Package: ggalt (via r-universe)

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Title Extra Coordinate Systems, 'Geoms', Statistical Transformations, Scales and Fonts for 'ggplot2'

Version 0.6.1

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Description A compendium of new geometries, coordinate systems, statistical transformations, scales and fonts for 'ggplot2', including splines, 1d and 2d densities, univariate average shifted histograms, a new map coordinate system based on the 'PROJ.4'-library along with geom_cartogram() that mimics the original functionality of geom_map(), formatters for ``bytes'', a stat_stepribbon() function, increased 'plotly' compatibility and the 'StateFace' open source font 'ProPublica'. Further new functionality includes lollipop charts, dumbbell charts, the ability to encircle points and coordinate-system-based text annotations.

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LazyData true

URL https://github.com/hrbrmstr/ggalt

BugReports https://github.com/hrbrmstr/ggalt/issues

Encoding UTF-8

Depends R (>= 3.2.0), ggplot2 (>= 2.2.1)

Suggests testthat, gridExtra, knitr, rmarkdown, ggthemes, reshape2

Imports utils, graphics, datasets, grDevices, plyr, dplyr, RColorBrewer, KernSmooth, proj4, scales, grid, gtable, ash, maps, MASS, extrafont, tibble, plotly (>= 3.4.1)

RoxygenNote 7.2.3

VignetteBuilder knitr

Collate 'annotate_textp.r' 'annotation_ticks.r' 'coord_proj.r' 'formatters.r' 'fortify.r' 'position-dodgev.R' 'geom2plotly.r' 'geom_ash.r' 'geom_bkde.r' 'geom_bkde2d.r' 'geom_spikelines.R' 'geom_dumbbell.R' 'geom_cartogram.r' 'geom_encircle.r'

'geom_horizon.r' 'geom_lollipop.r' 'geom_table.r'
'geom_twoway_bar.r' 'geom_xspline.r' 'geom_xspline2.r'
'geom_ubar.r' 'stat-stepribbon.r' 'ggalt-package.r'
'grob_absolute.r' 'guide_axis.r' 'stateface.r' 'utils.r'
'zzz.r'

Repository https://hrbrmstr.r-universe.dev

RemoteUrl https://github.com/hrbrmstr/ggalt

RemoteRef HEAD

RemoteSha 8941f8c9b13ac38ca0cf6500951017c35241de28

Contents

`annotate_textp` *Text annotations in plot coordinate system*

Description

Annotates the plot with text. Compared to `annotate("text",...)`, the placement of the annotations is specified in plot coordinates (from 0 to 1) instead of data coordinates.

Usage

```
annotate_textp(
  label,
  x,
  y,
  facets = NULL,
  hjust = 0,
  vjust = 0,
  color = "black",
  alpha = NA,
  family = theme_get()$text$family,
  size = theme_get()$text$size,
  fontface = 1,
  lineheight = 1,
  box_just = ifelse(c(x, y) < 0.5, 0, 1),
  margin = unit(size/2, "pt")
)
```

Arguments

label	text annotation to be placed on the plot
x, y	positions of the individual annotations, in plot coordinates (0..1) instead of data coordinates!
facets	facet positions of the individual annotations
hjust, vjust	horizontal and vertical justification of the text relative to the bounding box
color	alpha, family, size, fontface, lineheight font properties
alpha, family, size, fontface, lineheight	standard aesthetic customizations
box_just	placement of the bounding box for the text relative to x,y coordinates. Per default, the box is placed to the center of the plot. Be aware that parts of the box which are outside of the visible region of the plot will not be shown.
margin	margins of the bounding box

Examples

```
p <- ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point()
p <- p + geom_smooth(method = "lm", se = FALSE)
p + annotate_textp(x = 0.9, y = 0.35, label="A relative linear\nrelationship", hjust=1, color="red")
```

---

annotation_ticks *Annotation: tick marks*

Description

This annotation adds tick marks to an axis

Usage

```
annotation_ticks(
  sides = "b",
  scale = "identity",
  scaled = TRUE,
  short = unit(0.1, "cm"),
  mid = unit(0.2, "cm"),
  long = unit(0.3, "cm"),
  colour = "black",
  size = 0.5,
  linetype = 1,
  alpha = 1,
  color = NULL,
  ticks_per_base = NULL,
  ...
)
```

Arguments

sides	a string that controls which sides of the plot the log ticks appear on. It can be set to a string containing any of "trbl", for top, right, bottom, and left.
scale	character, vector of type of scale attributed to each corresponding side, Default: 'identity'
scaled	is the data already log-scaled? This should be TRUE (default) when the data is already transformed with log10() or when using scale_y_log10(). It should be FALSE when using coord_trans(y = "log10").
short	a grid::unit() object specifying the length of the short tick marks
mid	a grid::unit() object specifying the length of the middle tick marks. In base 10, these are the "5" ticks.
long	a grid::unit() object specifying the length of the long tick marks. In base 10, these are the "1" (or "10") ticks.
colour	Colour of the tick marks.
size	Thickness of tick marks, in mm.
linetype	Linetype of tick marks (solid, dashed, etc.)
alpha	The transparency of the tick marks.
color	An alias for colour.
ticks_per_base	integer, number of minor ticks between each pair of major ticks, Default: NULL
...	Other parameters passed on to the layer

Details

If scale is of length one it will be replicated to the number of sides given, but if the length of scale is larger than one it must match the number of sides given. If ticks_per_base is set to NULL the function infers the number of ticks per base to be the base of the scale - 1, for example log scale is base exp(1) and log10 and identity are base 10. If ticks_per_base is given it follows the same logic as scale.

