

Package ‘ggHoriPlot’

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Type Package

Title Horizon Plots for 'ggplot2'

Version 1.0.1

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Description A user-friendly, highly customizable R package for building horizon plots in the 'ggplot2' environment.

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URL <https://rivasiker.github.io/ggHoriPlot/>,
<https://github.com/rivasiker/ggHoriPlot>,
<https://CRAN.R-project.org/package=ggHoriPlot>

BugReports <https://github.com/rivasiker/ggHoriPlot/issues>

Depends ggplot2, R (>= 2.10)

Imports dplyr, glue, magrittr, stringr, tidyr

Suggests ggthemes, knitr, patchwork, rmarkdown, testthat (>= 3.0.0), tidyverse, utils

VignetteBuilder knitr

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climate_CPH	<i>Average temperature in Copenhagen</i>
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Description

A dataset containing the average temperature in degrees Celsius for Copenhagen between the year 1995 and 2019.

Usage

```
climate_CPH
```

Format

A data frame with 9,132 rows and 9 variables:

Region geographic region

Country country

State state or territory

City city or town

Month month

Day day

Year year

AvgTemperature average temperature in Fahrenheit

date_mine data in yyyy-mm-dd format

Source

<https://www.kaggle.com/sudalairajkumar/daily-temperature-of-major-cities>

climate_US	<i>Average temperature in major cities of the US</i>
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Description

A dataset containing the average temperature in Fahrenheit for major cities in the US for the year 2000.

Usage

climate_US

Format

A data frame with 57,828 rows and 9 variables:

Region geographic region

Country country

State state or territory

City city or town

Month month

Day day

Year year

AvgTemperature average temperature in Fahrenheit

date_mine data in yyyy-mm-dd format

Source

<https://www.kaggle.com/sudalairajkumar/daily-temperature-of-major-cities>

<https://benschmidt.org/2014/06/05/optimally-ordering-geographical-entities-in-linear-space/>

COVID	<i>Distribution of COVID-19 cases in Asia</i>
-------	---

Description

A dataset containing the geographic distribution of COVID-19 cases in Asia during 2020.

Usage

COVID

Format

A data frame with 12,695 rows and 3 variables:

date_mine date of the measurement in yyyy-mm-dd format

y standardized number of cases

countriesAndTerritories countries and territories in Asia

Source

<https://www.ecdc.europa.eu/en/publications-data/download-todays-data-geographic-distribution-covid>

geom_horizon

Horizon plots

Description

This function builds horizon plots in ggplot2. It allows for the customization of the origin and the horizon scale.

Usage

```
geom_horizon(  
  mapping = NULL,  
  data = NULL,  
  position = "identity",  
  ...,  
  na.rm = FALSE,  
  show.legend = TRUE,  
  origin = "midpoint",  
  horizonscale = 6,  
  rm.outliers = FALSE,  
  reverse = FALSE,  
  mirror = FALSE,  
  inherit.aes = TRUE  
)
```

```
stat_horizon(  
  mapping = NULL,  
  data = NULL,  
  geom = "ribbon",  
  position = "identity",  
  ...,  
  na.rm = FALSE,  
  show.legend = TRUE,  
  inherit.aes = TRUE,  
  origin = "midpoint",
```

```

  horizonscale = 6,
  rm.outliers = FALSE,
  reverse = FALSE,
  mirror = FALSE
)

```

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	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 <code>ggplot()</code> . 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. 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. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).
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>colour = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired <code>geom/stat</code> .
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. It can also be a named logical vector to finely select the aesthetics to display.
origin	Origin of the horizon plot. It can either be a string, namely "midpoint" (the default), "median", "mean", "min" or "quantiles", or a user-specified number.
horizonscale	Cutpoints of the horizon plot. It can either be an integer specifying the number of ranges (default is 6), or a user-supplied numeric vector with the cutpoints defining the different ranges.
rm.outliers	If <code>TRUE</code> , all the values below $\text{quantile}(y, 0.25) - 1.5 \cdot \text{IQR}(y)$ and above $\text{quantile}(y, 0.75) + 1.5 \cdot \text{IQR}(y)$ are excluded from the origin and cutpoint calculations (default is <code>FALSE</code>). @param reverse If <code>TRUE</code> , the horizon peaks for the values below the origin are reversed (default is <code>FALSE</code>).
reverse	IF <code>TRUE</code> , the horizon peaks for all the values below the origin are reversed (default is <code>FALSE</code>).
mirror	If <code>TRUE</code> , the horizon peaks for all the values are reversed (default is <code>FALSE</code>).
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. <code>borders()</code> .
geom	Used geom, default to 'ribbon'

Details

A horizon plot is a special type of area plot in which the original data is transformed based on an origin and a horizon scale. The data is cut in different intervals, and the further the data is from the origin, the deeper its color usually is. All the intervals above the origin are then stacked on top of one another, keeping the intervals closest to the origin in the bottom and the furthest away ones on top. Likewise, the intervals below the origin are normally given a different color palette and they are stacked in a similar manner in the same area as the intervals above the origin. You can learn more about how horizon plots are built in vignette('ggHorPlot') or at https://bernatgel.github.io/karyoploter_tutorial/Tutorial/PlotHorizon/PlotHorizon.html.

