

# Package ‘rethomics’

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**Type** Package

**Title** Rethomics, a package to analyse high-throughput animal behaviour data.

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**Description** This package was primarily developed to study sleep and circadian rhythm in fruit flies in combination with the ethoscope platform (<http://gilestrolab.github.io/ethoscope/>).

**License** GPL (>=3.0)

**Depends** R (>= 2.15.0),  
MASS,  
RSQLite,  
data.table,  
ggplot2,  
reshape2,  
tools

**LazyLoad** TRUE

**Collate** 'ethoscope\_io.R'  
'dam\_io.R'  
'helpers.R'  
'plots.R'  
'sleep.R'  
'utils\_time.R'  
'utils\_path.R'  
'utils\_misc.R'  
'datasets.R'

**URL** <https://github.com/gilestrolab/rethomics>

**RoxygenNote** 5.0.1

**Suggests** testthat,  
devtools,  
parallel

R topics documented:

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boutAnalysis	<i>Finds ‘bouts’ in categorical time series.</i>
--------------	--

---

Description

This function is used to find contiguous regions of unique value in a – potentially irregular – uni-variate time series.

Usage

```
boutAnalysis(var, data)
```

Arguments

- |      |                                    |
|------|------------------------------------|
| var  | the column variable to use in data |
| data | a data.table                       |

**Value**

A data.table with columns for the unique value of the bout variable, bout start time, and bout length (ie. duration). Bout analysis will be performed by individual (data.table key), which adds additional columns. There is one row for each bout.

**See Also**

rle to perform a run length transform manually

**Examples**

```
set.seed(1)
# 1000 points the first 500 points should have higher chance to be 1 than the last 500:
y_var <- round(c(runif(500,0,1),
                  runif(500,0,0.75)))
# first 500 points are for individual "A", next 500 points are for "B":
dt <- data.table( y = y_var,
                 t = rep(1:500,2)*12,
                 id = rep(c("A","B"),each=500),key="id")
bout_dt <- boutAnalysis(y,dt)
summary <- bout_dt[,
  .(n=.N,
    mean_duration=mean(length))
  ,by=c(key(bout_dt),"y")]
print(summary)
```

---

buildEthoscopeQuery	<i>Build a query for loading ethoscope dat; using the date of experiments and devices name to retrieve result files.</i>
---------------------	--

---

**Description**

This function is designed to list and select experimental files. In general, end-users will want to retrieve path to their experimental files according to the date and ID of the video monitor without having to understand the underlying directory structure.

**Usage**

```
buildEthoscopeQuery(result_dir, query = NULL, use_cached = FALSE)
```

**Arguments**

result_dir	The location of the result directory (i.e. the folder containing all the data).
query	An optional query formatted as a dataframe (see details).
use_cached	whether cache files should be used

## Details

The optional argument `query` is expected to be a table where every row maps an experiment. In many respects, it is similar to the `what` argument in [loadEthoscopeData](#). The only difference is that it does not have a `path` column. Instead, it must contain two columns:

- `date` The date and time when the experiment started formatted either as 'yyyy-mm-dd' or 'yyyy-mm-dd\_hh:mm:ss'. In the former case, there may be several matching experiments to a single time (starting the same day). When this happens, *only the last* is returned, and a warning message is displayed.
- `machine_name` The name of the machine that acquired the data.

The result is meant to be used directly, as the `what` argument, by [loadEthoscopeData](#) (see examples).

## Value

The query extended with the requested paths. When `query` is not specified, the function returns a table with all available files.

## Note

The ethoscope platform store data in a hard-coded directory structure `/root_dir/machine_id/machine_name/datetime/files` where:

- `machine_id` Is, in principle, a universally unique identifier of the acquisition device.
- `machine_name`, a human friendly name for acquisition device. In practice, this is expected to be unique within laboratory.
- `datetime`, the date and time of the start of the experiment

## See Also

[cacheEthoscopeData](#) to build a cached data directory.