Author(s)

Jonathan Sidi

Examples

```
p <- ggplot(msleep, aes(bodywt, brainwt)) + geom_point()

# Default behavior

# add identity scale minor ticks on y axis
p + annotation_ticks(sides = 'l')

# add identity scale minor ticks on x,y axis
p + annotation_ticks(sides = 'lb')

# Control number of minor ticks of each side independently

# add identity scale minor ticks on x,y axis
p + annotation_ticks(sides = 'lb', ticks_per_base = c(10,5))

# log10 scale
p1 <- p + scale_x_log10()

# add minor ticks on log10 scale
p1 + annotation_ticks(sides = 'b', scale = 'log10')

# add minor ticks on both scales
p1 + annotation_ticks(sides = 'lb', scale = c('identity','log10'))

# add minor ticks on both scales, but force x axis to be identity
p1 + annotation_ticks(sides = 'lb', scale = 'identity')

# log scale
p2 <- p + scale_x_continuous(trans = 'log')

# add minor ticks on log scale
p2 + annotation_ticks(sides = 'b', scale = 'log')

# add minor ticks on both scales
p2 + annotation_ticks(sides = 'lb', scale = c('identity','log'))

# add minor ticks on both scales, but force x axis to be identity
p2 + annotation_ticks(sides = 'lb', scale = 'identity')
```

---

byte_format *Bytes formatter: convert to byte measurement and display symbol.*

Description

Bytes formatter: convert to byte measurement and display symbol.

Usage

```
byte_format(symbol = "auto", units = "binary", only_highest = TRUE)

Kb(x)

Mb(x)

Gb(x)

bytes(x, symbol = "auto", units = c("binary", "si"), only_highest = FALSE)
```

Arguments

symbol	byte symbol to use. If "auto" the symbol used will be determined by the maximum value of x. Valid symbols are "b", "K", "Mb", "Gb", "Tb", "Pb", "Eb", "Zb", and "Yb", along with their upper case equivalents and "iB" equivalents.
units	which unit base to use, "binary" (1024 base) or "si" (1000 base) for ISI units.
only_highest	Whether to use the unit of the highest number or each number uses its own unit.
x	a numeric vector to format

Value

a function with three parameters, x, a numeric vector that returns a character vector, symbol a single or a vector of byte symbol(s) (e.g. "Kb") desired and the measurement units (traditional binary or si for ISI metric units).

References

Units of Information (Wikipedia) : http://en.wikipedia.org/wiki/Units_of_information

Examples

```
byte_format()(sample(3000000000, 10))
bytes(sample(3000000000, 10))
Kb(sample(3000000000, 10))
Mb(sample(3000000000, 10))
Gb(sample(3000000000, 10))
```

---

coord_proj *Similar to* coord_map *but uses the PROJ.4 library/package for projection transformation*

Description

The representation of a portion of the earth, which is approximately spherical, onto a flat 2D plane requires a projection. This is what coord_proj does, using the proj4::project() function from the proj4 package.

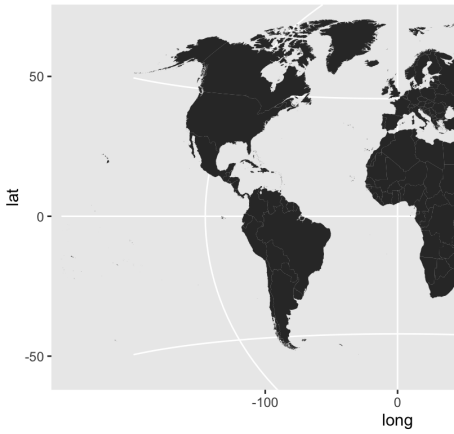
Usage

```
coord_proj(
  proj = NULL,
  inverse = FALSE,
  degrees = TRUE,
  ellps.default = "sphere",
  xlim = NULL,
  ylim = NULL
)
```

Arguments

proj	projection definition. If left NULL will default to a Robinson projection
inverse	if TRUE inverse projection is performed (from a cartographic projection into lat/long), otherwise projects from lat/long into a cartographic projection.
degrees	if TRUE then the lat/long data is assumed to be in degrees, otherwise in radians
ellps.default	default ellipsoid that will be added if no datum or ellipsoid parameter is specified in proj. Older versions of PROJ.4 didn't require a datum (and used sphere by default), but 4.5.0 and higher always require a datum or an ellipsoid. Set to NA if no datum should be added to proj (e.g. if you specify an ellipsoid directly).
xlim	manually specify x limits (in degrees of longitude)
ylim	manually specify y limits (in degrees of latitude)

Details



A sample of the output from `coord_proj()` using the Winkel-Tripel projection: "

Note

It is recommended that you use `geom_cartogram` with this coordinate system

When `inverse` is `FALSE` `coord_proj` makes a fairly large assumption that the coordinates being transformed are within -180:180 (longitude) and -90:90 (latitude). As such, it truncates all longitude & latitude input to fit within these ranges. More updates to this new `coord_` are planned.

Examples

```
## Not run:
# World in Winkel-Tripel

# U.S.A. Albers-style
usa <- world[world$region == "USA",]
usa <- usa[!(usa$subregion %in% c("Alaska", "Hawaii")),]

gg <- ggplot()
gg <- gg + geom_cartogram(data=usa, map=usa,
                    aes(x=long, y=lat, map_id=region))
gg <- gg + coord_proj(
             paste0("+proj=aea +lat_1=29.5 +lat_2=45.5 +lat_0=37.5 +lon_0=-96",
                    " +x_0=0 +y_0=0 +ellps=GRS80 +datum=NAD83 +units=m +no_defs"))
gg

# Showcase Greenland (properly)
greenland <- world[world$region == "Greenland",]

gg <- ggplot()
gg <- gg + geom_cartogram(data=greenland, map=greenland,
                    aes(x=long, y=lat, map_id=region))
gg <- gg + coord_proj(
             paste0("+proj=stere +lat_0=90 +lat_ts=70 +lon_0=-45 +k=1 +x_0=0",
                    " +y_0=0 +ellps=WGS84 +datum=WGS84 +units=m +no_defs"))
gg

## End(Not run)
```

`fortify.table` *Fortify contingency tables*

Description

Fortify contingency tables

Usage

```
## S3 method for class 'table'
fortify(model, data, ...)
```

Arguments

model	the contingency table
data	data (unused)
...	(unused)

GeomTicks *Base ggproto classes for ggplot2*

Description

If you are creating a new geom, stat, position, or scale in another package, you'll need to extend from ggplot2::Geom, ggplot2::Stat, ggplot2::Position, or ggplot2::Scale.

See Also

ggplot2-ggproto

---

geom_bkde *Display a smooth density estimate.*

Description

A kernel density estimate, useful for displaying the distribution of variables with underlying smoothness.

