

# Package ‘ggetho’

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**Title** Visualisation of High-Throughput Behavioural (i.e. Ethomics) Data

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**Version** 0.3.4

**Description** Extension of 'ggplot2' providing layers, scales and preprocessing functions useful to represent behavioural variables that are recorded over multiple animals and days. This package is part of the rethomics framework <<http://rethomics.github.io/>>.

**Depends** R (>= 3.00),  
ggplot2,  
behavr

**Imports** data.table,  
stringr,  
scales,  
labeling,  
rlang

**Suggests** testthat,  
covr,  
knitr,  
zeitgebr

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

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

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

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geom_peak	<i>Visualise peaks in a power spectrum or periodogram</i>
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**Description**

This function draws points on the x-y coordinates of selected peaks and write their (y) value on the bottom of the plot.

**Usage**

```
geom_peak(mapping = NULL, data = NULL, stat = "identity",
  position = "identity", ..., na.rm = TRUE, show.legend = NA,
  inherit.aes = TRUE, peak_rank = 1, conversion = hours)
```

**Arguments**

mapping	Set of aesthetic mappings created by <a href="#">aes()</a> or <a href="#">aes_()</a> . If specified and inherit.aes = TRUE (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 NULL, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot()</a> . A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify()</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a data.frame., and will be used as the layer data.
stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	Other arguments passed on to <a href="#">layer()</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like color = "red" or size = 3. They may also be parameters to the paired geom/stat.
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. It can also be a named logical vector to finely select the aesthetics to display.
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> .
peak_rank	numerical vector specifying the rank(s) of peak(s) to draw
conversion	function to convert values of x to a specific unit. The default, <code>hours</code> , will write x (time) in decimal hours.

## Details

In the input data, peaks are encoded as an additional column/aesthetic with values corresponding to peak ranks (and 0 when the point is not a peak). In other word, the mapping must provide x, y and peak. Only peaks matching `peak_rank` will be drawn (see example).

## References

- The relevant [rethomic tutorial section](#)

## See Also

- [ggperio](#) to create a periodogram
- [zeitgebr::find\\_peaks](#) to automatically add a peak column on periodogram data

Other layers: [stat\\_bar\\_tile\\_etho](#), [stat\\_ld\\_annotatons](#), [stat\\_pop\\_etho](#)

## Examples

```
# We make a data frame by hand with five rows
# There are two peaks: in position 4 and 2

df <- data.frame(x = hours(1:5),
                 y = c(1, 2, 0, 4, 1),
                 peak = c(0, 2, 0, 1, 0))

# We draw the plot as a line
p1 <- ggplot(df, aes(x, y, peak = peak)) +
  geom_line() +
  scale_x_hours()

p1
# Now we could add the peak values as an extra layer:
# The first peak
p1 + geom_peak()
# The first and second peak
p1 + geom_peak(peak_rank = 1:2)
# The second only
p1 + geom_peak(peak_rank = 2)

# Just like with other geoms,
# we can change colour, size, alpha, shape, ... :
p1 + geom_peak(colour = "red", size = 10, alpha = .5, shape = 20)
```

```
## In the context of circadian analysis,
# Using the zeitgebr package:

require(zeitgebr)
# We make toy data
metadata <- data.table(id = sprintf("toy_experiment|%02d", 1:40),
                      region_id = 1:40,
                      condition = c("A", "B"),
                      sex = c("M", "M", "F", "F"))
dt <- toy_activity_data(metadata, seed = 107)
# We shift period of the group "A" by 0.01
dt[, t := ifelse(xmv(condition) == "A", t, t * 1.01)]
# We compute a periodogram for each individual
per_dt <- periodogram(moving, dt, FUN = chi_sq_periodogram)
per_dt <- find_peaks(per_dt)
out <- ggperio(per_dt, aes(y = power - signif_threshold, colour = condition, peak = peak)) +
  stat_pop_etho() +
  facet_wrap(~ id, labeller = id_labeller)

out
out + geom_peak(colour="black")
```

---

ggetho

---

*Prepare a ggplot object to represent behavioural data*


---

## Description

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

## Usage

```
ggetho(data, mapping, summary_FUN = mean,
       summary_time_window = mins(30), time_wrap = NULL, time_offset = 0,
       multiplot = NULL, multiplot_period = hours(24), ...)
```