## Examples

```
# Some sample data are store in the package:
sample_dir <- getSampleDataPath(get_sample_dir = TRUE)
result_dir <- paste(sample_dir, "ethoscope", sep="/")

query <- data.table(
  machine_name = c("E_029", "E_014", "E_014"),
  date = c("2016-01-25", "2016-01-25", "2016-02-17")
)
query_path <- buildEthoscopeQuery(result_dir, query)
# now we have mapped a query to a path:
print(query)
```

---

cacheEthoscopeData	<i>Caches incrementally db files to R native files</i>
--------------------	--

---

### Description

This function is meant to be run by heavy users who want to speed up reading ethoscope file. It will essentially preload all data in a result directory into a cached directory with the same structure. .rdb and .idx files are generated instead of .db file. In practice, this function will be run every day to fetch and cache new data.

### Usage

```
cacheEthoscopeData(result_dir, cached_dir, dry_run = F)
```

### Arguments

result_dir	The location of the result directory (i.e. the folder containing all the data).
cached_dir	The location of the directory where data should be saved.
dry_run	The location of the directory where data should be saved.

---

checkColumns	<i>Checks if the expected columns are all in a given character vector. Through error if not</i>
--------------	---

---

### Description

Checks if the expected columns are all in a given character vector. Through error if not

### Usage

```
checkColumns(expected_colnames, cols)
```

### Arguments

expected_colnames	the colnmaes that should be in a dt
cols	the actual column names

---

curateDeadAnimals	<i>Finds when an animal is 'dead' and removes the all consecutive data</i>
-------------------	--

---

### Description

In this context, death is defined by very long periods of immobility.

### Usage

```
curateDeadAnimals(data, max_immobile_live = hours(12))
```

### Arguments

data	the data (i.e a data.table) from a <i>single</i> region. It must contain, at least, the columns tand moving.
max_immobile_live	the longest duration an alive animal can remain immobile before being considered dead.

### Value

A data table similar to data where late time points have potentially been removed

### Note

Death is assumed to be irreversible. Therefore, if an animal is classified as dead, all subsequent data is removed.

### See Also

[sleepAnnotation](#) and [sleepDAMAnnotation](#) to define movement and add a moving column.

### Examples

```
# Let us load some sample data
data(dam_data)
dt <- dam_data[,
  sleepDAMAnnotation(.SD),
  by=key(dam_data)]
# let us have a look at the pattern of movement.
# Some animals (e.g. 06, 21, 24) died early.
overviewPlot(moving,dt,normalise_var_per_id = FALSE)
dt_curated <- dt[,curateDeadAnimals(.SD,hours(15)),by=key(dt)]
# Note that some data has been removed.
# Also, no data was there for region_id == 06, therefore, it is removed altogether
overviewPlot(moving, dt_curated, normalise_var_per_id = FALSE)
#####
# A simple way to compute total lifespan of each remaining animal:
lifespan_dt <- dt_curated[,
```

```
.(lifespan = max(t) - min(t))  
,by=key(dt_curated)]
```

---

dam_data	<i>A simple rethomics data imported form a Trikinetics DAM2 file.</i>
----------	---

---

**Description**

A 32 animal, 5 days DAM2, single monitor data set formatted in a conventinal rethomics data.table (i.e. has experiment\_id, region\_id and t columns). A dummy variable, condition, was also added for illustration purposes.

**Usage**

```
dam_data
```

**Format**

a data.table where each row is a single observation of one unique animal at one unique time

**Author(s)**

Anne Petzold, 2015-07-02

**Source**

Gilestro lab, Imperial college, London

---

days	<i>Trivially converts days to seconds</i>
------	---

---

**Description**

Trivially converts days to seconds

**Usage**

```
days(x)
```

**Arguments**

x                      number of days

**Value**

the corresponding number of seconds

**See Also**[hours mins](#)


---

ethogramPlot	<i>Displays the temporal and inter-individual average of a variable of interest.</i>
--------------	--

---

**Description**

This function produces a graph where the variable of interest and time are on the y and x axes, respectively. It can be used to visualise temporal trends per groups of conditions. The response variable, y, is grouped by time windows of defined size.

