

Package ‘ggetho’

September 10, 2017

Title Visualise High-Throughput Behavioural (i.e. Ethomics) Data

Date 2017-07-25

Version 0.3.0.9003

Description Uses ggplot to represent animal behaviour data, generally recorded over multiple days.

Depends ggplot2,
behavr

Imports data.table,
hms

Suggests testthat

License GPL-3

Encoding UTF-8

LazyData true

URL <https://github.com/rethomics/ggetho>

BugReports <https://github.com/rethomics/ggetho/issues>

RoxygenNote 6.0.1

Roxygen list(markdown = TRUE)

R topics documented:

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|---------|--------------------------------------|
| boot_ci | <i>Bootstrap confidence interval</i> |
|---------|--------------------------------------|

Description

Compute the mean of a variable, and the quantiles after bootstrap resampling.

Usage

```
boot_ci(y, r = 5000, ci = 0.95)
```

Arguments

| | |
|----|--|
| y | Numeric vector |
| r | Number of replicates to draw. |
| ci | Confidence interval to draw from the empirical distribution. |

See Also

boot_ci is intended to be used as the method argument of [stat_pop_etho](#). Other functions, such as [ggplot2::mean_se](#), can be used to generate error bars.

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|--------|--|
| ggetho | <i>Prepare a ggplot object to represent behavioural data</i> |
|--------|--|

Description

This function summarises a variable of interest (y or z axis) in order to subsequently represent it over time (x axis) (either using ggplot2 or the of plotting functions provided in ‘ggetho’).

Usage

```
ggetho(data, mapping, summary_FUN = mean, summary_time_window = mins(30),
       time_wrap = NULL, time_offset = NULL, ...)
```

Arguments

| | |
|---------------------|--|
| data | behavr table containing the data and metadata |
| mapping | default list of aesthetic mappings to use for plot |
| summary_FUN | method (function) used to summarise variable over time (typically, the mean) |
| summary_time_window | width (in seconds) of the time window to compute a summary on |
| time_wrap | time (in seconds) used to wrap the data (see details) |
| time_offset | time offset (i.e. phase, in seconds) when using time_wrap |
| ... | additional arguments to be passed to ggplot2::ggplot() |

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)`. Instead of representing data from the start of the day, it can be done from any offset, using `time_offset`. For instance, `time_offset = hours(12)` puts the circadian reference (ZT0) in the middle of the plot.

Value

an initial plot object that can be further edited.

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See Also

- [stat_pop_etho](#) to show population trend by aggregating individuals over time
- [stat_tile_etho](#) to show variable of interest as colour intensity
- [stat_ld_annotations](#) to show light and dark phases on the plot

Examples

```
# We start by making a to dataset with 20 animals
library(behavr)
query <- data.frame(experiment_id="toy_experiment",
                    region_id=1:20,
                    condition=c("A","B"))
dt <- toy_activity_data(query,3)
# We build a plot object with nothing inside (just the axis)
# we want to show proportion of time sleeping on the y axis:
pl <- ggetho(dt, aes(y=asleep))
pl
# Sometimes, the variable of interest is not on the y axis, but on z axis (colour scale).
# When we do not provide a y axis,
# ggetho will make a ID for each animal and display them on separate rows
pl <- ggetho(dt, aes(z=asleep))
pl
# this one is the same type, but groups the animals by condition
pl <- ggetho(dt, aes(z=asleep,y=condition))
pl
# we want to summarise (wrap) data along a circadian day:
pl <- ggetho(dt, aes(y=asleep), time_wrap=hours(24))
pl
```

stat_ld_annotations *Compute and display light/dark annotations onto a plot object*

Description

This function is used to show light and dark (L and D) phases as boxes on top a plot.

Usage

```
stat_ld_annotations(mapping = NULL, data = NULL, position = "identity",
  ld_colours = c("white", "black"), ypos = "auto", height = "auto",
  period = hours(24), phase = 0, ..., na.rm = FALSE,
  show.legend = FALSE, inherit.aes = TRUE)
```

Arguments

| | |
|---------------|---|
| mapping | Set of aesthetic mappings created by aes or aes_ . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping. |
| data | The data to be displayed in this layer. There are three options: If <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to ggplot . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data. |
| position | Position adjustment, either as a string, or the result of a call to a position adjustment function. |
| ld_colours | character vector of length 2 naming the colours for light and dark phases, respectively. The default is white and black. |
| ypos, height | The position and height of the annotation on the y axis. The defaults, "auto" will put the labels below any data. |
| period, phase | period and phase (in seconds) of the LD cycle. |
| ... | other arguments passed on to layer . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat. |
| na.rm | If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed. |
| show.legend | logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes. |
| inherit.aes | If <code>FALSE</code> , overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders . |

See Also

Useful links:

- [ggetho](#) to generate a plot object
- [TODO Tutorial](#) for this function

Other layers: [stat_pop_etho](#), [stat_tile_etho](#)

Examples

```
library(behavr)
# we start by making a to dataset with 20 animals
query <- data.frame(experiment_id="toy_experiment",
                    region_id=1:20,
                    condition=c("A","B"))
dt <- toy_activity_data(query,3)
# We build a plot object
pl <- ggetho(dt, aes(y=asleep)) + stat_pop_etho()
pl + stat_ld_annotiations()
# different colours (e.g. DD)
pl + stat_ld_annotiations(ld_colour=c("grey", "black"))
# shorter period
pl + stat_ld_annotiations(period=hours(22), phase=hours(3))
# on a tile plot:
pl <- ggetho(dt, aes(z=asleep)) + stat_tile_etho()
pl + stat_ld_annotiations()
```

| | |
|---------------|--|
| stat_pop_etho | <i>Compute and display a population aggregate for a behavioural variable of interest</i> |
|---------------|--|

Description

This function displays the temporal (time on the x axis) trend of variable of interest, on the y axis as a line with error bars.