## Arguments

data	<a href="#">behavr::behavr</a> 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
multiplot	integer, greater than two, or NULL, the default (see details)

```

multiplot_period
    the duration of the period when mutiplotting (see details)
...
    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.

Multiplotting is a generalisation of double-plotting, triple-plotting... This type or representation is useful to understand periodic behaviours. When `multiplot` is *not* NULL, data is repeated as many time as its value, along the x axis. The y axis is then the period (typically the day) onset. It is possible to set duration of the period, which is typically 24 h to arbitrary values using the `multiplot_period` argument.

## Value

An initial plot object that can be further edited.

## References

- The relevant [rethomic tutorial section](#)

## 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 dataset with 20 animals
metadata <- data.table(id = sprintf("toy_experiment|%02d", 1:20),
                      condition = c("A", "B"))
dt <- toy_activity_data(metadata, 3)
# We build a plot object with nothing inside (just the axis)
# we want to show proportion of time sleeping on the y axis:
p1 <- ggetho(dt, aes(y = asleep))
p1
# 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 an ID for each animal and display them on separate rows
p1 <- ggetho(dt, aes(z = asleep))
p1
# this one is the same type, but it groups the animals by condition
p1 <- ggetho(dt, aes(z = asleep, y = condition))
p1
# sorting with paste

```

```

p1 <- ggetho(dt, aes(z = asleep, y = paste(condition, id)))
p1

# we want to summarise (wrap) data along a circadian day:
p1 <- ggetho(dt, aes(y = asleep), time_wrap = hours(24))
p1

# double-plotted actogram:
p1 <- ggetho(dt,
             aes(z = moving),
             multiplot = 2,
             multiplot_period = hours(24))
p1
# then use `+ stat_tile_etho()` , or `+ stat_bar_tile_etho()`

```

---

ggperio

---

*Prepare a ggplot object to represent periodogram data*


---

## Description

This function summarises periodogram data (containing periodograms of multiple individual), to show period on the x axis, and power (or equivalent) on the y axis.

## Usage

```
ggperio(data, mapping = aes(x = period, y = power), ...)
```

## Arguments

data	<a href="#">behavr::behavr</a> table containing the data and metadata
mapping	default list of aesthetic mappings to use for plot
...	additional arguments to be passed to <a href="#">ggplot2::ggplot()</a>

## References

- The relevant [rethomic tutorial section](#)

## See Also

- [ggetho](#) to plot time series
- [geom\\_peak](#) to draw peaks on a periodogram
- [zeitgebr::periodogram](#) to compute periodograms in a first place

## Examples

```
require(zeitgebr)
# We make toy data
metadata <- data.table(id = sprintf("toy_experiment|%02d", 1:40),
                       region_id = 1:40,
                       condition = c("A", "B"),
                       sex = c("M", "M", "F", "F"))
dt <- toy_activity_data(metadata, seed = 107)
# We shift period of the group "A" by 0.01
dt[, t := ifelse(xmv(condition) == "A", t, t * 1.01)]
# We compute a periodogram for each individual
per_dt <- periodogram(moving, dt, FUN = chi_sq_periodogram)

# Then we display them as an average
out <- ggperio(per_dt, aes(y = power, colour = condition))
out + stat_pop_etho()

out <- ggperio(per_dt, aes(y = power - signif_threshold, colour = condition))
out + stat_pop_etho()
out <- ggperio(per_dt, aes(y = power - signif_threshold, colour = condition))
out + stat_pop_etho() + facet_wrap(~ id, labeller = id_labeller)
```

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ggspectro

---

*Prepare a ggplot object to represent spectrogram data*


---

## Description

This function summarises spectrogram data (containing spectrograms of multiple individual), to show period on the y axis, time on the x axis and power on the z axis (*e.g.* as a colour).