**Usage**

```
ethogramPlot(y, data, condition = NULL, facet_var = NULL,
  summary_time_window = mins(30), normalise_var_per_id = FALSE,
  error_bar = NULL, time_wrap = NULL, time_unit_conversion = days)
```

**Arguments**

y	The variable of interest.
data	The data.table containing the data. It must have a column with the same name as y.
condition	An optional grouping factor to order rows.
facet_var	An optional grouping factor to draw group in each row of a faceted plot
summary_time_window	the width (in seconds) of the time window used to draw each “pixel”.
normalise_var_per_id	whether each row is to be normalised (using $\text{new\_x} = (x - \text{mean}(x))/\text{sd}(x)$ ).
error_bar	what type of error bar should be used see details.
time_wrap	the time (in seconds) used to wrap the data (see details).
time_unit_conversion	a function to convert time in the x axis. typically, days, hours or mins.

**Details**

time\_wrap is typically used to express time relatively to the start of the the day. In other words, it can help be used to pull all days together in one representative day. In this case, time\_wrap=hours(24)‘.

At the moment, four types of error bars (error\_bar) are supported:

- ‘sd’ The standard error
- ‘sem’ The standard error of the mean (*i.e.*  $\frac{sd}{\sqrt{n}}$ )
- ‘gauss\_ci’ The gaussian 95% confidence interval (*i.e.*  $1.96 \cdot \frac{sd}{\sqrt{n}}$ )
- ‘boot\_ci’ A standard 95% bootstrap resampling confidence interval. This is done over 5000 replicates. This can be quite *slow*, but is often more statistically sound.



**Value**

A ggplot object that can be plotted directly, or modified.

**See Also**

[overviewPlot](#) to show per-individual patterns

**Examples**

```
data(sleep_sexual_dimorphism)
my_data <- sleep_sexual_dimorphism
# Fraction of animal asleep over time:
p <- ethogramPlot(asleep, my_data)
# We would like to show that per group:
p <- ethogramPlot(asleep, my_data, condition=sex)
print(p)
# We can also put error bars:
p <- ethogramPlot(asleep, my_data, condition=sex, error_bar="sem")
print(p)
# we can also use a condition to split data per row (ggplot faceting):
p <- ethogramPlot(asleep, my_data, condition=sex, facet_var=experiment_id, error_bar="sem")
print(p)
# p is simply a ggplot object, so we can change things:
print(p + labs(title="MY own title"))
# Let us play with several error bars:
p <- ethogramPlot(asleep, my_data, condition=sex, error_bar="sd")
p
p <- ethogramPlot(asleep, my_data, condition=sex, error_bar="sem")
p
p <- ethogramPlot(asleep, my_data, condition=sex, error_bar="gauss_ci")
p
# this one is a bit slow
p <- ethogramPlot(asleep, my_data, condition=sex, error_bar="boot_ci")
p
data(dam_data)
# Time, on the x axis, in hours via
p <- ethogramPlot(activity,
  dam_data,
  condition,
  error_bar = "sem",
  time_unit_conversion=hours # this is where you set time in hours
)
p
# summarise/wrap data in one day
p <- ethogramPlot(activity,
  dam_data,
  condition,
  error_bar = "sem",
  time_wrap=days(1) # this argument does the job
)
p
```

---

getSampleDataPath	<i>Get the absolute path to a sample file.</i>
-------------------	--

---

### Description

This function is only for testing (and trying) purposes. It provides a way to access raw data (e.g. db files and dam text files) contained within this package.

### Usage

```
getSampleDataPath(path = NULL, get_sample_dir = FALSE)
```

### Arguments

path	The relative path and name of the samples to be loaded. When path is NULL, the function returns the list of all available samples.
get_sample_dir	whether the function return the root directory of the sample data, nistead of sample files.

### See Also

[loadEthoscopeData](#) to read raw experimental data.

---

hours	<i>Trivially converts hours to seconds</i>
-------	--

---

### Description

Trivially converts hours to seconds

### Usage

```
hours(x)
```

### Arguments

x	number of hours
---	-----------------

### Value

the corresponding number of seconds

### See Also

[days mins](#)

---

loadDailyDAM2Data	<i>Retrieves DAM2 data from daily saved files</i>
-------------------	---

---

## Description

Uses a query mechanism to get data from a DAM2 array. This is useful when data has been saved, by day, in individual files for each monitor.