Usage

```
geom_bkde(
  mapping = NULL,
  data = NULL,
  stat = "bkde",
  position = "identity",
  bandwidth = NULL,
  range.x = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_bkde(
  mapping = NULL,
  data = NULL,
  geom = "area",
```

```
  position = "stack",
  kernel = "normal",
  canonical = FALSE,
  bandwidth = NULL,
  gridsize = 410,
  range.x = NULL,
  truncate = TRUE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

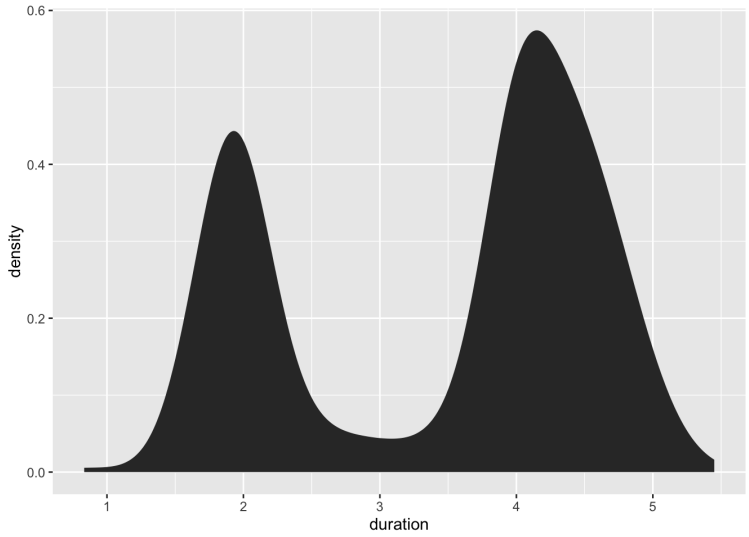
Arguments

mapping	Set of aesthetic mappings created by 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)).
position	Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
bandwidth	the kernel bandwidth smoothing parameter. see bkde for details. If NULL, it will be computed for you but will most likely not yield optimal results.
range.x	vector containing the minimum and maximum values of x at which to compute the estimate. see bkde for details
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().
...	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.
geom, stat	Use to override the default connection between geom_bkde and stat_bkde.

`kernel`	character string which determines the smoothing kernel. see bkde for details
`canonical`	logical flag: if TRUE, canonically scaled kernels are used. see bkde for details
`gridsize`	the number of equally spaced points at which to estimate the density. see bkde for details.
`truncate`	logical flag: if TRUE, data with x values outside the range specified by range.x are ignored. see bkde for details

Details

A sample of the output from `geom_bkde()`:



Aesthetics

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

- `x`
- `y`
- `alpha`
- `color`
- `fill`
- `linetype`
- `size`

Computed variables

density density estimate

count density * number of points - useful for stacked density plots

scaled density estimate, scaled to maximum of 1

See Also

See geom_histogram, geom_freqpoly for other methods of displaying continuous distribution. See geom_violin for a compact density display.

Examples

```
data(geyser, package="MASS")

ggplot(geyser, aes(x=duration)) +
  stat_bkde(alpha=1/2)

ggplot(geyser, aes(x=duration)) +
  geom_bkde(alpha=1/2)

ggplot(geyser, aes(x=duration)) +
 stat_bkde(bandwidth=0.25)

ggplot(geyser, aes(x=duration)) +
  geom_bkde(bandwidth=0.25)
```

---

geom_bkde2d *Contours from a 2d density estimate.*

Description

Perform a 2D kernel density estimation using bkde2D and display the results with contours. This can be useful for dealing with overplotting

Usage

```
geom_bkde2d(
  mapping = NULL,
  data = NULL,
  stat = "bkde2d",
  position = "identity",
  bandwidth = NULL,
  range.x = NULL,
  lineend = "butt",
  contour = TRUE,
  linejoin = "round",
  linemitre = 1,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_bkde2d(
```

```
  mapping = NULL,
  data = NULL,
  geom = "density2d",
  position = "identity",
  contour = TRUE,
  bandwidth = NULL,
  grid_size = c(51, 51),
  range.x = NULL,
  truncate = TRUE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

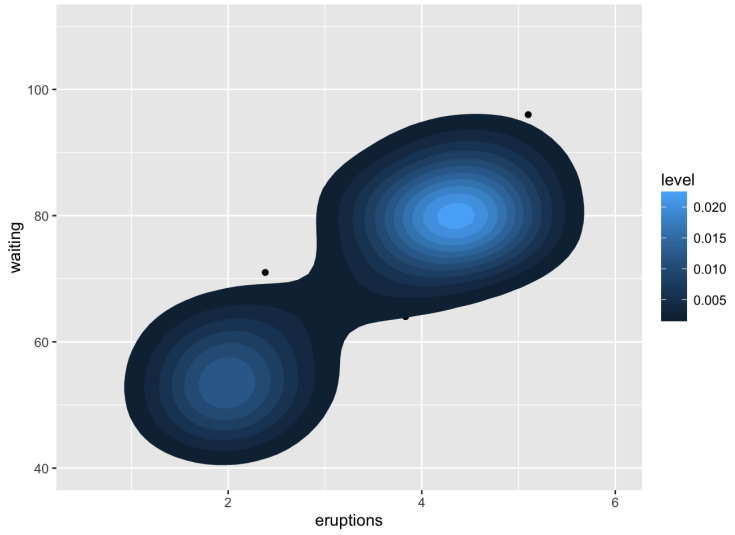
Arguments

mapping	Set of aesthetic mappings created by 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, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")
position	Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
bandwidth	the kernel bandwidth smoothing parameter. see bkde2D for details. If NULL, it will be computed for you but will most likely not yield optimal results. see bkde2D for details
range.x	a list containing two vectors, where each vector contains the minimum and maximum values of x at which to compute the estimate for each direction. see bkde2D for details
lineend	Line end style (round, butt, square).
contour	If TRUE, contour the results of the 2d density estimation
linejoin	Line join style (round, mitre, bevel).
linemitre	Line mitre limit (number greater than 1).