## Usage

```
ggspectro(data, mapping = aes(), summary_FUN = mean,
          summary_time_window = mins(30), time_wrap = NULL, time_offset = 0,
          ...)
```

## Arguments

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

## Examples

```
library(zeitgebr)
data(dams_sample)
dt <- dams_sample
spect_dt <- spectrogram(activity, dt)
p1 <- ggspectro(spect_dt, time_wrap = hours(24)) + stat_tile_etho() + scale_y_hours(log=T) +
  stat_ld_annotiations(ld_colours = c("grey", "black"))
p1 + facet_grid(period_group ~ .)
p1 + facet_wrap(~ id)
```

---

id\_labeller

*A facet labeller for id*


---

## Description

This function returns a [ggplot2::labeller](#) that displays the id on several lines to improve readability.

## Usage

```
id_labeller(labels)
```

## Arguments

labels	Data frame of labels. Usually contains only one element, but faceting over multiple factors entails multiple label variables.
--------	---

## See Also

[ggplot2::labeller](#), to make your own labellers

## Examples

```
library(behavr)
metadata <- data.frame(
  id = sprintf("2017-09-01 20:00:12|toy_experiment_a_very_long_name|%02d", 1:20),
  condition = c("A", "B"))
dt <- toy_activity_data(metadata, duration = hours(2))
p1 <- ggetho(dt, aes(y = asleep)) + stat_pop_etho()
## Without labelling
p1 + facet_wrap(~ id)

## With labeller
p1 + facet_wrap(~ id, labeller = id_labeller)
```



---

stat_bar_tile_etho	<i>Display a variable of interest either as a colour intensity value or as a bar height</i>
--------------------	---

---

## Description

These functions show the temporal trend (time on the x axis) of a variable of interest (z axis) as either colour intensity (stat\_tile\_etho) or using the hight of the tiles (stat\_bar\_tile\_etho). In both cases, the y axis is a discrete variable such as a treatment or the id of individuals.

## Usage

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

```
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 <a href="#">aes()</a> or <a href="#">aes_()</a> . If specified and inherit.aes = TRUE (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 NULL, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot()</a> . A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify()</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a data.frame., and will be used as the layer data.
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 <a href="#">layer()</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like color = "red" or size = 3. They may also be parameters to the paired geom/stat.
method	function used to compute the aggregate, when/if grouping several individuals on the same row. The default is fuction is <a href="#">mean</a> . <a href="#">median</a> , <a href="#">min</a> , <a href="#">max</a> are examples of alternatives.
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. It can also be a named logical vector to finely select the aesthetics to display.
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> .

## References

- The relevant [rethomic tutorial section](#)

## See Also

- [ggetho](#) to generate a plot object
- [stat\\_pop\\_etho](#) to show population trend by aggregating individuals over time
- [stat\\_ld\\_annotations](#) to show light and dark phases on the plot

Other layers: [geom\\_peak](#), [stat\\_ld\\_annotations](#), [stat\\_pop\\_etho](#)

## Examples

```
# We start by making a to dataset with 20 animals
metadata <- data.frame(id = sprintf("toy_experiment | %02d", 1:20),
                      age = c(1, 5, 10, 20),
                      condition = c("A", "B"))

print(metadata)
dt <- toy_activity_data(metadata, 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()

# We can sort by adding condition AND id on the y axis:
pl <- ggetho(dt, aes(z = asleep, y = interaction(id, condition)))
pl + stat_tile_etho()
# Same if we want to sort by age
pl <- ggetho(dt, aes(z = asleep, y = interaction(id, age)))
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)
# We can also use stat_bar_tile as an alternative
pl + stat_bar_tile_etho()
```

---

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 = "bottom", height = 0.03, period = hours(24), phase = 0,
  l_duration = hours(12), outline = "black", x_limits = c(NA, NA),
  ..., na.rm = FALSE, show.legend = FALSE, inherit.aes = TRUE)
```

## Arguments

mapping	Set of aesthetic mappings created by <code>aes()</code> or <code>aes_()</code> . 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 <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>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
ld_colours	character vector of length two setting the colours for light and dark phases, respectively. The default is <code>c("white", "black")</code> .
ypos	position and height of the annotation on the y axis. It can be either "top" or "bottom". The default, "bottom" will put the labels below any data.
height	relative height of the rectangles. The default is 3 percent (0.03).
period, phase, l_duration	period, phase and duration of the L phase (in seconds) of the LD cycle.
outline	colour of the border of the rectangles. A value of <code>NA</code> draws no border.
x_limits	numerical vector of length 2 for the start and end of the annotations (in seconds). The default, <code>c(NA, NA)</code> , uses the full range of the plotted data.
...	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 <code>geom/stat</code> .