## Usage

```
loadDailyDAM2Data(result_dir, query, reference_hour = 9, tz = "UTC",
  verbose = TRUE, FUN = NULL, ...)
```

## Arguments

result_dir	the root directory where all daily data are saved
query	a formatted query used to request data (see detail).
reference_hour	the hour, in the day, to use as t_0 reference. This should be expressed on Greenwich Meridian Time.
tz	the time zone on which the DAM2 data was saved (e.g. Europe/London -> British Summer Time)
verbose	whether to print progress (a logical).
FUN	an optional function to transform the data from each 'region' (i.e. a data.table) immediately after it has been loaded.
...	extra arguments to be passed to FUN

## Details

query must be a data.table. Conceptually, each row of the query describes the conditions in one channel (when region\_id is specified), or in each monitor (when it is not). It should have the following columns:

- machine\_id the name of the machine used (e.g. 'M002').
- start\_date the first day of the requested experiment (e.g. '2014-12-28').
- stop\_date the last day of the requested experiment (e.g. '2014-12-30').
- region\_id the channel (between 1 and 32) in what the animal was in (e.g. '20'). This is an optional column. If not provided, all 32 channels are loaded with the same conditions.
- ... arbitrary columns to associate conditions/treatments/genotypes/... to the previous columns

## Value

A data.table where every row is an individual measurement. That is an activity at a unique time (t) in a unique channel (region\_id), and from a unique result date/experiment (experiment\_id). The time is expressed in seconds. For each different combination of start\_date and machine\_id in the query, an individual experiment\_id is generated.

**Note**

the daily data should be saved in a hard-coded directory structure `root_dir/yyyy/mm/mdd/mddMxyz.txt`, where:

- yyyy Is the year (e.g. 2014)
- mm and dd, the formatted month and day, respectively (e.g. mm=12 and dd=28).
- xyz, the number of the monitor (e.g 003)

**See Also**

[loadDAM2Data](#) to load data from a regular DAM2 file

---

loadDAM2Data	<i>Retrieves DAM2 data from continuous files</i>
--------------	--

---

**Description**

Uses a query mechanism to get data from a DAM2 array. This is useful when using the default behaviour of Trikinetics software where data is simply appended to a single long file per monitor.

**Usage**

```
loadDAM2Data(query, FUN = NULL, ...)
```

**Arguments**

query	a formatted query used to request data (see detail).
FUN	an optional function to transform the data from each 'region' (i.e. a data.table) immediately after it has been loaded.
...	extra arguments to be passed to FUN

**Details**

query must be a data.table. Conceptually, each row of the query describes the conditions in one channel (when `region_id` is specified), or in each monitor (when it is not). It should have the following columns:

- path the location of your data file (e.g. 'C:/User/me/Desktop/Monitor3.txt').
- start\_date the first day of the requested experiment (e.g. '2014-12-28').
- stop\_date the last day of the requested experiment (e.g. '2014-12-30').
- region\_id the channel (between 1 and 32) in what the animal was in (e.g. '20'). This is an optional column. If not provided, all 32 channels are loaded with the same conditions.
- ... arbitrary columns to associate conditions/treatments/genotypes/... to the previous columns

**Value**

A data.table where every row is an individual measurement. That is an activity at a unique time (t) in a unique channel (region\_id), and from a unique result date/experiment (experiment\_id). The time is expressed in seconds. For each different combination of start\_date and file in the query, an individual experiment\_id is generated.

**See Also**

[loadSingleDAM2File](#) to load DAM data that is saved by day

**Examples**

```
# This is a simple, single sample dam2 file:
sample_file <- getSampleDataPath('misc/DAMfile.dam')
query = data.table(path=sample_file,
                    # note the time (10:00) is added as reference time
                    start_date="2015-07-02_10-00-00",
                    stop_date="2015-07-07",
                    region_id=c(1:32),condition=rep(letters[1:2],each=16))

print(query)
dt <- loadDAM2Data(query)
ethogramPlot(activity,dt,condition) + scale_x_continuous(breaks=0:10/2)
dt <- loadDAM2Data(query,FUN= sleepDAMAnnotation)
ethogramPlot(asleep,dt,condition) + scale_x_continuous(breaks=0:10/2)
```

---

loadEthoscopeData	<i>Read data from a result file.</i>
-------------------	--------------------------------------

---

**Description**

This function is used to convert all the information contained in a result file generated by the ethoscope platform <http://gilestrolab.github.io/ethoscope/> (i.e a .db file) into an R 'data.table'.

