Package ‘ggridges’

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Description Ridgeline plots provide a convenient way of visualizing changes in distributions over time or space. This package enables the creation of such plots in 'ggplot2'.

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License GPL-2 | file LICENSE
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**Aus_athletes**

**R topics documented:**

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**Description**

This dataset is equivalent to ais from the DAAG package.

**Usage**

Aus_athletes

**Format**

An object of class data.frame with 202 rows and 13 columns.

**References**


**Examples**

# none yet
Catalan_elections

Results from Catalan regional elections (1980-2015)

Description

Data from Catalan regional elections for 949 municipalities, from 11 elections spanning the years 1980-2015. The data was obtained and processed from Idescat.cat by Marc Belzunces (Twitter: @marcbeldata).

Usage

Catalan_elections

Format

A tibble with 20764 rows and 4 variables:

- **Municipality**
- **Year**
- **Option** The voter option; either "Indy" or "Unionist"
- **Percent** The percentage of the voters choosing the given option

geom_density_line

Smoothed density estimates drawn with a ridgeline rather than area

Description

This function is a drop-in replacement for ggplot2’s `geom_density()`. The only difference is that the geom draws a ridgeline (line with filled area underneath) rather than a polygon.

Usage

```r
geom_density_line(
  mapping = NULL,
  data = NULL,
  stat = "density",
  position = "identity",
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```
Arguments

mapping  Set of aesthetic mappings created by `aes()` or `aes_()`. 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 `ggplot()`.
A `data.frame`, 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 `data.frame`, and will be used as the layer data. A function can be created from a `formula` (e.g. `~ head(.x,10)`).

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 `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "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. `borders()`.

See Also

See `geom_density()`.

Examples

```r
library(ggplot2)
ggplot(diamonds, aes(carat)) +
  geom_density_line()

ggplot(diamonds, aes(carat)) +
  geom_density_line(adjust = 1/5)
ggplot(diamonds, aes(carat)) +
  geom_density_line(adjust = 5)

ggplot(diamonds, aes(depth, colour = cut)) +
  geom_density_line(alpha = 0.5) +
  xlim(55, 70)
ggplot(diamonds, aes(depth, fill = cut, colour = cut)) +
```
**geom_density_ridges**

```r
geom_density_line(alpha = 0.1) +
xlim(55, 70)
```

---

**Description**

`geom_density_ridges` arranges multiple density plots in a staggered fashion, as in the cover of the famous Joy Division album Unknown Pleasures.

**Usage**

```r
gem_density_ridges(
  mapping = NULL,
  data = NULL,
  stat = "density_ridges",
  position = "points_sina",
  panel_scaling = TRUE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

```r
gem_density_ridges2(
  mapping = NULL,
  data = NULL,
  stat = "density_ridges",
  position = "points_sina",
  panel_scaling = TRUE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

**Arguments**

- **mapping**: Set of aesthetic mappings created by `aes()` or `aes()`. 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 `ggplot()`.
  - A `data.frame`, or other object, will override the plot data.
  - 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_density_ridges

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.
panel_scaling  If TRUE, the default, relative scaling is calculated separately for each panel. If FALSE, relative scaling is calculated globally.
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.

...  other arguments passed on to layer(). 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.

Details

By default, this geom calculates densities from the point data mapped onto the x axis. If density calculation is not wanted, use stat="identity" or use geom_ridgeline. The difference between geom_density_ridges and geom_ridgeline is that geom_density_ridges will provide automatic scaling of the ridgelines (controlled by the scale aesthetic), whereas geom_ridgeline will plot the data as is. Note that when you set stat="identity", the height aesthetic must be provided.

Note that the default stat_density_ridges makes joint density estimation across all datasets. This may not generate the desired result when using faceted plots. As an alternative, you can set stat = "density" to use stat_density. In this case, it is required to add the aesthetic mapping height = ..density.. (see examples).

Aesthetics

Required aesthetics are in bold.

• x
• y
• group Defines the grouping. Not needed if a categorical variable is mapped onto y, but needed otherwise. Will typically be the same variable as is mapped to y.
• height The height of each ridgeline at the respective x value. Automatically calculated and provided by stat_density_ridges if the default stat is not changed.
• scale A scaling factor to scale the height of the ridgelines relative to the spacing between them. A value of 1 indicates that the maximum point of any ridgeline touches the baseline right above, assuming even spacing between baselines.
• rel_min_height Lines with heights below this cutoff will be removed. The cutoff is measured relative to the overall maximum, so rel_min_height=0.01 would remove everything that is 1\ ridgelines. Default is 0, so nothing is removed. alpha
• colour, fill, group, alpha, linetype, size, as in geom_ridgeline.
• point_shape, point_colour, point_size, point_fill, point_alpha, point_stroke, as in geom_ridgeline.
Examples