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. It can also be a named logical vector to finely select the aesthetics to display.
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> .

## References

- The relevant [rethomic tutorial section](#)

## See Also

- [ggetho](#) to generate a plot object

Other layers: [geom\\_peak](#), [stat\\_bar\\_tile\\_etho](#), [stat\\_pop\\_etho](#)

## Examples

```
library(behavr)
# We start by making a to dataset with 20 animals
metadata <- data.frame(id = sprintf("toy_experiment | %02d", 1:20),
                      condition = c("A", "B"))
dt <- toy_activity_data(metadata, 3)
# We build a plot object
pl <- ggetho(dt, aes(y = asleep)) + stat_pop_etho()
pl + stat_ld_annotatations()
# We can also put the annotations in the background:
pl <- ggetho(dt, aes(y = asleep)) +
  stat_ld_annotatations(outline = NA) +
  stat_pop_etho()

pl
# Different colours (e.g. DD)
pl + stat_ld_annotatations(ld_colour = c("grey", "black"))
# Shorter period
pl + stat_ld_annotatations(period = hours(22), phase = hours(3))
# On a tile plot:
pl <- ggetho(dt, aes(z = asleep)) + stat_tile_etho()
pl + stat_ld_annotatations()
```

---

stat\_pop\_etho

---

*Compute and display a population aggregate for a variable of interest*


---

## Description

This function displays the temporal (time on the x axis) trend of variable of interest, on the y axis as a line with confidence interval as a shaded area.

**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 <a href="#">aes()</a> or <a href="#">aes_()</a> . 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 <a href="#">ggplot()</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify()</a> 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.
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 <a href="#">layer()</a> . 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 confidence intervals. It should return <code>(y, ymin and ymax)</code> . The default is <a href="#">ggplot2::mean_se</a> , which computes the mean + or - standard error. <a href="#">ggplot2::mean_cl_boot</a> can be used instead to generate bootstrap confidence interval instead.
method.args	List of additional arguments passed on to the modelling function defined by <code>method</code> .
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. It can also be a named logical vector to finely select the aesthetics to display.
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. <a href="#">borders()</a> .

**References**

- The relevant [rethomic tutorial section](#)

**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
- [ggplot2::stat\\_smooth](#) to understand how to change the type of confidence interval, line colour and so forth

Other layers: [geom\\_peak](#), [stat\\_bar\\_tile\\_etho](#), [stat\\_ld\\_annotatons](#)

## Examples

```
library(behavr)
metadata <- data.frame(id = sprintf("toy_experiment | %02d", 1:20),
                       age=c(1, 5, 10, 20),
                       condition=c("A", "B"))
dt <- toy_activity_data(metadata, 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()
# We could want to aggregate several days of data to one circadian day (i.e. time wrapping)
# here, we also plot the invert of moving (!moving)
pl <- ggetho(dt, aes(y = !moving), time_wrap = hours(24))
pl + stat_pop_etho()
```

---

time\_scales

*Scales for durations*


---

## Description

A set of scales used to represent experimental durations.

## Usage

```
scale_x_days(name = "Time", breaks = waiver(),
             minor_breaks = waiver(), labels = waiver(), limits = NULL,
             expand = waiver(), oob = scales::censor, na.value = NA_real_,
             position = "bottom", time_wrap = NULL, unit = "day", log = FALSE)

scale_y_days(name = "Time", breaks = waiver(),
             minor_breaks = waiver(), labels = waiver(), limits = NULL,
             expand = waiver(), oob = scales::censor, na.value = NA_real_,
```

```

position = "left", time_wrap = NULL, unit = "day", log = FALSE)

scale_x_hours(name = "Time", breaks = waiver(),
  minor_breaks = waiver(), labels = waiver(), limits = NULL,
  expand = waiver(), oob = scales::censor, na.value = NA_real_,
  position = "bottom", time_wrap = NULL, unit = "h", log = FALSE)

scale_y_hours(name = "Time", breaks = waiver(),
  minor_breaks = waiver(), labels = waiver(), limits = NULL,
  expand = waiver(), oob = scales::censor, na.value = NA_real_,
  position = "left", time_wrap = NULL, unit = "h", log = FALSE)

scale_x_seconds(name = "Time", breaks = waiver(),
  minor_breaks = waiver(), labels = waiver(), limits = NULL,
  expand = waiver(), oob = scales::censor, na.value = NA_real_,
  position = "bottom", time_wrap = NULL, unit = "s", log = FALSE)

scale_y_seconds(name = "Time", breaks = waiver(),
  minor_breaks = waiver(), labels = waiver(), limits = NULL,
  expand = waiver(), oob = scales::censor, na.value = NA_real_,
  position = "left", time_wrap = NULL, unit = "s", log = FALSE)