**Usage**

```
loadEthoscopeData(what, min_time = 0, max_time = Inf,
                  reference_hour = NULL, verbose = TRUE, columns = NULL, ncores = 1,
                  FUN = NULL, ...)
```

**Arguments**

what	an object describing which file(s) to load and, optionally, associated variables/conditions (see details).
min_time	exclude data before min_time (in seconds). This time is relative to the start of the experiment.
max_time	exclude data after max_time (in seconds). It is also relative to the start of the experiment.

reference_hour	the hour, in the day, to use as t_0 reference. When unspecified, time will be relative to the start of the experiment.
verbose	whether to print progress (a logical).
columns	an optionnal vector of columns to be selected from the db file. Time (t) is always implicitly selected.
ncores	the number of cores to use for optionnal parallel processing.
FUN	an optional function to transform the data from each 'region' (i.e. a data.table) immediately after it has been loaded.
...	extra arguments to be passed to FUN

### Details

what can be one of two objects:

- A character vector. In which case, it is assumed that each element is the path to a different file to load.
- A dataframe. The dataframe *must* have a column named 'path'. The path basename will be used as a unique identifier for a specific experiment (experiment\_id). Arbitrary column can be added to map experimental conditions to file name. In addition, the dataframe can have a column named region\_id. When defined, only the specified combinations of path and region\_id will be loaded. This allows to map additional conditions (i.e. data frame columns) to specific regions/files. When additional conditions are provided, they will result in creation of custom columns in the output of this function.

### Value

A data.table where every row is an individual measurement. That is a position at a unique time (t) in a unique region (region\_id), and from a unique result file/experiment (experiment\_id). The time is expressed in seconds. Distance units (e.g. xy position, height/width) are expressed as a fraction of the width of the region they originate from.

### See Also

[loadEthoscopeMetaData](#) To display global informations about a specific file.

### Examples

```
# First of all, let us load files from the data sample included within this package.
# Most likely, you will already have your own data files.
sample_files <- c("ethoscope/014/E_014/2016-01-25_21-36-04/2016-01-25_21-36-04_014.db",
                 "ethoscope/029/E_029/2016-01-25_21-14-55/2016-01-25_21-14-55_029.db")

# Extract the files in your computer
paths <- sapply(sample_files, getSampleDataPath)
# Now, `paths` is just a vector of file names:
print(paths)
#####
#####
```

```

# Case 1: load ALL REGIONS from a SINGLE FILE
validation_data_file <- paths[1]
# `validation_data_file` is simply the path to the .db file in your computer
dt <- loadEthoscopeData(validation_data_file)
print(dt)
#####
# Case 2: load ALL REGIONS from MULTIPLE FILES
# we pass all the files we want to load as the `what` argument
dt <- loadEthoscopeData(paths)
# Note the column `experiment_id` in dt. It tells us which file/experiment
# each measurement originates from.
print(dt)

#####
# Case 3: load ALL REGIONS from MULTIPLE FILES AND add CONDITIONS
# Let us imagine that each file/experiment
# was acquired under different experimental condition.
# We can encode this information in a 'master-table' (i.e a data.frame)
# in which a column named `path` maps experimental condition(s).
# For instance, 2 different treatments:
master_table <- data.frame(path=paths, treatment=c("control", "drug_A"))
# Let us check our table:
print(master_table)
# The table looks OK, so we load the actual data
dt <- loadEthoscopeData(master_table)
# Note that `dt` now contains a column for your treatment.
print(colnames(dt))
# This makes it easier to perform things such as average per treatment.
print(dt[,.(mean_x = mean(x)),by="treatment"])
#####
# Case 4: load SELECTED REGIONS from MULTIPLE FILE, WITH CONDITIONS
# Sometimes, different regions contain different conditions.
# If the master table has a column named `region_id`,
# only the specified regions will be returned.
# Let us assume that we want to replicate case 3,
# but, now, we load only the first 20 regions.
master_table <- data.table(path=paths,
                           treatment=c("control", "drug_A"),
                           region_id=rep(1:20,each= 2))
# We could also imagine that every even region contains a male,
# whilst every odd one has a female:
master_table[, sex := ifelse(region_id %% 2, "male", "female" )]
# Note that we have now two conditions.
# Let us check our new table:
print(master_table)
# Then we can load our data:
dt <- loadEthoscopeData(master_table)
# This is simply a subset of data, so many regions are missing
# lets display the regions we ended up with
print(dt[,.(NA),by=key(dt)])

# For most complicated cases, you would probably have pre-generated the
# master-table (e.g. as a csv file) before analysing the results.