Usage

```
stat_pop_etho(mapping = NULL, data = NULL, geom = "smooth",
              position = "identity", ..., method = mean_se, method.args = list(),
              show.legend = NA, inherit.aes = TRUE)
```

Arguments

| | |
|---------|---|
| mapping | Set of aesthetic mappings created by aes or aes_ . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping. |
|---------|---|

| | |
|-------------|--|
| data | <p>The data to be displayed in this layer. There are three options:</p> <p>If NULL, the default, the data is inherited from the plot data as specified in the call to <code>ggplot</code>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <code>fortify</code> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>., and will be used as the layer data.</p> |
| geom | The geometric object to use display the data |
| position | Position adjustment, either as a string, or the result of a call to a position adjustment function. |
| ... | other arguments passed on to <code>layer</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat. |
| method | function used to compute the aggregate and error bars. It should return (y, ymin and ymax). The default is <code>ggplot2::mean_se</code> , which computes the mean + or - standard error. <code>boot_ci</code> can be used instead to generate bootstrap confidence interval. |
| method.args | List of additional arguments passed on to the modelling function defined by method. |
| show.legend | logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. |
| inherit.aes | If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders</code> . |

See Also

- `ggetho` to generate a plot object
- `stat_tile_etho` to show variable of interest as colour intensity
- `stat_ld_annotatons` to show light and dark phases on the plot
- TODO Tutorial for this function

Other layers: `stat_ld_annotatons`, `stat_tile_etho`

Examples

```
library(behavr)
# we start by making a to dataset with 20 animals
query<- data.frame(experiment_id="toy_experiment",
                    region_id=1:20,
                    condition=c("A","B"),
                    age=c(1, 5, 10, 20))

print(query)
dt <- toy_activity_data(query,seed=3)
# We build a plot object
pl <- ggetho(dt, aes(y=asleep))
```

```
# A standard plot of the whole population:
pl + stat_pop_etho()
# We can also split by condition, and display the two population on different facets:
pl + stat_pop_etho() + facet_grid(condition ~ .)

# Instead, we can use different colour for separate conditions:
pl <- ggetho(dt, aes(y=asleep, colour=condition))
pl + stat_pop_etho()

#sometimes, we also have numeric condition (e.g. age)
pl <- ggetho(dt, aes(y=asleep, colour=age))
pl + stat_pop_etho()
# sometimes we want to aggregate several days of data to one circadian day (i.e. time wrapping)
pl <- ggetho(dt, aes(y=moving), time_wrap=hours(24))
pl + stat_pop_etho()
```

| | |
|----------------|---|
| stat_tile_etho | <i>Display a behavioural variable of interest as colour intensity value</i> |
|----------------|---|

Description

This function shows the temporal trend (time on the x axis) of a variable of interest as colour intensity (z axis). The y axis is a discrete variable such as a treatment or the id of animals.

Usage

```
stat_tile_etho(mapping = NULL, data = NULL, geom = "raster",
  position = "identity", ..., method = mean, method.args = list(),
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE)
```

Arguments

| | |
|----------|---|
| mapping | Set of aesthetic mappings created by aes or aes_ . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping. |
| data | <p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to ggplot.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>., and will be used as the layer data.</p> |
| geom | The geometric object to use display the data |
| position | Position adjustment, either as a string, or the result of a call to a position adjustment function. |

| | |
|-------------|--|
| ... | other arguments passed on to layer . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat. |
| method | function used to compute the aggregate, when grouping individuals on the same row. The default is mean . median , min , max are other examples of other functions one can use. |
| method.args | List of additional arguments passed on to the modelling function defined by method. |
| na.rm | If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed. |
| show.legend | logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. |
| inherit.aes | If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders . |

See Also

- [ggetho](#) to generate a plot object
- [stat_pop_etho](#) to show population trend by aggregating individuals over time
- [stat_ld_annotatons](#) to show light and dark phases on the plot
- TODO Tutorial for this function <http://gilestrolab.github.io/rethomics/tutorial/todo>

Other layers: [stat_ld_annotatons](#), [stat_pop_etho](#)

Examples

```
library(behavr)
# we start by making a to dataset with 20 animals
query<- data.frame(experiment_id="toy_experiment",
                    region_id=1:20,
                    condition=c("A","B"),
                    age=c(1, 5, 10, 20))

print(query)
dt <- toy_activity_data(query,seed=3)
# We build a plot object
pl <- ggetho(dt, aes(z=asleep))
# A standard plot one row per animal:
pl + stat_tile_etho()
# We can also group animals per condition and calculate the average sleep
pl <- ggetho(dt, aes(z=asleep, y=condition))
pl + stat_tile_etho()
# Instead, of the average, maybe we want to show the highest (max)
# possible value of sleep for any time point
pl + stat_tile_etho(method=max)
```


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