```r
library(ggplot2)

# set the 'rel_min_height' argument to remove tails
ggplot(iris, aes(x = Sepal.Length, y = Species)) +
  geom_density_ridges(rel_min_height = 0.005) +
  scale_y_discrete(expand = c(0.01, 0)) +
  scale_x_continuous(expand = c(0.01, 0)) +
  theme_ridges()

# set the 'scale' to determine how much overlap there is among the plots
ggplot(diamonds, aes(x = price, y = cut)) +
  geom_density_ridges(scale = 4) +
  scale_y_discrete(expand = c(0.01, 0)) +
  scale_x_continuous(expand = c(0.01, 0)) +
  theme_ridges()

# the same figure with colors, and using the ggplot2 density stat
ggplot(diamonds, aes(x = price, y = cut, fill = cut, height = ..density..)) +
  geom_density_ridges(scale = 4, stat = "density") +
  scale_y_discrete(expand = c(0.01, 0)) +
  scale_x_continuous(expand = c(0.01, 0)) +
  scale_fill_brewer(palette = 4) +
  theme_ridges() + theme(legend.position = "none")

# use geom_density_ridges2() instead of geom_density_ridges() for solid polygons
ggplot(iris, aes(x = Sepal.Length, y = Species)) +
  geom_density_ridges2() +
  scale_y_discrete(expand = c(0.01, 0)) +
  scale_x_continuous(expand = c(0.01, 0)) +
  theme_ridges()
```

Description

Plots the sum of the y and height aesthetics versus x, filling the area between y and y + height with a color. Thus, the data mapped onto y and onto height must be in the same units. If you want relative scaling of the heights, you can use `geom_density_ridges` with `stat = "identity"`.

Usage

```r
geom_ridgeline(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  na.rm = FALSE,
  inherit.aes = TRUE )
```

Plot a ridgeline (line with filled area underneath)
Arguments

- **mapping**
  Set of aesthetic mappings created by `aes()` or `aes_()`. 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 `ggplot()`.
  - A `data.frame`, or other object, will override the plot data.
  - 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.

- **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.

- **...**
  other arguments passed on to `layer()`. 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.

Details

In addition to drawing ridgelines, this geom can also draw points if they are provided as part of the dataset. The stat `stat_density_ridges()` takes advantage of this option to generate ridgeline plots with overlaid jittered points.

Aesthetics

Required aesthetics are in bold.

- **x**
- **y**
- **height** Height of the ridgeline, measured from the respective y value. Assumed to be positive, though this is not required.
- **group** Defines the grouping. Required when the dataset contains multiple distinct ridgelines. Will typically be the same variable as is mapped to y.
- **scale** A scaling factor to scale the height of the ridgelines. A value of 1 indicates that the heights are taken as is. This aesthetic can be used to convert height units into y units.
• min_height A height cutoff on the drawn ridgelines. All values that fall below this cutoff will be removed. The main purpose of this cutoff is to remove long tails right at the baseline level, but other uses are possible. The cutoff is applied before any height scaling is applied via the scale aesthetic. Default is 0, so negative values are removed.
• colour Color of the ridgeline
• fill Fill color of the area under the ridgeline
• alpha Transparency level of fill. Not applied to color. If you want transparent lines, you can set their color as RGBA value, e.g. #FF0000A0 for partially transparent red.
• group Grouping, to draw multiple ridgelines from one dataset
• linetype Linetype of the ridgeline
• size Line thickness
• point_shape, point_colour, point_size, point_fill, point_alpha, point_stroke Aesthetics applied to points drawn in addition to ridgelines.

Examples

library(ggplot2)

d <- data.frame(x = rep(1:5, 3), y = c(rep(0, 5), rep(1), rep(3, 5)),
                height = c(0, 1, 3, 4, 0, 1, 2, 3, 5, 4, 0, 5, 4, 4, 1))
ggplot(d, aes(x, y, height = height, group = y)) + geom_ridgeline(fill="lightblue")

geom_ridgeline_gradient

Plot ridgelines and ridgeline plots with fill gradients along the x axis

Description

The geoms geom_ridgeline_gradient and geom_density_ridges_gradient work just like geom_ridgeline and geom_density_ridges except that the fill aesthetic can vary along the x axis. Because filling with color gradients is fraught with issues, these geoms should be considered experimental. Don’t use them unless you really need to. Note that due to limitations in R’s graphics system, transparency (alpha) has to be disabled for gradient fills.

Usage

geom_ridgeline_gradient(
    mapping = NULL,
    data = NULL,
    stat = "identity",
    position = "identity",
    na.rm = FALSE,
    gradient_lwd = 0.5,
    show.legend = NA,
geom_ridgeline_gradient

geom_density_ridges_gradient(
  mapping = NULL,
  data = NULL,
  stat = "density_ridges",
  position = "points_sina",
  panel_scaling = TRUE,
  na.rm = TRUE,
  gradient_lwd = 0.5,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

Arguments

  mapping       Set of aesthetic mappings created by aes() or aes_. 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 ggplot().
                A data.frame, or other object, will override the plot data.
                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.

  na.rm         If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

  gradient_lwd  A parameter to needed to remove rendering artifacts inside the rendered gradients. Should ideally be 0, but often needs to be around 0.5 or higher.

  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.

  ...           other arguments passed on to layer(). 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.

  panel_scaling Argument only to geom_density_ridges_gradient. If TRUE, the default, relative scaling is calculated separately for each panel. If FALSE, relative scaling is calculated globally.
Examples