```

---

`loadEthoscopeMetaData` *Retrieves metadata from a result file.*

---

### Description

This function is used to obtain metadata – such as ‘time and date of the experiment’, ‘acquisition device’, ‘version of the software’ and such– embedded in a result file generated by the ethoscope platform.

### Usage

```
loadEthoscopeMetaData(FILE)
```

### Arguments

`FILE`                      the name of the input file.

### Value

A list containing fields for metadata entries

### See Also

[loadEthoscopeData](#) to load raw data.

### Examples

```
FILE <- "ethoscope/014/E_014/2016-01-25_21-36-04/2016-01-25_21-36-04_014.db"
path <- getSampleDataPath(FILE)
out <- loadEthoscopeMetaData(path)
names(out)
```

---

`loadSingleDAM2File`      *Read a text file formatted as DAM2 into a single data table.*

---

### Description

This function is used to load data from DAM2 devices as a `data.table`.

### Usage

```
loadSingleDAM2File(FILE, start_date = -Inf, stop_date = +Inf, tz = "",
  verbose = TRUE)
```



**Arguments**

FILE	the name of the input file.
start_date	the starting date formatted as "yyyy-mm-dd" or "yyyy-mm-dd_hh-mm-ss"
stop_date	the last day of the experiment. Same format as start_date
tz	the time zone of the computer saving the file. By default, tz is taken from the computer running this function
verbose	whether to print progress (a logical).

**Value**

a data table with an activity (number of beam crosses) variable, a region\_id (channel) variable and a posix time stamp.

**See Also**

[loadDAM2Data](#) To load data from a query.

**Examples**

```
## Not run:
FILE <- "Monitor53.txt"
out <- loadSingleDAM2File(FILE)
#histogram of x marginal distribution
hist(out[roi_id == 1, x], nclass=100)

## End(Not run)
## Not run:
# More realistic example where we have experimental conditions, and
we want to resample data at 1.0Hz.
# First, the conditions:
conditions <- cbind(roi_id=1:32, expand.grid(treatment=c(T,F), genotype=LETTERS[1:4]))
print(conditions)

## End(Not run)
```

---

makeLDAnnotation	<i>Put white and black bars under a plot to show Dark and Light phases.</i>
------------------	---

---

**Description**

Put white and black bars under a plot to show Dark and Light phases.

**Usage**

```
makeLDAnnotation(pl, time_conversion_unit = days, period = hours(24),
  offset = 0, size = 0.02)
```

**Arguments**

`p1` A ggplot object to be annotated.  
`time_conversion_unit` The time conversion function used in `p1`.  
`period` The period, in seconds  
`offset` A number, lower than the period to shift the bar left or right  
`size` The height of the bar. It is expressed in percent of the graph height

**Value**

A ggplot object that can be plotted directly, or modified.

**Examples**

```

data(sleep_sexual_dimorphism)
my_data <- sleep_sexual_dimorphism
# Fraction of animal asleep over time:
p <- overviewPlot(asleep, my_data, condition=sex)
p <- makeLDAnnotation(p)
print(p)
p <- ethogramPlot(asleep, my_data, condition=sex, error_bar="sem")
p <- makeLDAnnotation(p)
print(p)

```

---

maxVelocityClassifier *Motion classifier based on maximum velocity.*

---

**Description**

Defines whether an animal is moving according to its subpixel velocity. It requires a variable named `xy_dist_log10x1000` in the `.db` file.