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().
...	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.
geom	default geom to use with this stat
grid_size	vector containing the number of equally spaced points in each direction over which the density is to be estimated. see bkde2D for details
truncate	logical flag: if TRUE, data with x values outside the range specified by range.x are ignored. see bkde2D for details

Details

A sample of the output from geom_bkde2d():



Computed variables

Same as stat_contour

See Also

geom_contour for contour drawing geom, stat_sum for another way of dealing with overplotting

Examples

```
m <- ggplot(faithful, aes(x = eruptions, y = waiting)) +
       geom_point() +
       xlim(0.5, 6) +
       ylim(40, 110)

m + geom_bkde2d(bandwidth=c(0.5, 4))

m + stat_bkde2d(bandwidth=c(0.5, 4), aes(fill = ..level..), geom = "polygon")

# If you map an aesthetic to a categorical variable, you will get a
# set of contours for each value of that variable
set.seed(4393)
dsmall <- diamonds[sample(nrow(diamonds), 1000), ]
d <- ggplot(dsmall, aes(x, y)) +
       geom_bkde2d(bandwidth=c(0.5, 0.5), aes(colour = cut))
d

# If we turn contouring off, we can use use geoms like tiles:
d + stat_bkde2d(bandwidth=c(0.5, 0.5), geom = "raster",
                aes(fill = ..density..), contour = FALSE)

# Or points:
d + stat_bkde2d(bandwidth=c(0.5, 0.5), geom = "point",
                aes(size = ..density..),  contour = FALSE)
```

---

geom_cartogram *Map polygons layer enabling the display of show statistical information*

Description

This replicates the old behaviour of `geom_map()`, enabling specifying of `x` and `y` aesthetics.

Usage

```
geom_cartogram(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  ...,
  map,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

mapping	Set of aesthetic mappings created by 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, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")
...	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.
map	Data frame that contains the map coordinates. This will typically be created using fortify on a spatial object. It must contain columns x, long or longitude, y, lat or latitude and region or id.
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().

Aesthetics

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

- map_id
- alpha
- colour
- fill
- group
- linetype
- size
- x
- y

Examples

```
## Not run:
# When using geom_polygon, you will typically need two data frames:
# one contains the coordinates of each polygon (positions),  and the
# other the values associated with each polygon (values).  An id
# variable links the two together

ids <- factor(c("1.1", "2.1", "1.2", "2.2", "1.3", "2.3"))

values <- data.frame(
  id = ids,
  value = c(3, 3.1, 3.1, 3.2, 3.15, 3.5)
)

positions <- data.frame(
  id = rep(ids, each = 4),
  x = c(2, 1, 1.1, 2.2, 1, 0, 0.3, 1.1, 2.2, 1.1, 1.2, 2.5, 1.1, 0.3,
  0.5, 1.2, 2.5, 1.2, 1.3, 2.7, 1.2, 0.5, 0.6, 1.3),
  y = c(-0.5, 0, 1, 0.5, 0, 0.5, 1.5, 1, 0.5, 1, 2.1, 1.7, 1, 1.5,
  2.2, 2.1, 1.7, 2.1, 3.2, 2.8, 2.1, 2.2, 3.3, 3.2)
)

ggplot() +
  geom_cartogram(aes(x, y, map_id = id), map = positions, data=positions)

ggplot() +
  geom_cartogram(aes(x, y, map_id = id), map = positions, data=positions) +
  geom_cartogram(data=values, map=positions, aes(fill = value, map_id=id))

ggplot() +
  geom_cartogram(aes(x, y, map_id = id), map = positions, data=positions) +
  geom_cartogram(data=values, map=positions, aes(fill = value, map_id=id)) +
  ylim(0, 3)

# Better example
crimes <- data.frame(state = tolower(rownames(USArrests)), USArrests)
crimesm <- reshape2::melt(crimes, id = 1)

if (require(maps)) {

  states_map <- map_data("state")

  ggplot() +
    geom_cartogram(aes(long, lat, map_id = region), map = states_map, data=states_map) +
    geom_cartogram(aes(fill = Murder, map_id = state), map=states_map, data=crimes)

  last_plot() + coord_map("polyconic")

  ggplot() +
    geom_cartogram(aes(long, lat, map_id=region), map = states_map, data=states_map) +
    geom_cartogram(aes(fill = value, map_id=state), map = states_map, data=crimesm) +
    coord_map("polyconic") +
```

```
    facet_wrap( ~ variable)
}

## End(Not run)
```

`geom_dumbbell` *Dumbbell charts*

Description

The dumbbell geom is used to create dumbbell charts.

Usage

```
geom_dumbbell(
  mapping = NULL,
  data = NULL,
  ...,
  colour_x = NULL,
  size_x = NULL,
  colour_xend = NULL,
  size_xend = NULL,
  dot_guide = FALSE,
  dot_guide_size = NULL,
  dot_guide_colour = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  position = "identity"
)
```

Arguments

`mapping`	Set of aesthetic mappings created by `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)`).

...	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.
colour_x	the colour of the start point
size_x	the size of the start point
colour_xend	the colour of the end point
size_xend	the size of the end point
dot_guide	if TRUE, a leading dotted line will be placed before the left-most dumbbell point
dot_guide_size, dot_guide_colour	singe-value aesthetics for dot_guide
na.rm	If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.
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().
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.

Details

Dumbbell dot plots — dot plots with two or more series of data — are an alternative to the clustered bar chart or slope graph.

Aesthetics

@section Aesthetics: geom_segment()understands the following aesthetics (required aesthetics are in bold):

- x
- y
- xend***or***yend
- alpha
- colour
- group
- linetype
- linewidth

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Examples

```
library(ggplot2)

df <- data.frame(trt=LETTERS[1:5], l=c(20, 40, 10, 30, 50), r=c(70, 50, 30, 60, 80))

ggplot(df, aes(y=trt, x=l, xend=r)) +
  geom_dumbbell(size=3, color="#e3e2e1",
                colour_x = "#5b8124", colour_xend = "#bad744",
                dot_guide=TRUE, dot_guide_size=0.25) +
  labs(x=NULL, y=NULL, title="ggplot2 geom_dumbbell with dot guide") +
  theme_minimal() +
  theme(panel.grid.major.x=element_line(size=0.05))