```r
library(ggplot2)

# Example for 'geom_ridgeline_gradient()'

d <- data.frame(
  x = rep(1:5, 3) + c(rep(0, 5), rep(0.3, 5), rep(0.6, 5)),
  y = c(rep(0, 5), rep(1, 5), rep(3, 5)),
  height = c(0, 1, 3, 4, 0, 1, 2, 3, 5, 4, 0, 5, 4, 4, 1)
)

ggplot(d, aes(x, y, height = height, group = y, fill = factor(x+y))) +
  geom_ridgeline_gradient() +
  scale_fill_viridis_d(direction = -1) +
  theme(legend.position = 'none')

# Example for 'geom_density_ridges_gradient()'

ggplot(lincoln_weather, aes(x = 'Mean Temperature [F]', y = 'Month', fill = stat(x))) +
  geom_density_ridges_gradient(scale = 3, rel_min_height = 0.01) +
  scale_x_continuous(expand = c(0, 0)) +
  scale_y_discrete(expand = c(0, 0)) +
  scale_fill_viridis_c(name = "Temp. [F]", option = "C") +
  coord_cartesian(clip = "off") +
  labs(title = 'Temperatures in Lincoln NE in 2016') +
  theme_ridges(font_size = 13, grid = TRUE) +
  theme(axis.title.y = element_blank())
```

---

**geom_vridgeline**  
Plot a vertical ridgeline (ridgeline rotated 90 degrees)

**Description**

Plots the sum of the x and width aesthetics versus y, filling the area between x and x + width with a color. Just like `geom_ridgeline()`, but with y and x replaced.

**Usage**