**Usage**

```
maxVelocityClassifier(data, velocity_threshold = 0.006)
```

**Arguments**

`data` the data.table containing behavioural features used for movement classification.  
`velocity_threshold` velocity above which an animal is classified as ‘moving’.

**Value**

a data table with the columns `moving` (logical, TRUE iff. motion was detected) and `t_round` (the ‘rounded’ time). There is one row per rounded time point.

**See Also**

[sleepAnnotation](#) to apply this function to all subsequent time windows.

---

mins	<i>Trivially converts minutes to seconds</i>
------	--

---

**Description**

Trivially converts minutes to seconds

**Usage**

```
mins(x)
```

**Arguments**

x                      number of minutes

**Value**

the corresponding number of seconds

**See Also**

[days](#) [hours](#)

---

multiple_iterative_y_mazes	<i>Unprocessed ethoscope data of animals waling in a y maze.</i>
----------------------------	--

---

**Description**

An ,8 animal, single region\_id data set formatted in a conventinal rethomics data.table (i.e. has experiment\_id, region\_id and t columns).

**Usage**

```
multiple_iterative_y_mazes
```

**Format**

a data.table where each row is a single observation of one unique animal at one unique time

**Author(s)**

Diana Bicazan, 2015-08-05

**Source**

Gilestro lab, Imperial college, London

---

overviewPlot	<i>Displays, per individual, the temporal average of a variable of interest.</i>
--------------	--

---

**Description**

This function produces a tiled representation in which every row represents one individual (i.e. from a unique combination of region and experiment). The x axis represents time in days. The values of the variable of interest are represented by different colour intensities.

**Usage**

```
overviewPlot(y, data, condition = NULL, summary_time_window = mins(30),
  normalise_var_per_id = FALSE, time_wrap = NULL,
  time_unit_conversion = days)
```

**Arguments**

y	The variable of interest
data	The data.table containing the data. It must have a column with the same name as y.
condition	An optional grouping factor to order rows.
summary_time_window	the width (in seconds) of the time window used to draw each pixel.
normalise_var_per_id	whether each row is to be normalised, using $\text{new\_y} = (y - \text{mean}(y))/\text{sd}(y)$ .
time_wrap	the time (in seconds) used to wrap the data (see details).
time_unit_conversion	a function to convert time in the x axis. typically, days, hours or mins.

**Details**

time\_wrap is typically used to express time relatively to the start of the the day. In other words, it can help be used to pull all days together in one representative day. In this case, time\_wrap=hours(24)‘.

**Value**

A ggplot object that can be plotted directly or modified.

**See Also**

[ethogramPlot](#) To show trend by aggregating individuals over time.

## Examples

```
# Load sample data, it is already annotated for sleep, has sex=='male' or sex=="female"
data(sleep_sexual_dimorphism)
my_data <- sleep_sexual_dimorphism
# let us have a look of the max velocity as a measure of activity
p <- overviewPlot(max_velocity,my_data)
print(p)
# what about sleep amount?
p <- overviewPlot(asleep,my_data)
print(p)
# we can also group by condition. For instance by sex:
p <- overviewPlot(asleep,my_data,condition = sex)
print(p)
# p is simply a ggplot object, so we can change things:
print(p + labs(title="MY own title"))
##### time wrapping example
data(dam_data)
# the original plot:
p <- overviewPlot(activity,dam_data)
p
# summarise/wrap activity in one `day`
p <- overviewPlot(activity,dam_data,time_wrap=hours(24))
p
#####expresses time in hours:
p <- overviewPlot(activity,dam_data, time_unit_conversion=hours)
p
```

---

sleepAnnotation	<i>Determines whether an animal is asleep</i>
-----------------	---

---

## Description

This function uses a motion classifier to first decide whether an animal is moving during a given time window. Then, it defines sleep as contiguous immobility for a minimal duration.

