03 um and original data is 1 pixel, xyscalar = 0.03
tmObj <- correctTrackMateData(dataList = tmObj, xyscalar = 0.03)</pre>
```

find_distances	Find distance between xy coordinate and a series of other xy coordi-
	nates

# Description

Find distance between xy coordinate and a series of other xy coordinates

# Usage

```
find_distances(xx, yy, df)
```

## Arguments

xx	x coord of point for comparison
уу	y coord of point for comparison
df	data frame containing x and y columns for other points

#### Value

numeric vector of distances

find\_td\_A2

find\_td\_A1

Track Density - Find area A1

# Description

Track Density - Find area A1

## Usage

```
find_td_A1(x, r)
```

# Arguments

x value radius

#### Value

numeric variable

 $find_td_A2$ 

Track Density - Find area A2

# Description

Track Density - Find area A2

# Usage

# Arguments

x valuey valuer radius

# Value

numeric variable

find\_td\_area 7

find\_td\_area

Track Density - Find search area

#### **Description**

Find the area of the intersection of the circle centered at xy with radius r and the radius with vertical sides at a and horizontal sides at b. xy, a, and b must be vectors of length 2, and xy must lie within the rectangle.

#### Usage

```
find_td_area(r, xy, a, b)
```

#### **Arguments**

```
r radius of search circle
xy numeric vector (length 2)
a numeric vector (length 2)
b numeric vector (length 2)
```

#### Value

numeric variable

#### **Examples**

```
find_td_area(r=2, xy=c(4, 4), a=c(0, 8), b=c(0, 5))
```

fittingJD

Fitting jump distance (JD) data

#### **Description**

Jump Distances have been calculated for a given time lag. They can be described by fitting curves to the data, either using a histogram or cumulative probability density function. Firtting to a histogram is sensitive to binning parameters and ECDF performs better for general use. The idea behind this analysis is given in: - Weimann et al. (2013) A quantitative comparison of single-dye tracking analysis tools using Monte Carlo simulations. PloS One 8, e64287. - Menssen & Mani (2019) A Jump-Distance-Based Parameter Inference Scheme for Particulate Trajectories, Biophysical Journal, 117: 1, 143-156. The bulk of this code is taken from trackR by JuG

```
fittingJD(
    df,
    mode = "ECDF",
    nPop = 1,
    init,
    units = c("um", "s"),
    timeRes = 1,
    breaks = 100
)
```

#### **Arguments**

df	data frame with a column named jump of jump distances
mode	string indicated ECDF (default) or hist (histogram)
nPop	number of populations of diffusing species (1, 2 or 3)
init	initialisation parameters for the nls fit for example list(D2 = 200, D1 = 0.1) or list(D2 = 0.01, D1=0.1, D3=10, D4=100)
units	character vector to describe units (defaults are um, micrometres and s, seconds)
timeRes	time resolution per unit of jump. Frame interval is $0.5~\mathrm{s}$ and jump interval is two steps, timeRes = 1.
breaks	number of bins for histogram. With ECDF breaks can be high e.g. 100, for mode = "hist" they should be low, perhaps 30.

#### Value

ggplot

#### **Examples**

```
xmlPath <- "~/Desktop/FakeTracks.xml"
tmObj <- readTrackMateXML(XMLpath = xmlPath)
tmObj <- correctTrackMateData(tmObj, xyscalar = 0.04)
jdObj <- calculateJD(dataList = tmObj, deltaT = 2)
jdDF <- jdObj[[1]]
fittingJD(df = jdDF, mode = "ECDF", nPop = 2, breaks = 100, timeRes = 0.06)</pre>
```

 ${\it makeSummaryReport}$ 

Make Summary Report

#### **Description**

Generate several plots to visualise TrackMate data and generate a report. The use of um is because ggsave does not currently save unicode to PDF reliably. The code is switchable to accommodate making a "report" (one dataset) or a "summary" (several related datasets combined)