```r
geom_vridgeline(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...)
```
Arguments

mapping Set of aesthetic mappings created by \texttt{aes()} or \texttt{aes()}. If specified and \texttt{inherit.aes = TRUE} (the default), it is combined with the default mapping at the top level of the plot. You must supply \texttt{mapping} if there is no plot mapping.

data The data to be displayed in this layer. There are three options:
If \texttt{NULL}, the default, the data is inherited from the plot data as specified in the call to \texttt{ggplot()}.
A \texttt{data.frame}, or other object, will override the plot data.
A function will be called with a single argument, the plot data. The return value must be a \texttt{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.

na.rm If \texttt{FALSE}, the default, missing values are removed with a warning. If \texttt{TRUE}, missing values are silently removed.

show.legend logical. Should this layer be included in the legends? \texttt{NA}, the default, includes if any aesthetics are mapped. \texttt{FALSE} never includes, and \texttt{TRUE} always includes.

inherit.aes If \texttt{FALSE}, overrides the default aesthetics, rather than combining with them.

\texttt{...} other arguments passed on to \texttt{layer()}. These are often aesthetics, used to set an aesthetic to a fixed value, like \texttt{color = "red"} or \texttt{size = 3}. They may also be parameters to the paired geom/stat.

Aesthetics

Required aesthetics are in bold.

- \texttt{x}
- \texttt{y}
- \texttt{width} Width of the ridgeline, measured from the respective \texttt{x} value. Assumed to be positive, though this is not required.
- \texttt{group} Defines the grouping. Required when the dataset contains multiple distinct ridgelines. Will typically be the same variable as is mapped to \texttt{x}.
- \texttt{scale} A scaling factor to scale the widths of the ridgelines. A value of 1 indicates that the widths are taken as is. This aesthetic can be used to convert \texttt{width} units into \texttt{x} units.
- \texttt{min\_width} A width cutoff on the drawn ridgelines. All values that fall below this cutoff will be removed. The main purpose of this cutoff is to remove long tails right at the baseline level, but other uses are possible. The cutoff is applied before any width scaling is applied via the \texttt{scale} aesthetic. Default is 0, so negative values are removed.
- \texttt{color} Color of the ridgeline
- \texttt{fill} Fill color of the area under the ridgeline
- \texttt{alpha} Transparency level of \texttt{fill}. Not applied to \texttt{color}. If you want transparent lines, you can set their color as RGBA value, e.g. \texttt{#FF0000A0} for partially transparent red.
- \texttt{group} Grouping, to draw multiple ridgelines from one dataset
- \texttt{linetype} Linetype of the ridgeline
- \texttt{size} Line thickness
Examples

```r
library(ggplot2)

d <- data.frame(y = rep(1:5, 3), x = c(rep(0, 5), rep(1, 5), rep(3, 5)),
               width = c(0, 1, 3, 4, 0, 1, 2, 3, 5, 4, 0, 5, 4, 4, 1))
ggplot(d, aes(x, y, width = width, group = x)) + geom_vridgeline(fill="lightblue")

ggplot(iris, aes(x=Species, y=Sepal.Width, width = ..density.., fill=Species)) +
geom_vridgeline(stat="ydensity", trim=FALSE, alpha = 0.85, scale = 2)
```

---

**ggridges**

*Ridgeline plots with ggplot2*

---

**Description**

Please see the package vignettes for usage instructions. For a quick start, check out the examples for `geom_density_ridges()`.

---

**lincoln_weather**

*Weather in Lincoln, Nebraska in 2016.*

---

**Description**

A dataset containing weather information from Lincoln, Nebraska, from 2016. Originally downloaded from Weather Underground by Austin Wehrwein, http://austinwehrwein.com/. The variables are listed below. Most are self-explanatory. Max, mean, and min measurements are calculated relative to the specific day of measurement.

**Usage**

`lincoln_weather`

**Format**

A tibble with 366 rows and 24 variables:

- **CST** Day of the measurement
- **Max Temperature [F]**
- **Mean Temperature [F]**
- **Min Temperature [F]**
- **Max Dew Point [F]**
- **Mean Dew Point [F]**
- **Min Dewpoint [F]**
Max Humidity
Mean Humidity
Min Humidity
Max Sea Level Pressure [In]
Mean Sea Level Pressure [In]
Min Sea Level Pressure [In]
Max Visibility [Miles]
Mean Visibility [Miles]
Min Visibility [Miles]
Max Wind Speed [MPH]
Mean Wind Speed [MPH]
Max Gust Speed [MPH]
Precipitation [In]
CloudCover
Events Specific weather events, such as rain, snow, or fog
WindDir [Degrees]
Month The month in which the measurement was taken

---

**position_points_jitter**

*Randomly jitter the points in a ridgeline plot*

---

**Description**

This is a position adjustment specifically for `geom_density_ridges()` and related geoms. It only jitters the points drawn by these geoms, if any. If no points are present, the plot remains unchanged. The effect is similar to `position_jitter()`: points are randomly shifted up and down and/or left and right.

**Usage**

```r
position_points_jitter(  
    width = 0,  
    height = 0.2,  
    yoffset = 0,  
    adjust_vlines = FALSE,  
    seed = NULL  
)  
```
position_points_sina

Arguments

- **width**: Width for horizontal jittering. By default set to 0.
- **height**: Height for vertical jittering, applied in both directions (up and down). By default 0.2.
- **yoffset**: Vertical offset applied in addition to jittering.
- **adjust_vlines**: If TRUE, adjusts vertical lines (as are drawn for quantile lines, for example) to align with the point cloud.
- **seed**: Random seed. If set to NULL, the current random number generator is used. If set to NA, a new random random seed is generated. If set to a number, this number is used as seed for jittering only.

See Also

Other position adjustments for ridgeline plots: position_points_sina, position_raincloud

Examples