## Usage

```
sleepAnnotation(data, time_window_length = 10, min_time_immobile = 60 * 5,
  motion_classifier_FUN = maxVelocityClassifier, ...)
```

## Arguments

data	the data (i.e a data.table) from a <i>single</i> region. It must contain, at least, the columns 't', 'x' and 'y'.
time_window_length	The number of seconds to be used by the motion classifier. This corresponds to the sampling period of the output data.

```

min_time_immobile
    the minimal duration (in s) after which an immobile animal is scored as 'asleep'.
motion_classifier_FUN
    the function used to classify movement.
...
    extra arguments to be passed to motion_classifier_FUN

```

**Value**

A data table similar to data with additional variables/annotations (i.e. 'moving', 'asleep').

**Note**

The resulting data will only have one data point every time\_window\_length seconds.

**See Also**

[loadEthoscopeData](#) to load data and optionally apply analysis on the fly.

**Examples**

```

# Let us load some sample data
data(tube_monitor_validation)
# We will start only with region 2:
dt_region2 <- tube_monitor_validation[region_id==2,]
sleep_dt <- sleepAnnotation(dt_region2)
print(sleep_dt)
# We make a sleep 'barcode'
ggplot(sleep_dt, aes(t,region_id,fill=asleep)) + geom_tile()
# A bit of data.table wizardry to apply that to each experiment and region:
sleep_dt <- tube_monitor_validation[,sleepAnnotation(.SD),by=key(tube_monitor_validation)]
# The same bare code for all regions
ggplot(sleep_dt, aes(t,region_id,fill=asleep)) + geom_tile()

```

---

sleepDAMAnnotation	<i>Determines whether an animal is asleep using beam crossing activity</i>
--------------------	--

---

**Description**

Sleep as contiguous inactivity (absence of beam crossing) for a minimal duration.

**Usage**

```

sleepDAMAnnotation(data, time_window_length = 60, min_time_immobile = 60 *
  5)

```

**Arguments**

**data** the data (i.e a data.table) from a *single* region. It must contain, at least, the columns t, x and y.

**time\_window\_length** The number of seconds to be used by the motion classifier. This corresponds to the sampling period of the output data.

**min\_time\_immobile** the minimal duration (in s) after which an immobile animal is scored as 'asleep'.

**Value**

A data table similar to data with additional variables/annotations (i.e. 'moving', 'asleep').

**Note**

The resulting data will only have one data point every time\_window\_length seconds.

**See Also**

[loadDAM2Data](#) To load DAM2 data first/ apply this function to each animal.

**Examples**

```
# Let us load some sample data
data(dam_data)
dam_data[,
          sleepDAMAnnotation(.SD),
          by=key(dam_data)]
```

---

sleep\_sexual\_dimorphism

*Sample of ethoscope data showing difference between males and females.*

---

**Description**

A sleep-annotated 56 animal data set. Movement was defined for 10s time windows. conventional rethomics data.table (i.e. has experiment\_id, region\_id and t columns).

**Usage**

```
sleep_sexual_dimorphism
```

**Format**

a data.table where each row is a single observation of one unique animal at one unique time

**Author(s)**

Quentin Geissmann, 2015-06-13

**Source**

Gilestro lab, Imperial college, London

---

tube\_monitor\_validation

*A dataset to validate tracking algorithms.*

---

**Description**

A 20 animal single monitor data set formatted in a conventional rethomics data.table (i.e. has experiment\_id, region\_id and t columns). Only raw tracking values are present in dataset.

**Usage**

tube\_monitor\_validation

**Format**

a data.table where each row is a single observation of one unique animal at one unique time

**Author(s)**

Quentin Geissmann, 2015-05-02

**Source**

Gilestro lab, Imperial college, London

---

virtualBeamCrossClassif

*Motion classifier based on beam crosses.*

---

**Description**

Defines whether an animal is moving. This is achieved by computing the number of crossed of a "virtual beam" in the middle of its region (i.e. at  $x=0.5$ ). This emulate the type of data generated by DAM2.

**Usage**

virtualBeamCrossClassif(data)



**Arguments**

`data` the data.table containing behavioural features used for movement classification.

**Value**

a data table with the columns `moving` (logical, TRUE iff. motion was detected) and `t_round` (the 'rounded' time). There is one row per rounded time point.

**See Also**

[maxVelocityClassifier](#) to define movement by maximum velocity, which is more accurate, instead.

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