

# Package ‘sleepr’

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**Title** Analyse Activity and Sleep Behaviour

**Date** 2017-08-17

**Version** 0.0.0.9000

**Description** Use behavioural variables to score activity and infer sleep from bouts of immobility.

**Depends** R ( $\geq 3.00$ ),  
behavr

**Imports** data.table

**Suggests** testthat,  
covr,  
knitr

**Remotes** rethomics/behavr

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

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

**BugReports** <https://github.com/rethomics/sleepr/issues>

**RoxygenNote** 6.0.1

**Roxygen** list(markdown = TRUE)

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bout_analysis	<i>Find "bouts" in categorical time series</i>
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### Description

This function is used to find contiguous regions of unique value in a – potentially irregular/heterogeneous – univariate categorical time series.

### Usage

```
bout_analysis(var, data)
```

### Arguments

var	name of the variable to use from data
data	<a href="#">data.table</a> containing behavioural variable from one or multiple animals. When it has a key, unique values, are assumed to represent unique individuals (e.g. in a <a href="#">behavr</a> table). Otherwise, it analysis the data as coming from a single animal. data must have a column t representing time.

### Value

an object of the same type as data (i.e. [data.table::data.table](#) or [behavr::behavr](#)). Each row is a specific bout characterised by three columns.

- t – its *onset*
- duration – its length
- <var> – a column with the same name as var. The value of var for this bout.

### References

- The relevant [rethomic tutorial section](#) – on sleep analysis

### See Also

- [sleep\\_annotation](#) – to generate a binary sleep variable
- [rle](#) run length encoding function – on which this analysis is based

### Examples

```
# Bout analysis on binary variable:
dt <- toy_dam_data()
dt[, moving := activity > 0]
bdt <- bout_analysis(moving,dt)
print(bdt)
# With multiple states
dt <- toy_ethoscope_data()
# we discretise x position in three states: left, middle and right (1/3 each)
```

```
dt[, location := as.character( cut(x,
                                breaks = c(0.0, .33, .67, 1.0),
                                labels = c("left", "middle", "right")))]

bdt <- bout_analysis(location, dt)
```

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curate\_dead\_animals      *Remove – irrelevant – data after individual have died*

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## Description

This function detects when individuals have died base on their first (very) long bout of immobility. Following data (which may include spurious artefact of movement) are removed.

## Usage

```
curate_dead_animals(data, moving_var = moving, time_window = hours(24),
  prop_immobile = 0.01, resolution = 24)
```

## Arguments

data	<a href="#">data.table</a> containing behavioural variable from or one multiple animals. When it has a key, unique values, are assumed to represent unique individuals (e.g. in a <a href="#">behavr</a> table). Otherwise, it analysis the data as coming from a single animal. data must have a column t representing time.
moving_var	logical variable in data used to define the moving (alive) state (default is moving)
time_window	window during which to define death (default is one day)
prop_immobile	proportion of immobility that counts as "dead" during time_window (see details)
resolution	how much scanning windows overlap. Expressed as a factor (see details).

## Details

This function scans the time series looking for "death" in the right (future) data, within time\_window. Death is defined as `mean(moving_var) < prop_immobile` within a time window. Moving window start every time\_window/resolution. resolution = 1 is fast but means no overlap. The default would score an animal as dead it does not move more than *one percent of the time* for at least *one day*. All data following "death" are removed.

## Value

an object of the same type as data (i.e. [data.table::data.table](#) or [behavr::behavr](#)).

## References

- The relevant [rethomic tutorial section](#) – on high-resolution survival analysis

**See Also**

- [sleep\\_annotation](#) – to score movement and sleep

**Examples**

```
dt1 <- toy_activity_data()
#all movement after day 3 is set at 0
dt1[t > days(3), moving := FALSE]
# one artefact of movement is detected at day 3.5
dt1[t == days(3.5), moving := TRUE]

dt2 <- curate_dead_animals(dt1)
dt3 <- curate_dead_animals(dt1, prop_immobile = 0)
## Not run:
library(ggplot2)
ggplot(data=dt1[, test:=1], aes(t, as.numeric(moving))) +
  geom_line(data=dt1[, test:=1]) +
  geom_line(data=dt2[, test:=2]) +
  geom_line(data=dt3[, test:=3]) +
  facet_grid(test ~ .) +
  scale_x_time()

## End(Not run)
```

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motion\_detectors

*Motion detector for Ethocope data*


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**Description**

Defines whether a *single animal* is moving according to:

**Usage**

```
max_velocity_detector(data, time_window_length,
  velocity_correction_coef = 0.003, masking_duration = 6)

max_velocity_detector_legacy(data, velocity_threshold = 0.006)

virtual_beam_cross_detector(data, time_window_length)
```

**Arguments**

**data** [data.table::data.table](#) containing behavioural variables of a *single animal* (no id). It must have the columns `xy_dist_log10x1000` (for computing subpixel velocity), `x` (beam cross), `t` and `has_interacted` (whether a stimulus was delivered).