Value

'ggplot2' layer for building a horizon plot.

Orientation

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the orientation parameter, which can be either "x" or "y". The value gives the axis that the geom should run along, "x" being the default orientation you would expect for the geom.

Aesthetics

geom_horizon() understands the following aesthetics (required aesthetics are in bold):

- x
- y
- xend
- alpha
- colour
- fill

Examples

```
# Generate data
huron <- data.frame(year = 1875:1972, level = as.vector(LakeHuron))

# Basic plot with default colors
h <- ggplot(huron) + geom_horizon(aes(year, level))

# Add color scheme
h + theme_void() + scale_fill_hcl()

# Add cupoints
ggplot(huron) +
  geom_horizon(aes(year, level, fill = ..Cutpoints..)) +
```

```
theme_void() +  
scale_fill_hcl()
```

rmsk

Distribution of repeats along the human genome

Description

A dataset containing the percentage of simple repeats in 100 kb windows along the human genome (hg38).

Usage

```
rmsk
```

Format

A data frame with 30,885 rows and 4 variables:

genoName chromosome name
bin starting coordinate of window
bin_2 end coordinate of window
p_repeat percentage of repeats

Source

<https://genome.ucsc.edu/cgi-bin/hgTrackUi?g=rmsk>

scale_fill_hcl

Create your own discrete scale

Description

These functions allow you to specify your own set of mappings from levels in the data to aesthetic values.

Usage

```
scale_fill_hcl(..., palette = "RdYlBu", reverse = FALSE)
```

Arguments

...	Arguments passed on to <code>ggplot2::discrete_scale</code>
scale_name	The name of the scale that should be used for error messages associated with this scale.
name	The name of the scale. Used as the 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"> • <code>NULL</code> for no breaks • <code>waiver()</code> for the default breaks (the scale limits) • A character vector of breaks • A function that takes the limits as input and returns breaks as output. Also accepts rlang <code>lambda</code> function notation.
labels	One of: <ul style="list-style-type: none"> • <code>NULL</code> for no labels • <code>waiver()</code> for the default labels computed by the transformation object • A character vector giving labels (must be same length as breaks) • A function that takes the breaks as input and returns labels as output. Also accepts rlang <code>lambda</code> function notation.
limits	One of: <ul style="list-style-type: none"> • <code>NULL</code> to use the default scale values • A character vector that defines possible values of the scale and their order • A function that accepts the existing (automatic) values and returns new ones. Also accepts rlang <code>lambda</code> function notation.
na.translate	Unlike continuous scales, discrete scales can easily show missing values, and do so by default. If you want to remove missing values from a discrete scale, specify <code>na.translate = FALSE</code> .
na.value	If <code>na.translate = TRUE</code> , what aesthetic value should the missing values be displayed as? Does not apply to position scales where <code>NA</code> is always placed at the far right.
drop	Should unused factor levels be omitted from the scale? The default, <code>TRUE</code> , uses the levels that appear in the data; <code>FALSE</code> uses all the levels in the factor.
guide	A function used to create a guide or its name. See <code>guides()</code> for more information.
super	The super class to use for the constructed scale
palette	the name of the palette to generate colors from. A list of all available palettes can be found by running <code>colorspace::hcl_palettes()</code> (default is "RdYlBu").
reverse	If <code>TRUE</code> , the order of the colors is reversed (default is <code>FALSE</code>)

Details

The functions `'scale_colour_manual()'`, `'scale_fill_manual()'`, `'scale_size_manual()'`, etc. work on the aesthetics specified in the scale name: `'colour'`, `'fill'`, `'size'`, etc. However, the functions

'scale_colour_manual()' and 'scale_fill_manual()' also have an optional 'aesthetics' argument that can be used to define both 'colour' and 'fill' aesthetic mappings via a single function call (see examples). The function 'scale_discrete_manual()' is a generic scale that can work with any aesthetic or set of aesthetics provided via the 'aesthetics' argument.

Value

Scale layer for the fill aesthetic.

sports_time	<i>Peaks times for sports and leisure activities</i>
-------------	--

Description

A dataset containing the peak time for doing 29 sports and leisure activities.

Usage

```
sports_time
```

Format

A data frame with 8,092 rows and 3 variables:

activity name of the activity

time time of the day, in hhmm format

p standardized peak

Source

<https://github.com/halhen/viz-pub/blob/master/sports-time-of-day/activity.tsv>

<https://eagereyes.org/blog/2017/joy-plots>

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