```r
library(ggplot2)

# default jittered points
ggplot(iris, aes(x = Sepal.Length, y = Species)) +
  geom_density_ridges(jittered_points = TRUE, position = "points_jitter", alpha = 0.7)

# simulating a rug
ggplot(iris, aes(x = Sepal.Length, y = Species)) +
  geom_density_ridges(jittered_points = TRUE, point_shape = '|', alpha = 0.7, point_size = 2,
                      position = position_points_jitter(width = 0.02, height = 0))
```

Description

This is a position adjustment specifically for `geom_density_ridges()` and related geoms. It only jitters the points drawn by these geoms, if any. If no points are present, the plot remains unchanged. The effect is similar to a sina plot: Points are randomly distributed to fill the entire shaded area representing the data density.

Usage

`position_points_sina(rel_min = 0.02, rel_max = 0.98, seed = NULL)`

Arguments

- **rel_min**: The relative minimum value at which a point can be placed.
- **rel_max**: The relative maximum value at which a point can be placed.
- **seed**: See `position_points_jitter`.
position_raincloud

See Also

Other position adjustments for ridgeline plots: position_points_jitter, position_raincloud

Examples

```r
library(ggplot2)

ggplot(iris, aes(x = Sepal.Length, y = Species)) +
  geom_density_ridges(jittered_points = TRUE, position = "points_sina", alpha = 0.7)
```

Description

This is a position adjustment specifically for `geom_density_ridges()` and related geoms. It only jitters the points drawn by these geoms, if any. If no points are present, the plot remains unchanged. The effect is similar to `position_points_jitter()`, only that by default the points lie all underneath the baseline of each individual ridgeline.

Usage

```r
position_raincloud(
  width = 0,
  height = 0.4,
  ygap = 0.05,
  adjust_vlines = FALSE,
  seed = NULL
)
```

Arguments

- `width`: Width for horizontal jittering. By default set to 0.
- `height`: Total height of point cloud. By default 0.4.
- `ygap`: Vertical gap between ridgeline baseline and point cloud.
- `adjust_vlines`: If TRUE, adjusts vertical lines (as are drawn for quantile lines, for example) to align with the point cloud.
- `seed`: Random seed. See `position_points_jitter`.

Details

The idea for this position adjustment comes from Micah Allen, who proposed this type of plot in a blog post on March 15, 2018.

See Also

Other position adjustments for ridgeline plots: position_points_jitter, position_points_sina
**reduce**

*Reduce a list to a single value by iteratively applying a binary function*

**Description**

Inspired by `reduce()` from the *purrr* package

**Usage**

```r
reduce(.x, .f, ..., .init)
```

**Arguments**

- `.x` A list or atomic vector.
- `.f` A 2-argument function. The function will be passed the accumulated value as the first argument and the "next" value as the second argument.
- `...` Additional arguments passed on to `.f`.
- `.init` If supplied, will be used as the first value to start the accumulation, rather than using `.x[[1]]`. This is useful if you want to ensure that `reduce` returns a correct value when `.x` is empty. If missing, and `.x` is empty, will throw an error.

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---

**scale_cyclical**

*Create a discrete scale that cycles between values*

**Description**

The readability of ridgeline plots can often be improved by alternating between fill colors and other aesthetics. The various cyclical scales make it easy to create plots with this feature, simply map your grouping variable to the respective aesthetic (e.g., fill) and then use `scale_fill_cyclical` to define the fill colors between you want to alternate. Note that the cyclical scales do not draw legends by default, because the legends will usually be wrong unless the labels are properly adjusted. To draw legends, set the `guide` argument to "legend", as shown in the examples.
Usage

scale_colour_cyclical(..., values)
scale_fill_cyclical(..., values)
scale_alpha_cyclical(..., values)
scale_linetype_cyclical(..., values)
scale_size_cyclical(..., values)

Arguments

... Common discrete scale parameters: name, breaks, labels, na.value, limits and guide. See discrete_scale for more details.

values The aesthetic values that the scale should cycle through, e.g. colors if it is a scale for the color or fill aesthetic.

Examples

library(ggplot2)

# By default, scale_cyclical sets 'guide = "none"', i.e., no legend
# is drawn
ggplot(diamonds, aes(x = price, y = cut, fill = cut)) +
  geom_density_ridges(scale = 4) +
  scale_fill_cyclical(values = c("#3030D0", "#9090F0"))

# However, legends can be turned on by setting 'guide = "legend"
ggplot(diamonds, aes(x = price, y = cut, fill = cut)) +
  geom_density_ridges(scale = 4) +
  scale_fill_cyclical(values = c("#3030D0", "#9090F0"),
                      guide = "legend", name = "Fill colors",
                      labels = c("dark blue", "light blue"))

# Cyclical scales are also available for the various other aesthetics
ggplot(diamonds, aes(x = price, y = cut, fill = cut,
                      color = cut, size = cut,
                      alpha = cut, linetype = cut)) +
  geom_density_ridges(scale = 4, fill = "blue") +
  scale_fill_cyclical(values = c("blue", "green")) +
  scale_color_cyclical(values = c("black", "white")) +
  scale_size_cyclical(values = c(2, 1)) +
  scale_alpha_cyclical(values = c(0.4, 0.8)) +
  scale_linetype_cyclical(values = c(1, 2))
Scales for point aesthetics

Description

These are various scales that can be applied to point aesthetics, such as point_color, point_fill, point_size. The individual scales all have the same usage as existing standard ggplot2 scales, only the name differs.

See Also

See `scale_vline_color_hue()` for specific scales for vline aesthetics and `scale_discrete_manual()` for a general discrete scale.

Examples

