Package ‘gghalves’

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Title Compose Half-Half Plots Using Your Favourite Geoms

Version 0.0.1

Description A ‘ggplot2’ extension for easy plotting of half-half geom combinations. Think half boxplot and half jitterplot, or half violinplot and half dotplot.

URL https://github.com/erocoar/gghalves

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Description

gghalves extensions to ggplot2

geom_half_boxplot

A half boxplot

Usage

geom_half_boxplot(mapping = NULL, data = NULL, stat = "boxplot", position = "dodge2", ..., side = "l", center = FALSE, outlier.colour = NULL, outlier.color = NULL, outlier.fill = NULL, outlier.shape = 19, outlier.size = 1.5, outlier.stroke = 0.5, outlier.alpha = NULL, notch = FALSE, notchwidth = 0.5, varwidth = FALSE, errorbar.draw = TRUE, errorbar.length = 0.5, 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 Use to override the default connection between geom_boxplot and stat_boxplot.
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.
The side of the half-geom, "l" for left and "r" for right, defaults to "l".

Boolean whether to center the half-boxplot instead of aligning it to its respective side.

Default aesthetics for outliers. Set to NULL to inherit from the aesthetics used for the box.

In the unlikely event you specify both US and UK spellings of colour, the US spelling will take precedence.

Sometimes it can be useful to hide the outliers, for example when overlaying the raw data points on top of the boxplot. Hiding the outliers can be achieved by setting outlier.shape = NA. Importantly, this does not remove the outliers, it only hides them, so the range calculated for the y-axis will be the same with outliers shown and outliers hidden.

Default aesthetics for outliers. Set to NULL to inherit from the aesthetics used for the box.

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- **outlier.stroke**
  Default aesthetics for outliers. Set to `NULL` to inherit from the aesthetics used for the box.
  In the unlikely event you specify both US and UK spellings of colour, the US spelling will take precedence.
  Sometimes it can be useful to hide the outliers, for example when overlaying the raw data points on top of the boxplot. Hiding the outliers can be achieved by setting `outlier.shape = NA`. Importantly, this does not remove the outliers, it only hides them, so the range calculated for the y-axis will be the same with outliers shown and outliers hidden.

- **outlier.alpha**
  Default aesthetics for outliers. Set to `NULL` to inherit from the aesthetics used for the box.
  In the unlikely event you specify both US and UK spellings of colour, the US spelling will take precedence.
  Sometimes it can be useful to hide the outliers, for example when overlaying the raw data points on top of the boxplot. Hiding the outliers can be achieved by setting `outlier.shape = NA`. Importantly, this does not remove the outliers, it only hides them, so the range calculated for the y-axis will be the same with outliers shown and outliers hidden.

- **notch**
  If `FALSE` (default) make a standard box plot. If `TRUE`, make a notched box plot. Notches are used to compare groups; if the notches of two boxes do not overlap, this suggests that the medians are significantly different.

- **notchwidth**
  For a notched box plot, width of the notch relative to the body (defaults to `notchwidth = 0.5`).

- **varwidth**
  If `FALSE` (default) make a standard box plot. If `TRUE`, boxes are drawn with widths proportional to the square-roots of the number of observations in the groups (possibly weighted, using the weight aesthetic).

- **errorbar.draw**
  Draw horizontal whiskers at the top and bottom (the IQR). Defaults to ‘TRUE’.

- **errorbar.length**
  Length of the horizontal whiskers (errorbar). Defaults to half the width of the half-boxplot

- **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
ggplot(iris, aes(x = Species, y = Petal.Width, fill = Species)) +
```
```r
geom_half_boxplot()

ggplot(iris, aes(x = Species, y = Petal.Width, fill = Species)) +
  geom_half_boxplot(side = "r")

ggplot(iris, aes(x = Species, y = Petal.Width, fill = Species)) +
  geom_half_boxplot(center = TRUE)
```

---

**geom_half_dotplot**  
Half dot plot with sensible parameter settings.

### Description

In a dot plot, the width of a dot corresponds to the bin width (or maximum width, depending on the binning algorithm), and dots are stacked, with each dot representing one observation.

### Usage

```r
geom_half_dotplot(mapping = NULL, data = NULL, position = "dodge",
                   ..., binwidth = NULL, binaxis = "y", method = "dotdensity",
                   binpositions = "bygroup", stackdir = "up", stackratio = 1,
                   dotsize = 1, stackgroups = FALSE, origin = NULL, right = TRUE,
                   width = NULL, drop = FALSE, 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)`).

- **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.

