# Package 'ggside'

July 21, 2021

**Type** Package

**Title** Side Grammar Graphics

**Version** 0.1.2

**Maintainer** Justin Landis <jtlandis314@gmail.com>

**Description** The grammar of graphics as shown in 'ggplot2' has provided an expressive API for users to build plots. 'ggside' extends 'ggplot2' by allowing users to add graphical information about one of the main panel's axis using a familiar 'ggplot2' style API with tidy data. This package is particularly useful for visualizing metadata on a discrete axis, or summary graphics on a continuous axis such as a boxplot or a density distribution.

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**Depends** ggplot2 (>= 3.0.0)

**Imports** grid, gtable, rlang, scales, glue, stats

**Suggests** tidyr, dplyr, testthat (>= 3.0.3), knitr, rmarkdown, vdiffr (>= 1.0.0), ggdendro, viridis

**Config/testthat/edition** 3

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-07-21 09:00:08 UTC

## R topics documented:

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`as_ggsideFacet` *Extending base ggproto classes for ggside*

---

## Description

S3 class that converts old Facet into one that is compatible with ggside. Can also update ggside on the object. Typically, the new ggproto will inherit from the object being replaced.

`check_scales_collapse` is a helper function that is meant to be called after the inherited Facet's compute_layout method

`sidePanelLayout` is a helper function that is meant to be called after the inherited Facet's compute_layout method and after `check_scales_collapse`

`map_data_ggside` is the mapping function used to replace all map_data method on FacetSideNull, FacetSideGrid, and FacetSideWrap. It is exported for conveniences of extensibility.

## Usage

```
as_ggsideFacet(facet, ggside)

check_scales_collapse(data, params)

sidePanelLayout(layout, ggside)

map_data_ggside(data, layout, params)
```

### Arguments

| | |
|---|---|
| facet | Facet ggproto Object to replace |
| ggside | ggside object to update |
| data | data passed through ggproto object |
| params | parameters passed through ggproto object |
| layout | layout computed by inherited ggproto Facet compute_layout method |

### Value

ggproto object that can be added to a ggplot object

### Extended Facets

The following is a list ggplot2 facets that are available to use by ggside base.

- FacetNull -> FacetSideNull
- FacetGrid -> FacetSideGrid
- FacetWrap -> FacetSideWrap

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## geom_xsidebar *Side bar Charts*

---

### Description

The xside and yside variants of geom_bar is geom_xsidebar and geom_ysidebar. These variants both inherit from geom_bar and only differ on where they plot data relative to main panels.

The xside and yside variants of geom_col is geom_xsidecol and geom_ysidecol. These variants both inherit from geom_col and only differ on where they plot data relative to main panels.

### Usage

```
geom_xsidebar(
  mapping = NULL,
  data = NULL,
  stat = "count",
  position = "stack",
  ...,
  width = NULL,
  na.rm = FALSE,
  orientation = "x",
  show.legend = NA,
  inherit.aes = TRUE
)

geom_ysidebar(
```

```
  mapping = NULL,
  data = NULL,
  stat = "count",
  position = "stack",
  ...,
  width = NULL,
  na.rm = FALSE,
  orientation = "y",
  show.legend = NA,
  inherit.aes = TRUE
)

geom_xsidecol(
  mapping = NULL,
  data = NULL,
  position = "stack",
  ...,
  width = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_ysidecol(
  mapping = NULL,
  data = NULL,
  position = "stack",
  ...,
  width = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  orientation = "y"
)
```

## 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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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` | Override the default connection between `geom_bar()` and `stat_count()`. |
| `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. |
| `width` | Bar width. By default, set to 90% of the resolution of the data. |
| `na.rm` | If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed. |
| `orientation` | The orientation of the layer. The default (`NA`) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting `orientation` to either `"x"` or `"y"`. See the *Orientation* section for more detail. |
| `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()`. |

## Value

XLayer or YLayer object to be added to a ggplot object

## Aesthetics

Required aesthetics are in bold.