```r
library(ggplot2)

# default scales
ggplot(iris, aes(x=Sepal.Length, y=Species, fill = Species)) +
  geom_density_ridges(
    aes(
      point_color = Species, point_fill = Species,
      point_shape = Species
    ),
    alpha = .4, jittered_points = TRUE
  ) +
  theme_ridges()

# modified scales
ggplot(iris, aes(x=Sepal.Length, y=Species, fill = Species)) +
  geom_density_ridges(
    aes(
      point_color = Species, point_fill = Species,
      point_shape = Species
    ),
    alpha = .4, point_alpha = 1,
    jittered_points = TRUE
  ) +
  scale_fill_hue(l = 50) +
  scale_point_color_hue(l = 20) +
  scale_point_fill_hue(l = 70) +
  scale_discrete_manual("point_shape", values = c(21, 22, 23)) +
  theme_ridges()
```
scale_vline  Scales for vline aesthetics

Description
These are various scales that can be applied to vline aesthetics, such as vline_color, vline_size, vline_linetype. The individual scales all have the same usage as existing standard ggplot2 scales, only the name differs.

See Also
See scale_point_color_hue() for specific scales for point aesthetics and scale_discrete_manual() for a general discrete scale.

Examples

```r
library(ggplot2)

# default scales
ggplot(iris, aes(x=Sepal.Length, y=Species, fill = Species, color = Species)) +
  geom_density_ridges(
    aes(vline_color = Species, vline_linetype = Species),
    alpha = .4, quantile_lines = TRUE
  ) +
  theme_ridges()

# modified scales
ggplot(iris, aes(x=Sepal.Length, y=Species, fill = Species, color = Species)) +
  geom_density_ridges(  
    aes(vline_color = Species),
    alpha = .4, quantile_lines = TRUE
  ) +
  scale_fill_hue(l = 50) +
  scale_vline_color_hue(l = 30) +
  theme_ridges()
```

stat_binline  Stat for histogram ridgeline plots

Description
Works like stat_bin except that the output is a ridgeline describing the histogram rather than a set of counts.
Usage

```r
stat_binline(
  mapping = NULL,
  data = NULL,
  geom = "density_ridges",
  position = "identity",
  ..., 
  binwidth = NULL,
  bins = NULL,
  center = NULL,
  boundary = NULL,
  breaks = NULL,
  closed = c("right", "left"),
  pad = TRUE,
  draw_baseline = TRUE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

- **mapping**: Set of aesthetic mappings created by `aes()` or `aes()`. 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 `ggplot()`.
  - A `data.frame`, 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 `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x,10)`).

- **geom**: Use to override the default connection between `geom_histogram()`/`geom_freqpoly()` and `stat_bin()`.

- **position**: Position adjustment, either as a string, or the result of a call to a position adjustment function.