```
makeSummaryReport(
  tmList,
  msdList,
  jumpList,
  tddf,
  titleStr = "",
  subStr = "",
  auto = FALSE,
  summary = FALSE
)
```

plotMSD 9

#### **Arguments**

tmList	list of trackmate data and calibration
msdList	MSD summary and alpha list = output from calculateMSD()
jumpList	list of a data frame of jump data and a variable to be passed to timeRes
tddf	data frame of track density data
titleStr	string used as the title for the report
subStr	string used as the subtitle for the report
auto	boolean which selects for returning the patchwork report or a list of the patchwork report and a data frame of summary
summary	boolean which selects for summary

#### Value

patchwork ggplot or a list of patchwork ggplot and data frame of summary data

#### **Examples**

```
xmlPath <- "~/Desktop/FakeTracks.xml"
tmObj <- readTrackMateXML(XMLpath = xmlPath)
tmObj <- correctTrackMateData(tmObj, xyscalar = 0.04)
tmDF <- tmObj[[1]]
calibrationDF <- tmObj[[2]]
msdObj <- calculateMSD(df = tmDF, method = "ensemble", N = 3, short = 8)
jdObj <- calculateJD(dataList = tmObj, deltaT = 1)
tdDF <- calculateTrackDensity(dataList = tmObj, radius = 1.5)
fileName <- tools::file_path_sans_ext(basename(xmlPath))
reportObj <- makeSummaryReport(tmList = tmObj, msdList = msdObj, jumpList = jdObj, tddf = tdDF,
titleStr = "Report", subStr = fileName, auto = TRUE)</pre>
```

plotMSD

Make a plot of MSD data

### Description

Generate a plot of MSD over a series of increasing time lags. Input is the output from CalculateMSD(), so the plot will display the ensemble or time-averaged MSD (whatever was requested) A fit to the first four points is displayed to evaluate alpha. Diffusion coefficient from this fit is displayed top-left.

```
plotMSD(
   df,
   units = c("um", "s"),
   bars = FALSE,
   xlog = FALSE,
   ylog = FALSE,
   auto = FALSE
)
```

10 plotNMSD

#### **Arguments**

df	MSD summary = output from calculateMSD()
units	character vector to describe units (defaults are um, micrometres and s, seconds)
bars	boolean to request error bars (1 x SD)
xlog	boolean to request log10 x axis
ylog	boolean to request log10 y axis
auto	boolean to request plot only, TRUE gives plot and D as a list

#### Value

ggplot or ggplot and variable

## **Examples**

```
xmlPath <- "~/Desktop/FakeTracks.xml"</pre>
datalist <- readTrackMateXML(XMLpath = xmlPath)</pre>
data <- datalist[[1]]</pre>
# use the ensemble method and only look at tracks with more than 8 points
msdobj <- calculateMSD(df = data, method = "ensemble", N = 3, short = 8)</pre>
msddf <- msdobj[[1]]</pre>
plotMSD(msddf, bars = FALSE)
```

Plot several (n) MSD curves

plotNMSD

## Description

Generate a plot of several MSD curves together with a summary curve.

# Usage

```
plotNMSD(df)
```

## **Arguments**

df

dataframe of MSD summary data from multiple datasets (labelled by dataid)

# Value

ggplot

plot\_tm\_allTracks 11

plot\_tm\_allTracks

Make a plot of all tracks

#### **Description**

Make a plot of all tracks

#### Usage

```
plot_tm_allTracks(
  input,
  summary = FALSE,
  xstr = "",
  ystr = "",
  alphaLevel = 0.5
)
```

## **Arguments**

input either a data frame of TrackMate data or list of TrackMate data frame and cali-

bration data frame

summary boolean to specify if plot is of one dataset or several related datasets

xstr string to label x-axis ystr string to label y-axis

alphaLevel numeric variable to set alpha for the plot

# Value

ggplot

plot\_tm\_alpha

Make a histogram of alpha values

# Description

Make a histogram of alpha values

```
plot_tm_alpha(
   df,
   median_alpha = NULL,
   xstr = "alpha (log2)",
   ystr = "Frequency"
)
```

#### **Arguments**

df data frame of alpha values

median\_alpha variable for adding label to plot

xstr string to label x-axis

ystr string to label y-axis

### Value

ggplot