```

## Arguments

name	The name of the scale. Used as axis or legend title. If <code>waiver()</code> , the default, the name of the scale is taken from the first mapping used for that aesthetic. If <code>NULL</code> , the legend title will be omitted.
breaks	One of: <ul style="list-style-type: none"> <li>• <code>NULL</code> for no breaks</li> <li>• <code>waiver()</code> for the breaks specified by <code>date_breaks</code></li> <li>• A <code>Date/POSIXct</code> vector giving positions of breaks</li> <li>• A function that takes the limits as input and returns breaks as output</li> </ul>
minor_breaks	One of: <ul style="list-style-type: none"> <li>• <code>NULL</code> for no breaks</li> <li>• <code>waiver()</code> for the breaks specified by <code>date_minor_breaks</code></li> <li>• A <code>Date/POSIXct</code> vector giving positions of minor breaks</li> <li>• A function that takes the limits as input and returns minor breaks as output</li> </ul>
labels	One of: <ul style="list-style-type: none"> <li>• <code>NULL</code> for no labels</li> <li>• <code>waiver()</code> for the default labels computed by the transformation object</li> <li>• A character vector giving labels (must be same length as breaks)</li> <li>• A function that takes the breaks as input and returns labels as output</li> </ul>
limits	A numeric vector of length two providing limits of the scale. Use <code>NA</code> to refer to the existing minimum or maximum.

expand	Vector of range expansion constants used to add some padding around the data, to ensure that they are placed some distance away from the axes. Use the convenience function <code>ggplot2::expand_scale()</code> to generate the values for the <code>expand</code> argument. The defaults are to expand the scale by 5% on each side for continuous variables, and by 0.6 units on each side for discrete variables.
oob	Function that handles limits outside of the scale limits (out of bounds). The default replaces out of bounds values with NA.
na.value	Missing values will be replaced with this value.
position	The position of the axis. "left" or "right" for vertical scales, "top" or "bottom" for horizontal scales
time_wrap	duration (in seconds) used to wrap the labels of the time axis
unit	the name of unit (string) to be used in the label (e.g. one could use "second" instead of "s")
log	logical, whether axis should be on a log-transformed

### Details

`time_wrap` is useful, for instance, to express time within a day (ZT), instead of absolute time.

### References

- The relevant [rethomic tutorial section](#)

### See Also

- [ggetho](#) to generate a plot object
- [ggplot2::scale\\_x\\_continuous](#), the default ggplot scale, to understand limits, breaks, labels and name

### Examples

```
# We generate some data
metadata <- data.frame(id = sprintf("toy_experiment | %02d", 1:20),
                      condition = c("A", "B"))
dt <- toy_activity_data(metadata, 3)
# Then, a simple plot
p1 <- ggetho(dt, aes(y = asleep)) + stat_pop_etho()
p1 + scale_x_hours(breaks = days(c(1, 2)))
p1 + scale_x_hours()
p1 + scale_x_days(breaks = days(c(1, 2)))
p1 + scale_x_days()

# To express time modulus `time_wrap`
# e.g. time n the day
p1 + scale_x_hours(time_wrap = hours(24)) +
  coord_cartesian(xlim=c(0, days(2)))

# On a shorter time scale
p1 <- ggetho(dt[t < hours(5)], aes(z = asleep)) + stat_tile_etho()
```



```
p1 + scale_x_hours()  
p1 + scale_x_hours(breaks = hours(1:4))  
p1 + scale_x_seconds(breaks = hours(1:4))
```

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