## with vertical dodging
df2 <- data.frame(trt = c(LETTERS[1:5], "D"),
                  l = c(20, 40, 10, 30, 50, 40),
                  r = c(70, 50, 30, 60, 80, 70))

ggplot(df2, aes(y=trt, x=l, xend=r)) +
  geom_dumbbell(size=3, color="#e3e2e1",
                colour_x = "#5b8124", colour_xend = "#bad744",
                dot_guide=TRUE, dot_guide_size=0.25,
                position=position_dodgev(height=0.4)) +
  labs(x=NULL, y=NULL, title="ggplot2 geom_dumbbell with dot guide") +
  theme_minimal() +
  theme(panel.grid.major.x=element_line(size=0.05))
```

---

geom_encircle *Automatically enclose points in a polygon*

Description

Automatically enclose points in a polygon

Usage

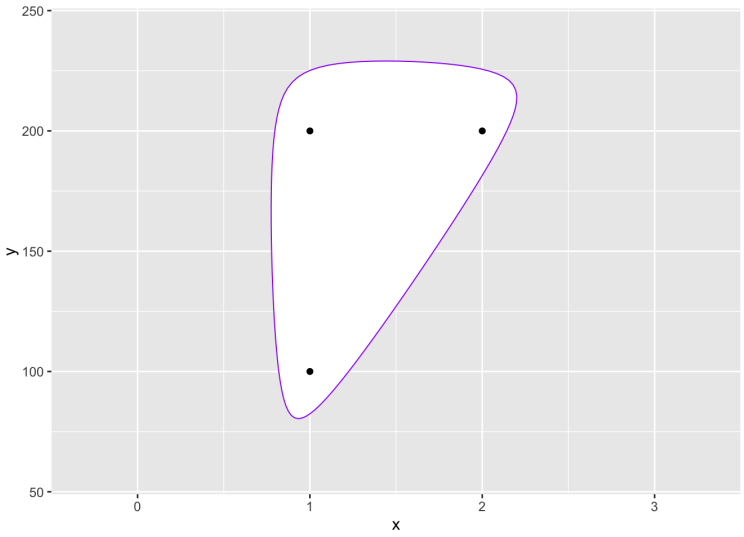
```
geom_encircle(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

Arguments

mapping	mapping
data	data
stat	stat
position	position
na.rm	na.rm
show.legend	show.legend
inherit.aes	inherit.aes
...	dots

Details

A sample of the output from geom_encircle():



Value

adds a circle around the specified points

Author(s)

Ben Bolker

Examples

```
d <- data.frame(x=c(1,1,2),y=c(1,2,2)*100)

gg <- ggplot(d,aes(x,y))
gg <- gg + scale_x_continuous(expand=c(0.5,1))
gg <- gg + scale_y_continuous(expand=c(0.5,1))
```

```
gg + geom_encircle(s_shape=1, expand=0) + geom_point()

gg + geom_encircle(s_shape=1, expand=0.1, colour="red") + geom_point()

gg + geom_encircle(s_shape=0.5, expand=0.1, colour="purple") + geom_point()

gg + geom_encircle(data=subset(d, x==1), colour="blue", spread=0.02) +
  geom_point()

gg +geom_encircle(data=subset(d, x==2), colour="cyan", spread=0.04) +
  geom_point()

gg <- ggplot(mpg, aes(displ, hwy))
gg + geom_encircle(data=subset(mpg, hwy>40)) + geom_point()
gg + geom_encircle(aes(group=manufacturer)) + geom_point()
gg + geom_encircle(aes(group=manufacturer,fill=manufacturer),alpha=0.4)+
       geom_point()
gg + geom_encircle(aes(group=manufacturer,colour=manufacturer))+
       geom_point()

ss <- subset(mpg,hwy>31 & displ<2)

gg + geom_encircle(data=ss, colour="blue", s_shape=0.9, expand=0.07) +
  geom_point() + geom_point(data=ss, colour="blue")
```

`geom_lollipop` *Lollipop charts*

Description

The lollipop geom is used to create lollipop charts.

Usage

```
geom_lollipop(
  mapping = NULL,
  data = NULL,
  ...,
  horizontal = FALSE,
  point.colour = NULL,
  point.size = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

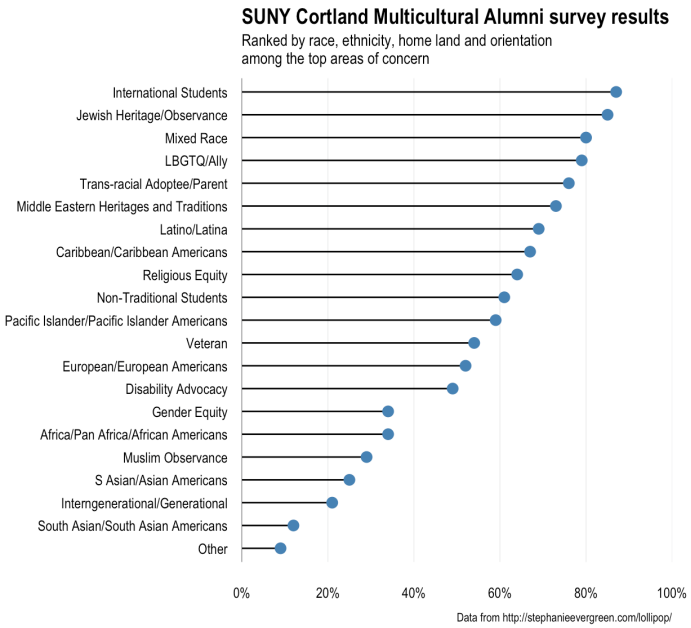
mapping	Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data	The data to be displayed in this layer. There are three options: If NULL, 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)).
...	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.
horizontal	horizontal is FALSE (the default), the function will draw the lollipops up from the X axis (i.e. it will set xend to x & yend to 0). If TRUE, it wiill set yend to y & xend to 0). Make sure you map the x & y aesthetics accordingly. This parameter helps avoid the need for coord_flip().
point.colour	the colour of the point
point.size	the size of the point
na.rm	If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.
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().

Details

Lollipop charts are the creation of Andy Cotgreave going back to 2011. They are a combination of a thin segment, starting at with a dot at the top and are a suitable alternative to or replacement for bar charts.

Use the horizontal parameter to abate the need for coord_flip() (see the Arguments section for details).

A sample of the output from geom_lollipop():



Aesthetics

@section Aesthetics: `geom_point()`understands the following aesthetics (required aesthetics are in bold):

- `x`
- `y`
- `alpha`
- `colour`
- `fill`
- `group`
- `shape`
- `size`
- `stroke`

Learn more about setting these aesthetics in `vignette("ggplot2-specs")`.

Examples

```
df <- data.frame(trt=LETTERS[1:10],
                 value=seq(100, 10, by=-10))

ggplot(df, aes(trt, value)) + geom_lollipop()

ggplot(df, aes(value, trt)) + geom_lollipop(horizontal=TRUE)
```

`geom_spikelines` *Draw spikelines on a plot*

Description

Segment reference lines that originate at an point

Usage

```
geom_spikelines(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  arrow = NULL,
  lineend = "butt",
  linejoin = "round",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

`mapping`	Set of aesthetic mappings created by `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, either as a `ggproto` `Geom` subclass or as a string naming the stat stripped of the `stat_` prefix (e.g. `"count"` rather than `"stat_count"`)
`position`	Position adjustment, either as a string naming the adjustment (e.g. `"jitter"` to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
`...`	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.

arrow	Arrow specification, as created by grid::arrow().
lineend	Line end style (round, butt, square).
linejoin	Line join style (round, mitre, bevel).
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().

