

Package ‘ggnormalviolin’

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Title A 'ggplot2' Extension to Make Normal Violin Plots

Version 0.1.2

Description Uses 'ggplot2' to create normally distributed violin plots with specified means and standard deviations. This function can be useful in showing hypothetically normal distributions and confidence intervals.

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URL <https://github.com/wjschne/ggnormalviolin>

BugReports <https://github.com/wjschne/ggnormalviolin/issues>

Imports dplyr, ggplot2, grid, magrittr, scales

Suggests spelling

Encoding UTF-8

Language en-US

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

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geom_normalviolin *Creates normal violins with specified means and standard deviations*

Description

Creates normal violins with specified means and standard deviations

Usage

```
geom_normalviolin(mapping = NULL, data = NULL, nsigma = 4,
  p_tail = 0, p_lower_tail = p_tail/2, p_upper_tail = p_tail/2,
  tail_fill = "black", tail_alpha = 0.4, width = 0.6,
  upper_limit = NA, lower_limit = NA, face_left = TRUE,
  face_right = TRUE, 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	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. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).
nsigma	The number of standard deviations each violin should extend
p_tail	The 2-tailed proportion that should be highlighted. Can be overridden with <code>p_lower_tail</code> and/or <code>p_upper_tail</code>
p_lower_tail	The proportion of the distribution that should be highlighted in the lower tail. Defaults to half of 'p_tail'.
p_upper_tail	The proportion of the distribution that should be highlighted in the upper tail. Defaults to half of 'p_tail'.
tail_fill	fill color for tails
tail_alpha	alpha value for tails
width	Width of normal violin
upper_limit	upper limit for polygons. Needed in case setting limits in <code>scale_y_continuous</code> or <code>ylim</code> distorts the polygons.
lower_limit	lower limit for polygons. Needed in case setting limits in <code>scale_y_continuous</code> or <code>ylim</code> distorts the polygons.

face_left	Display left half of violins. Defaults to 'TRUE'
face_right	Display right half of violins. Defaults to 'TRUE'
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> .
...	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 geom/stat.

Aesthetics

`geom_normviolin` understands the following aesthetics (required aesthetics are in bold):

- **x**
- **mu** (mean of the normal distribution)
- **sigma** (standard deviation of the normal distribution)
- width (width of violin)
- nsigma (number of standard deviations to which the violins extend)
- p_tail (2-tailed proportion of tails highlighted)
- p_upper_tail (proportion of upper tails highlighted)
- p_lower_tail (proportion of lower tails highlighted)
- face_left (display left half of violin?)
- face_right (display right half of violin?)
- color
- fill
- alpha (of fills)
- group
- linetype
- size (of lines)

Examples

```
library(ggplot2)
library(ggnormalviolin)

d <- data.frame(
  Distribution = c("A", "B"),
  Distribution_mean = c(80, 90),
  Distribution_sd = c(15, 10)
```

```
)  
ggplot(data = d, aes(x = Distribution)) +  
  geom_normalviolin(aes(mu = Distribution_mean,  
                        sigma = Distribution_sd))
```

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