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

velocity\_correction\_coef  
 an empirical coefficient to correct velocity with respect to variable framerate.

masking\_duration  
 number of second during which any movement is ignored (velocity is set to 0) after a stimulus is delivered (aka interaction).

velocity\_threshold  
 uncorrected velocity above which an animal is classified as ‘moving’ (for the legacy version).

### Details

- Validated and corrected subpixel velocity ([max\\_velocity\\_detector](#)), the most rigorous
- Uncorrected subpixel velocity ([max\\_velocity\\_detector\\_legacy](#))
- Crossing a virtual beam in the middle of the region of interest ([virtual\\_beam\\_cross\\_detector](#))

[max\\_velocity\\_detector](#) is the default movement classification for real-time ethoscope experiments. It is benchmarked against human-generated ground truth.

These functions are *rarely called directly*, but typically used is in the context of [sleep\\_annotation](#).

### Value

an object of the same type as data (i.e. [data.table::data.table](#) or [behavr::behavr](#)) with additional columns:

- moving Logical, TRUE iff. motion was detected.
- beam\_crosses The number of beam crosses (when the animal crosses  $x = 0.5$  – that is the midpoint of the region of interest) within the time window
- max\_velocity The maximal velocity within the time window. The resulting data is sampled at a period equals to time\_window\_length.

### See Also

- [sleep\\_annotation](#) – which requires a motion detector

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sleep_annotation	<i>Score sleep behaviour from immobility</i>
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### Description

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

### Usage

```
sleep_annotation(data, time_window_length = 10, min_time_immobile = 300,
  motion_detector_FUN = max_velocity_detector, ...)
```

```
sleep_dam_annotation(data, min_time_immobile = 300)
```

## Arguments

data	<a href="#">data.table</a> containing behavioural variable from or one multiple animals. When it has a key, unique values, are assumed to represent unique individuals (e.g. in a <a href="#">behavr</a> table). Otherwise, it analysis the data as coming from a single animal. data must have a column t representing time.
time_window_length	number of seconds to be used by the motion classifier. This corresponds to the sampling period of the output data.
min_time_immobile	Minimal duration (in s) of a sleep bout. Immobility bouts longer or equal to this value are considered as sleep.
motion_detector_FUN	function used to classify movement
...	extra arguments to be passed to motion_classifier_FUN.

## Details

The default `time_window_length` is 300 seconds – it is also known as the "5 minute rule". `sleep_annotation` is typically used for ethoscope data, whilst `sleep_dam_annotation` only works on DAM2 data. These functions are *rarely used directly*, but rather passed as an argument to a data loading function, so that analysis can be performed on the go.

## Value

a [behavr](#) table similar to data with additional variables/annotations (i.e. moving and asleep). The resulting data will only have one data point every `time_window_length` seconds.

## References

- The relevant [rethomic tutorial section](#) – on sleep analysis

## See Also

- [motion\\_detectors](#) – options for the `motion_detector_FUN` argument
- [bout\\_analysis](#) – to further analyse sleep bouts in terms of onset and length

## Examples

```
dt_one_animal <- toy_ethoscope_data(seed=2)
##### Ethoscope, corrected velocity classification #####
sleep_dt <- sleep_annotation(dt_one_animal, masking_duration=0)
print(sleep_dt)
# We could make a sleep 'barcode'
## Not run:
library(ggplot2)
ggplot(sleep_dt, aes(t,y="Animal 1",fill=asleep)) +
  geom_tile() + scale_x_time()

## End(Not run)
```

```
##### Ethoscope, virtual beam cross classification #####
sleep_dt2 <- sleep_annotation(dt_one_animal,
                             motion_detector_FUN=virtual_beam_cross_detector)

## Not run:
library(ggplot2)
ggplot(sleep_dt2, aes(t,y="Animal 1",fill=asleep)) +
  geom_tile() + scale_x_time()

## End(Not run)

##### DAM data, de facto beam cross classification #####
dt_one_animal <- toy_dam_data(seed=7)
sleep_dt <- sleep_dam_annotation(dt_one_animal)

## Not run:
library(ggplot2)
ggplot(sleep_dt, aes(t,y="Animal 1",fill=asleep)) +
  geom_tile() + scale_x_time()

## End(Not run)
```

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