Author(s)

Jonathan Sidi

Examples

```
mtcars$name <- rownames(mtcars)

p <- ggplot(data = mtcars, aes(x=mpg,y=disp)) + geom_point()

p + geom_spikelines(data = mtcars[mtcars$carb==4,],linetype = 2)

p + geom_spikelines(data = mtcars[mtcars$carb==4,],aes(colour = factor(gear)), linetype = 2)

## Not run:
require(ggrepel)
p + geom_spikelines(data = mtcars[mtcars$carb==4,],aes(colour = factor(gear)), linetype = 2) +
ggrepel::geom_label_repel(data = mtcars[mtcars$carb==4,],aes(label = name))

## End(Not run)
```

---

geom_stateface *Use ProPublica's StateFace font in ggplot2 plots*

Description

The label parameter can be either a 2-letter state abbreviation or a full state name. geom_stateface() will take care of the translation to StateFace font glyph characters.

Usage

```
geom_stateface(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  parse = FALSE,
  nudge_x = 0,
  nudge_y = 0,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

mapping	Set of aesthetic mappings created by 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, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")
position	Position adjustment, either as a string, or the result of a call to a position adjustment function. Cannot be jointy specified with nudge_x or nudge_y.
...	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.
parse	If TRUE, the labels will be parsed into expressions and displayed as described in ?plotmath.
nudge_x, nudge_y	Horizontal and vertical adjustment to nudge l abels by. Useful for offsetting text from points, particularly on discrete scales.
check_overlap	If TRUE, text that overlaps previous text in the same layer will not be plotted. check_overlap happens at draw time and in the order of the data. Therefore data should be arranged by the label column before calling geom_text(). Note that this argument is not supported by geom_label().

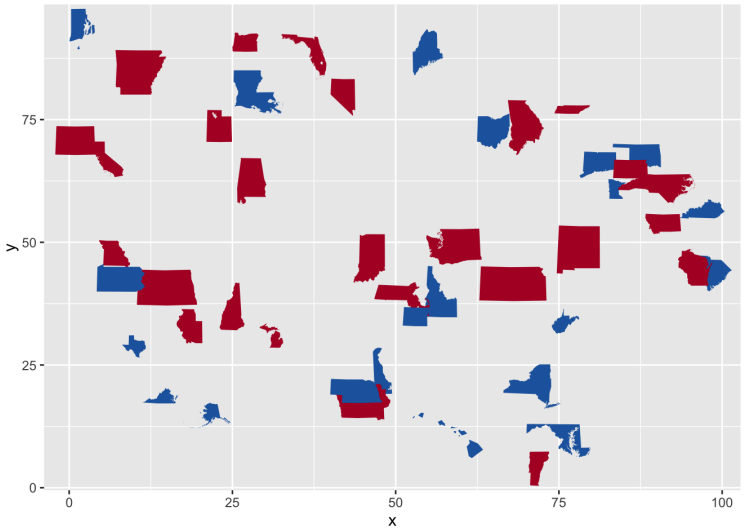
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also 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().

Details

The package will also take care of loading the StateFace font for PDF and other devices, but to use it with the on-screen ggplot2 device, you'll need to install the font on your system.

ggalt ships with a copy of the StateFace TTF font. You can run show_stateface() to get the filesystem location and then load the font manually from there.

A sample of the output from geom_stateface():



See Also

Other StateFace operations: load_stateface(), show_stateface()

Examples

```
## Not run:
library(ggplot2)
library(ggalt)

# Run show_stateface() to see the location of the TTF StateFace font
# You need to install it for it to work

set.seed(1492)
```

```
dat <- data.frame(state=state.abb,
                  x=sample(100, 50),
                  y=sample(100, 50),
                  col=sample(c("#b2182b", "#2166ac"), 50, replace=TRUE),
                  sz=sample(6:15, 50, replace=TRUE),
                  stringsAsFactors=FALSE)
gg <- ggplot(dat, aes(x=x, y=y))
gg <- gg + geom_stateface(aes(label=state, color=col, size=sz))
gg <- gg + scale_color_identity()
gg <- gg + scale_size_identity()
gg

## End(Not run)
```

---

geom_ubar *Uniform "bar" charts*

Description

I've been using geom_segment more to make "bar" charts, setting xend to whatever x is and yend to 0. The bar widths remain constant without any tricks and you have granular control over the segment width. I decided it was time to make a geom.

Usage

```
geom_ubar(
  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 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, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")
position	Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
...	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.
na.rm	If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.
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().

Aesthetics

'geom_ubar" understands the following aesthetics (required aesthetics are in bold):

- x
- y
- alpha
- colour
- group
- linetype
- size

Examples

```
library(ggplot2)

data(economics)
ggplot(economics, aes(date, uempmed)) +
  geom_ubar()
```

geom_xspline *Connect control points/observations with an X-spline*

Description

Draw an X-spline, a curve drawn relative to control points/observations. Patterned after `geom_line` in that it orders the points by `x` first before computing the splines.