- **binwidth**: The width of the bins. Can be specified as a numeric value or as a function that calculates width from unscaled x. Here, "unscaled x" refers to the original x values in the data, before application of any scale transformation. When specifying a function along with a grouping structure, the function will be called once per group. The default is to use `bins bins that cover the range of the data. You
should always override this value, exploring multiple widths to find the best to illustrate the stories in your data.

The bin width of a date variable is the number of days in each time; the bin width of a time variable is the number of seconds.

- **bins**: Number of bins. Overridden by `binwidth`. Defaults to 30.

- **center**: bin position specifiers. Only one, `center` or `boundary`, may be specified for a single plot. `center` specifies the center of one of the bins. `boundary` specifies the boundary between two bins. Note that if either is above or below the range of the data, things will be shifted by the appropriate integer multiple of `width`. For example, to center on integers use `width = 1` and `center = 0`, even if 0 is outside the range of the data. Alternatively, this same alignment can be specified with `width = 1` and `boundary = 0.5`, even if 0.5 is outside the range of the data.

- **boundary**: bin position specifiers. Only one, `center` or `boundary`, may be specified for a single plot. `center` specifies the center of one of the bins. `boundary` specifies the boundary between two bins. Note that if either is above or below the range of the data, things will be shifted by the appropriate integer multiple of `width`. For example, to center on integers use `width = 1` and `center = 0`, even if 0 is outside the range of the data. Alternatively, this same alignment can be specified with `width = 1` and `boundary = 0.5`, even if 0.5 is outside the range of the data.

- **breaks**: Alternatively, you can supply a numeric vector giving the bin boundaries. Overrides `binwidth`, `bins`, `center`, and `boundary`.

- **closed**: One of "right" or "left" indicating whether right or left edges of bins are included in the bin.

- **pad**: If `TRUE`, adds empty bins at either end of `x`. This ensures that the binline always goes back down to 0. Defaults to `TRUE`.

- **draw_baseline**: If `FALSE`, removes lines along 0 counts. 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. `borders()`.

### Examples

```r
library(ggplot2)

ggplot(iris, aes(x = Sepal.Length, y = Species, group = Species, fill = Species)) +
  geom_density_ridges(stat = "binline", bins = 20, scale = 2.2) +
  scale_y_discrete(expand = c(0, 0)) +
  scale_x_continuous(expand = c(0, 0)) +
  coord_cartesian(clip = "off") +
  theme_ridges()
```
**stat_density_ridges**

A function for creating density ridgeline plots.

```r
library(ggplot2movies)
library(dplyr)
library(regulomeUtils)

# Create a data frame
count_data <- data.frame(
  group = rep(letters[1:5], each = 10),
  mean = rep(1:5, each = 10)
)

# Count data
count_data$group <- factor(count_data$group, levels = letters[5:1])

# Calculate Poisson distribution
count_data$count <- rpois(nrow(count_data), count_data$mean)

# Plot
ggplot(count_data, aes(x = count, y = group, group = group)) +
  geom_density_ridges2(
    stat = "binline",
    aes(fill = group),
    binwidth = 1,
    scale = 0.95
  ) +
  geom_text(
    stat = "bin",
    aes(y = group + 0.9*stat(count/max(count)),
         label = ifelse(stat(count) > 0, stat(count), ""),
         vjust = 1.2, size = 3, color = "white", binwidth = 1
  ) +
  scale_x_continuous(breaks = c(0:12), limits = c(-.5, 13), expand = c(0, 0)) +
  scale_y_discrete(expand = c(0, 0)) +
  scale_fill_cyclical(values = c("#0000B0", "#7070D0")) +
  guides(y = "none") +
  coord_cartesian(clip = "off") +
  theme_ridges(grid = FALSE)
```

---

**stat_density_ridges**  
*Stat for density ridgeline plots*
Description

This stat is the default stat used by geom_density_ridges. It is very similar to stat_density, however there are a few differences. Most importantly, the density bandwidth is chosen across the entire dataset.