- **binwidth**  
  When method is "dotdensity", this specifies maximum bin width. When method is "histodot", this specifies bin width. Defaults to 1/30 of the range of the data.
geom_half_dotplot

binaxis
The axis to bin along, "x" (default) or "y"

method
"dotdensity" (default) for dot-density binning, or "histodot" for fixed bin widths (like stat_bin)

binpositions
When method is "dotdensity", "bygroup" (default) determines positions of the bins for each group separately. "all" determines positions of the bins with all the data taken together; this is used for aligning dot stacks across multiple groups.

stackdir
Which direction to stack the dots. "up" (default) places the half-dotplot on the right side. "down" on the left side.

stackratio
how close to stack the dots. Default is 1, where dots just just touch. Use smaller values for closer, overlapping dots.

dotsize
The diameter of the dots relative to binwidth, default 1.

stackgroups
should dots be stacked across groups? This has the effect that position = "stack" should have, but can’t (because this geom has some odd properties).

origin
When method is "histodot", origin of first bin

right
When method is "histodot", should intervals be closed on the right (a, b], or not [a, b)

width
When binaxis is "y", the spacing of the dot stacks for dodging.

drop
If TRUE, remove all bins with zero counts

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
There are two basic approaches: dot-density and histodot. With dot-density binning, the bin positions are determined by the data and ‘binwidth’, which is the maximum width of each bin. See Wilkinson (1999) for details on the dot-density binning algorithm. With histodot binning, the bins have fixed positions and fixed widths, much like a histogram.

When binning along the x axis and stacking along the y axis, the numbers on y axis are not meaningful, due to technical limitations of ggplot2. You can hide the y axis, as in one of the examples, or manually scale it to match the number of dots.

Computed variables

x  center of each bin, if binaxis is "x"
y  center of each bin, if binaxis is "x"

binwidth  max width of each bin if method is "dotdensity"; width of each bin if method is "histodot"
count  number of points in bin
ncount  count, scaled to maximum of 1
density  density of points in bin, scaled to integrate to 1, if method is "histodot"
ndensity  density, scaled to maximum of 1, if method is "histodot"
geom_half_point

References


Examples

ggplot(iris, aes(x = Species, y = Petal.Width, fill = Species)) +
  geom_half_dotplot(stackratio = .5, method = "histodot")

--

geom_half_point    Points with jitter for half geoms.

Description

Points with jitter for half geoms.

Usage

geom_half_point(mapping = NULL, data = NULL, stat = "HalfPoint",
  position = "dodge2", ..., side = "r",
  transformation = PositionJitter, transformation_params = list(width =
  NULL, height = NULL), 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.

side       The side on which to draw the half violin plot. "l" for left, "r" for right, defaults
to "l".
transformation  A 'Position' object to calculate the transformation of the points. Defaults to
'ggplot2::PositionJitter'.

transformation_params  A 'list' containing named parameter values for the 'transformation' object. De-
defaults to 'list(width = NULL, height = NULL)'. For 'ggplot2::PositionJitter',
keyword arguments can be 'width', 'height' and 'seed'.

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
ggplot(iris, aes(x = Species, y = Petal.Width, fill = Species)) +
  geom_half_point()

ggplot(iris, aes(x = Species, y = Petal.Width, fill = Species)) +
  geom_half_point(side = "l")
```

---

**geom_half_violin**  

**Half Violin plot**

**Description**

A violin plot is a compact display of a continuous distribution. It is a blend of [geom_boxplot()] and
[geom_density()]: a violin plot is a mirrored density plot displayed in the same way as a boxplot.

**Usage**

```r
geom_half_violin(mapping = NULL, data = NULL, stat = "half_ydensity",
  position = "dodge", ..., side = "1", draw_quantiles = NULL,
  trim = TRUE, scale = "area", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE)

stat_half_ydensity(mapping = NULL, data = NULL, geom = "half_violin",
  position = "dodge", ..., bw = "nrd0", adjust = 1,
  kernel = "gaussian", trim = TRUE, scale = "area", 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**
Use to override the default connection between `geom_violin` and `stat_ydensity`.

**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.

**side**
The side on which to draw the half violin plot. "l" for left, "r" for right, defaults to "l".

**draw_quantiles**
If not(`NULL`) (default), draw horizontal lines at the given quantiles of the density estimate.

**trim**
If `TRUE` (default), trim the tails of the violins to the range of the data. If `FALSE`, don’t trim the tails.

**scale**
if "area" (default), all violins have the same area (before trimming the tails).
- If "count", areas are scaled proportionally to the number of observations. If "width", all violins have the same maximum width.

**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()`.

**geom**
Use to override the default connection between `geom_violin` and `stat_ydensity`.

**bw**
The smoothing bandwidth to be used. If numeric, the standard deviation of the smoothing kernel. If character, a rule to choose the bandwidth, as listed in `stats::bw.nrd()`.

**adjust**
A multiplicative bandwidth adjustment. This makes it possible to adjust the bandwidth while still using the a bandwidth estimator. For example, `adjust = 1/2` means use half of the default bandwidth.

**kernel**
Kernel. See list of available kernels in `density()`.
References


See Also

[geom_half_violin()] for examples.

Examples

```r
ggplot(iris, aes(x = Species, y = Petal.Width, fill = Species)) + geom_half_violin()

ggplot(iris, aes(x = Species, y = Petal.Width, fill = Species)) + geom_half_violin(side = "r")
```
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