Usage

```
geom_xspline(
  mapping = NULL,
  data = NULL,
  stat = "xspline",
  position = "identity",
  na.rm = TRUE,
  show.legend = NA,
  inherit.aes = TRUE,
  spline_shape = -0.25,
  open = TRUE,
  rep_ends = TRUE,
  ...
)

stat_xspline(
  mapping = NULL,
  data = NULL,
  geom = "line",
  position = "identity",
  na.rm = TRUE,
  show.legend = NA,
  inherit.aes = TRUE,
  spline_shape = -0.25,
  open = TRUE,
  rep_ends = TRUE,
  ...
)
```

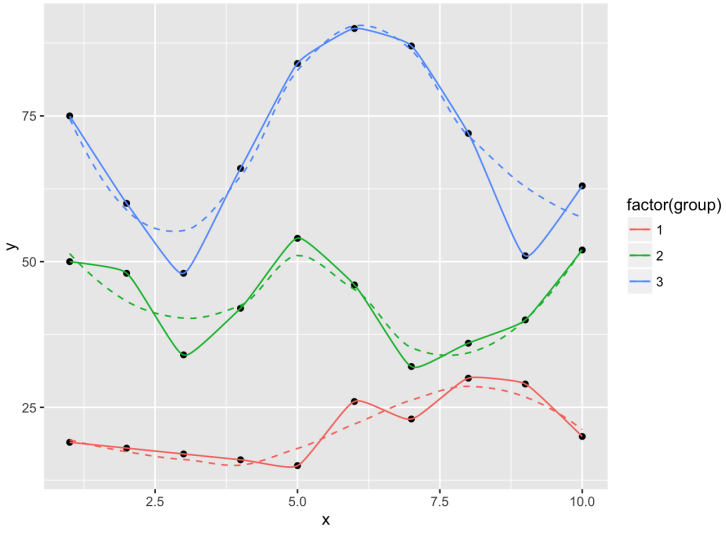
Arguments

`mapping`	Set of aesthetic mappings created by `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)`).
`position`	Position adjustment, either as a string naming the adjustment (e.g. `"jitter"` to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
`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()`.
`spline_shape`	A numeric vector of values between -1 and 1, which control the shape of the spline relative to the control points.
`open`	A logical value indicating whether the spline is an open or a closed shape.
`rep_ends`	For open X-splines, a logical value indicating whether the first and last control points should be replicated for drawing the curve. Ignored for closed X-splines.
`...`	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.
`geom, stat`	Use to override the default connection between `geom_xspline` and `stat_xspline`.

Details

A sample of the output from `geom_xspline()`:



An X-spline is a line drawn relative to control points. For each control point, the line may pass through (interpolate) the control point or it may only approach (approximate) the control point; the behaviour is determined by a shape parameter for each control point.

If the shape parameter is greater than zero, the spline approximates the control points (and is very similar to a cubic B-spline when the shape is 1). If the shape parameter is less than zero, the spline interpolates the control points (and is very similar to a Catmull-Rom spline when the shape is -1). If the shape parameter is 0, the spline forms a sharp corner at that control point.

For open X-splines, the start and end control points must have a shape of 0 (and non-zero values are silently converted to zero).

For open X-splines, by default the start and end control points are replicated before the curve is drawn. A curve is drawn between (interpolating or approximating) the second and third of each set of four control points, so this default behaviour ensures that the resulting curve starts at the first control point you have specified and ends at the last control point. The default behaviour can be turned off via the repEnds argument.

Aesthetics

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

- `x`
- `y`
- `alpha`
- `color`
- `linetype`
- `size`

Computed variables

- x
- y

References

Blanc, C. and Schlick, C. (1995), "X-splines : A Spline Model Designed for the End User", in *Proceedings of SIGGRAPH 95*, pp. 377-386. http://dept-info.labri.fr/~schlick/DOC/sig1.html

See Also

`geom_line`: Connect observations (x order); `geom_path`: Connect observations; `geom_polygon`: Filled paths (polygons); `geom_segment`: Line segments; `xspline`; `grid.xspline`

Other xspline implementations: `geom_xspline2()`

Examples

```
set.seed(1492)
dat <- data.frame(x=c(1:10, 1:10, 1:10),
                  y=c(sample(15:30, 10), 2*sample(15:30, 10),
                      3*sample(15:30, 10)),
                  group=factor(c(rep(1, 10), rep(2, 10), rep(3, 10)))
)

ggplot(dat, aes(x, y, group=group, color=group)) +
  geom_point() +
  geom_line()

ggplot(dat, aes(x, y, group=group, color=factor(group))) +
  geom_point() +
  geom_line() +
  geom_smooth(se=FALSE, linetype="dashed", size=0.5)

ggplot(dat, aes(x, y, group=group, color=factor(group))) +
  geom_point(color="black") +
  geom_smooth(se=FALSE, linetype="dashed", size=0.5) +
  geom_xspline(size=0.5)

ggplot(dat, aes(x, y, group=group, color=factor(group))) +
  geom_point(color="black") +
  geom_smooth(se=FALSE, linetype="dashed", size=0.5) +
  geom_xspline(spline_shape=-0.4, size=0.5)

ggplot(dat, aes(x, y, group=group, color=factor(group))) +
  geom_point(color="black") +
  geom_smooth(se=FALSE, linetype="dashed", size=0.5) +
  geom_xspline(spline_shape=0.4, size=0.5)

ggplot(dat, aes(x, y, group=group, color=factor(group))) +
  geom_point(color="black") +
  geom_smooth(se=FALSE, linetype="dashed", size=0.5) +
  geom_xspline(spline_shape=1, size=0.5)

ggplot(dat, aes(x, y, group=group, color=factor(group))) +
  geom_point(color="black") +
  geom_smooth(se=FALSE, linetype="dashed", size=0.5) +
  geom_xspline(spline_shape=0, size=0.5)

ggplot(dat, aes(x, y, group=group, color=factor(group))) +
  geom_point(color="black") +
  geom_smooth(se=FALSE, linetype="dashed", size=0.5) +
  geom_xspline(spline_shape=-1, size=0.5)
```

`geom_xspline2` *Alternative implemenation for connecting control points/observations with an X-spline*

Description

Alternative implemenation for connecting control points/observations with an X-spline

Usage

```
geom_xspline2(
  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 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)).
position	Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
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().
...	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.

Value

creates a spline curve

Author(s)

Ben Bolker

See Also

Other xspline implementations: `geom_xspline()`

`ggalt` *Extra Geoms, Stats, Coords, Scales & Fonts for 'ggplot2'*

Description

A package containing additional geoms, coords, stats, scales & fonts for ggplot2 2.0+

Author(s)

Bob Rudis (@hrbrmstr)

`load_stateface` *Load stateface font*

Description

Makes the ProPublica StateFace font available to PDF, PostScript, et. al. devices.

Usage