```
plot_tm_cumdistOverTime
```

Make a plot of cumulative distance over time

## Description

Make a plot of cumulative distance over time

## Usage

```
plot_tm_cumdistOverTime(
   input,
   summary = FALSE,
   xstr = NULL,
   ystr = NULL,
   alphaLevel = 0.1
)
```

#### **Arguments**

input either a data frame of TrackMate data or list of TrackMate data frame and cali-

bration data frame

summary boolean to specify if plot is of one dataset or several related datasets

xstr string to label x-axis
ystr string to label y-axis

alphaLevel numeric variable to set alpha for the plot

#### Value

ggplot

```
plot_tm_displacementHist
```

Make a histogram of displacements

#### **Description**

Make a histogram of displacements

#### Usage

```
plot_tm_displacementHist(
  input,
  summary = FALSE,
  xstr = NULL,
  ystr = NULL,
  auto = FALSE
)
```

# Arguments

input either a data frame of TrackMate data or list of TrackMate data frame and cali-

bration data frame

summary boolean to specify if plot is of one dataset or several related datasets

xstr string to label x-axis ystr string to label y-axis

auto boolean to switch between returning a ggplot and a list of ggplot and variable

#### Value

ggplot or list of ggplot and variable

```
plot_tm_displacementOverTime
```

Make a plot of displacement over time

## Description

Make a plot of displacement over time

# Usage

```
plot_tm_displacementOverTime(input, summary = FALSE, xstr = NULL, ystr = NULL)
```

## **Arguments**

input either a data frame of TrackMate data or list of TrackMate data frame and cali-

bration data frame

summary boolean to specify if plot is of one dataset or several related datasets

xstr string to label x-axis ystr string to label y-axis plot\_tm\_speed

#### Value

ggplot

plot\_tm\_neighbours

Make a histogram of track density (number of neighbours)

# **Description**

Make a histogram of track density (number of neighbours)

#### Usage

```
plot_tm_neighbours(df, auto = FALSE)
```

# Arguments

df data frame of TrackMate data

auto boolean to switch between returning a ggplot and a list of ggplot and variable

#### Value

ggplot or list of ggplot and variable

plot\_tm\_speed

Make a histogram of average speed

#### **Description**

Make a histogram of average speed

#### Usage

```
plot_tm_speed(input, summary = FALSE, xstr = NULL, ystr = NULL, auto = FALSE)
```

# Arguments

input either a data frame of TrackMate data or list of TrackMate data frame and cali-

bration data frame

summary boolean to specify if plot is of one dataset or several related datasets

xstr string to label x-axis ystr string to label y-axis

auto boolean to switch between returning a ggplot and a list of ggplot and variable

# Value

ggplot or list of ggplot and variable

readTrackMateXML 15

readTrackMateXML

Read TrackMate XML output files.

# **Description**

Produces a data frame of all spots from filtered tracks, ordered by track number. A warning is generated if the scaling is in pixels rather than real units.

## Usage

```
readTrackMateXML(XMLpath)
```

## Arguments

XMLpath

path to the xml file

#### Value

list of two data frames

## **Examples**

```
xmlPath <- "~/Desktop/FakeTracks.xml"
tmObj <- readTrackMateXML(XMLpath = xmlPath)
# get the track data in a data frame
tmDF <- tmObj[[1]]
# get the calibration data in a data frame
calibrationDF <- tmObj[[2]]</pre>
```

# **Index**

```
calculateAlpha, 2
calculateJD, 2
calculateMSD, 3
calculateTrackDensity, 4
correctTrackMateData, 4
find_distances, 5
find_td_A1, 6
find\_td\_A2, \color{red}{6}
find_td_area, 7
fittingJD, 7
makeSummaryReport, 8
plot_tm_allTracks, 11
plot_tm_alpha, 11
plot_tm_cumdistOverTime, 12
plot_tm_displacementHist, 13
plot_tm_displacementOverTime, 13
plot_tm_neighbours, 14
plot_tm_speed, 14
plotMSD, 9
plotNMSD, 10
readTrackMateXML, 15
```