Usage

stat_density_ridges(
  mapping = NULL,
  data = NULL,
  geom = "density_ridges",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  bandwidth = NULL,
  from = NULL,
  to = NULL,
  jittered_points = FALSE,
  quantile_lines = FALSE,
  calc_ecdf = FALSE,
  quantiles = 4,
  quantile_fun = quantile,
  n = 512,
  ...
)

Arguments

mapping Set of aesthetic mappings created by aes() or aes_(). 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 ggplot().
  A data.frame, or other object, will override the plot data.
  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 to display the data.
position Position adjustment, either as a string, or the result of a call to a position adjustment function.
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.
**stat_density_ridges**

- **bandwidth**: Bandwidth used for density calculation. If not provided, is estimated from the data.
- **from, to**: The left and right-most points of the grid at which the density is to be estimated, as in `density()`. If not provided, these are estimated from the data range and the bandwidth.
- **jittered_points**: If TRUE, carries the original point data over to the processed data frame, so that individual points can be drawn by the various ridgeline geoms. The specific position of these points is controlled by various position objects, e.g. `position_points_sina()` or `position_raincloud()`.
- **quantile_lines**: If TRUE, enables the drawing of quantile lines. Overrides the `calc_ecdf` setting and sets it to TRUE.
- **calc_ecdf**: If TRUE, `stat_density_ridges` calculates an empirical cumulative distribution function (ecdf) and returns a variable `ecdf` and a variable `quantile`. Both can be mapped onto aesthetics via `stat(ecdf)` and `stat(quantile)`, respectively.
- **quantiles**: Sets the number of quantiles the data should be broken into. Used if either `calc_ecdf` = TRUE or `quantile_lines` = TRUE. If quantiles is an integer then the data will be cut into that many equal quantiles. If it is a vector of probabilities then the data will cut by them.
- **quantile_fun**: Function that calculates quantiles. The function needs to accept two parameters, a vector x holding the raw data values and a vector probs providing the probabilities that define the quantiles. Default is `quantile`.
- **n**: The number of equally spaced points at which the density is to be estimated. Should be a power of 2. Default is 512.
- **...**: other arguments passed on to `layer()`. 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.

**Examples**

```r
library(ggplot2)

# Examples of coloring by ecdf or quantiles
ggplot(iris, aes(x = Sepal.Length, y = Species, fill = factor(stat(quantile)))) +
  stat_density_ridges(
    geom = "density_ridges_gradient",
    calc_ecdf = TRUE,
    quantiles = 5
  ) +
  scale_fill_viridis_d(name = "Quintiles") +
  theme_ridges()

ggplot(iris,
  aes(
    x = Sepal.Length, y = Species, fill = 0.5 - abs(0.5-stat(ecdf))
  )) +
  stat_density_ridges(geom = "density_ridges_gradient", calc_ecdf = TRUE) +
  scale_fill_viridis_c(name = "Tail probability", direction = -1) +
```
theme_ridges()

ggplot(iris,
  aes(
    x = Sepal.Length, y = Species, fill = factor(stat(quantile))
  )) +
  stat_density_ridges(
    geom = "density_ridges_gradient",
    calc_ecdf = TRUE, quantiles = c(0.025, 0.975)
  ) +
  scale_fill_manual(
    name = "Probability",
    values = c("FF0000A0", "A0A0A0A0", "#0000FFA0"),
    labels = c("(0, 0.025]", "(0.025, 0.975]", "(0.975, 1]"
  ) +
  theme_ridges()

theme_ridges  A custom theme specifically for use with ridgeline plots

Description

This theme has some special modifications that make ridgeline plots look better, such as properly aligned y axis labels. It can draw plots with and without background grids (see examples).

Usage

theme_ridges(
  font_size = 14,
  font_family = "",
  line_size = 0.5,
  grid = TRUE,
  center_axis_labels = FALSE
)

Arguments

font_size Overall font size. Default is 14.
font_family Default font family.
line_size Default line size.
grid If TRUE (default), a background grid is drawn. If FALSE, background is left empty.
center_axis_labels If TRUE, axis labels are drawn centered. If FALSE (default), axis labels are drawn right/top-aligned.
theme_ridges

Value

The theme.

Examples

library(ggplot2)

# Example with background grid
ggplot(iris, aes(x = Sepal.Length, y = Species, group = Species)) +
  geom_density_ridges(rel_min_height = 0.005) +
  scale_y_discrete(expand = c(0.01, 0)) +
  scale_x_continuous(expand = c(0.01, 0)) +
  theme_ridges()

# Example without background grid
ggplot(iris, aes(x = Sepal.Length, y = Species, group = Species)) +
  geom_density_ridges() +
  scale_y_discrete(expand = c(0.01, 0)) +
  scale_x_continuous(expand = c(0.01, 0)) +
  theme_ridges(grid = FALSE)
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