```
load_stateface()
```

See Also

Other StateFace operations: `geom_stateface()`, `show_stateface()`

position_dodgev *Vertically dodge position*

Description

Vertically dodge position

Usage

```
position_dodgev(height = NULL)
```

Arguments

height	numeric, height of vertical dodge, Default: NULL

Note

position-dodgev(): unmodified from lionel-/ggstance/R/position-dodgev.R 73f521384ae8ea277db5f7d5a2854004aa18f947

Author(s)

@ggstance authors

Examples

```
if(interactive()){

dat <- data.frame(
  trt = c(LETTERS[1:5], "D"),
  l = c(20, 40, 10, 30, 50, 40),
  r = c(70, 50, 30, 60, 80, 70)
)

ggplot(dat, aes(y=trt, x=l, xend=r)) +
 geom_dumbbell(size=3, color="#e3e2e1",
               colour_x = "#5b8124", colour_xend = "#bad744",
               dot_guide=TRUE, dot_guide_size=0.25,
               position=position_dodgev(height=0.8)) +
 labs(x=NULL, y=NULL, title="ggplot2 geom_dumbbell with dot guide") +
 theme_minimal() +
 theme(panel.grid.major.x=element_line(size=0.05))

 }
```

show_stateface *Show location of StateFace font*

Description

Displays the path to the StateFace font. For the font to work in the on-screen plot device for ggplot2, you need to install the font on your system

Usage

```
show_stateface()
```

See Also

Other StateFace operations: `geom_stateface()`, `load_stateface()`

stat_ash *Compute and display a univariate averaged shifted histogram (polynomial kernel)*

Description

See `bin1` & `ash1` for more information.

Usage

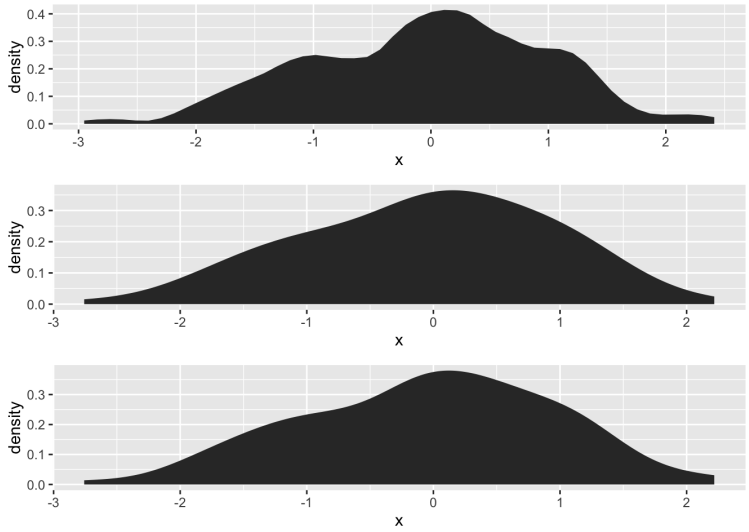
```
stat_ash(
  mapping = NULL,
  data = NULL,
  geom = "area",
  position = "stack",
  ab = NULL,
  nbin = 50,
  m = 5,
  kopt = c(2, 2),
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

Arguments

mapping	Set of aesthetic mappings created by 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 Geom
position	Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
ab	half-open interval for bins *[a,b)*. If no value is specified, the range of x is stretched by 5% at each end and used the interval.
nbin	number of bins desired. Default 50.
m	integer smoothing parameter; Default 5.
kopt	vector of length 2 specifying the kernel, which is proportional to *(1 - abs(i/m)^kopt(1))i^kopt(2)*; (2,2)=biweight (default); (0,0)=uniform; (1,0)=triangle; (2,1)=Epanechnikov; (2,3)=triweight.
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().
...	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.

Details

A sample of the output from stat_ash():



Aesthetics

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

- x
- alpha
- color
- fill
- linetype
- size

Computed variables

density ash density estimate

References

David Scott (1992), *"Multivariate Density Estimation,"* John Wiley, (chapter 5 in particular).

B. W. Silverman (1986), *"Density Estimation for Statistics and Data Analysis,"* Chapman & Hall.

Examples

```
# compare
library(gridExtra)
set.seed(1492)
dat <- data.frame(x=rnorm(100))
grid.arrange(ggplot(dat, aes(x)) + stat_ash(),
             ggplot(dat, aes(x)) + stat_bkde(),
             ggplot(dat, aes(x)) + stat_density(),
             nrow=3)
```

```
cols <- RColorBrewer::brewer.pal(3, "Dark2")
ggplot(dat, aes(x)) +
  stat_ash(alpha=1/2, fill=cols[3]) +
  stat_bkde(alpha=1/2, fill=cols[2]) +
  stat_density(alpha=1/2, fill=cols[1]) +
  geom_rug() +
  labs(x=NULL, y="density/estimate") +
  scale_x_continuous(expand=c(0,0)) +
  theme_bw() +
  theme(panel.grid=element_blank()) +
  theme(panel.border=element_blank())
```

`stat_stepribbon` *Step ribbon statistic*

Description

Provides stairstep values for ribbon plots

Usage

```
stat_stepribbon(
  mapping = NULL,
  data = NULL,
  geom = "ribbon",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  direction = "hv",
  ...
)
```

Arguments

`mapping`	Set of aesthetic mappings created by `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	which geom to use; defaults to "ribbon"
position	Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
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().
direction	hv for horizontal-veritcal steps, vh for vertical-horizontal steps
...	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.

References

https://groups.google.com/forum/?fromgroups=#!topic/ggplot2/9cFWHaH1CPs

Examples

```
x <- 1:10
df <- data.frame(x=x, y=x+10, ymin=x+7, ymax=x+12)

gg <- ggplot(df, aes(x, y))
gg <- gg + geom_ribbon(aes(ymin=ymin, ymax=ymax),
                       stat="stepribbon", fill="#b2b2b2")
gg <- gg + geom_step(color="#2b2b2b")
gg

gg <- ggplot(df, aes(x, y))
gg <- gg + geom_ribbon(aes(ymin=ymin, ymax=ymax),
                       stat="stepribbon", fill="#b2b2b2",
                       direction="hv")
gg <- gg + geom_step(color="#2b2b2b")
gg
```

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