- `x`
- `y`
- `fill` *or* `xfill` Fill color of the xsidebar
- `fill` *or* `yfill` Fill color of the ysidebar
- `width` specifies the width of each bar
- `height` specifies the height of each bar
- `alpha` Transparency level of `xfill` or `yfill`
- `size` size of the border line.

## See Also

geom_xsidehistogram, geom_ysidehistogram

## Examples

```
p <-ggplot(iris, aes(Sepal.Width, Sepal.Length, color = Species, fill = Species)) +
geom_point()

#sidebar - uses StatCount
p +
geom_xsidebar() +
geom_ysidebar()

#sidecol - uses Global mapping
p +
  geom_xsidecol() +
  geom_ysidecol()
```

---

geom_xsideboxplot *Side boxplots*

---

## Description

The xside and yside variants of geom_boxplot is geom_xsideboxplot and geom_ysideboxplot.

## Usage

```
geom_xsideboxplot(
  mapping = NULL,
  data = NULL,
  stat = "boxplot",
  position = "dodge2",
  ...,
  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,
  na.rm = FALSE,
  orientation = "x",
  show.legend = NA,
  inherit.aes = TRUE
)

geom_ysideboxplot(
```

```
  mapping = NULL,
  data = NULL,
  stat = "boxplot",
  position = "dodge2",
  ...,
  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,
  na.rm = FALSE,
  orientation = "y",
  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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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. |
| outlier.colour | Default aesthetics for outliers. Set to NULL to inherit from the aesthetics used for the box.<br>In the unlikely event you specify both US and UK spellings of colour, the US spelling will take precedence.<br>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.color` 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.fill` 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.shape` 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.size` 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.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).

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

`orientation` The orientation of the layer. The default (`NA`) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting `orientation` to either `"x"` or `"y"`. See the *Orientation* section for more detail.

`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()`.

## Value

XLayer or YLayer object to be added to a ggplot object

## See Also

geom_*sideviolin

## Examples

```
df <- expand.grid(UpperCase = LETTERS, LowerCase = letters)
df$Combo_Index <- as.integer(df$UpperCase)*as.integer(df$LowerCase)

p1 <- ggplot(df, aes(UpperCase, LowerCase)) +
```

```
geom_tile(aes(fill = Combo_Index))

#sideboxplots
#Note - Mixing discrete and continuous axis scales
#using xsideboxplots when the y aesthetic was previously
#mapped with a continuous varialbe will prevent
#any labels from being plotted. This is a feature that
#will hopefully be added to ggside in the future.

p1 + geom_xsideboxplot(aes(y = Combo_Index)) +
   geom_ysideboxplot(aes(x = Combo_Index))

#sideboxplots with swapped orientation
#Note - Discrete before Continuous
#If you are to mix Discrete and Continuous variables on
#one axis, ggplot2 prefers the discrete variable to be mapped
#BEFORE the continuous.
ggplot(iris, aes(Sepal.Width, Sepal.Length, color = Species)) +
    geom_xsideboxplot(aes(y = Species), orientation = "y") +
    geom_point()

#Alternatively, you can recast discrete as a factor and then
#a numeric
ggplot(iris, aes(Sepal.Width, Sepal.Length, color = Species))+
  geom_point() +
  geom_xsideboxplot(aes(y = as.numeric(Species)), orientation = "y") +
  geom_ysideboxplot(aes(x = as.numeric(Species)), orientation = "x")
```

---

`geom_xsidedensity` *Side density distributions*

---

## Description

The xside and yside variants of geom_density is geom_xsidedensity and geom_ysidedensity.

## Usage

```
geom_xsidedensity(
  mapping = NULL,
  data = NULL,
  stat = "density",
  position = "identity",
  ...,
  na.rm = FALSE,
  orientation = "x",
  show.legend = NA,
  inherit.aes = TRUE,
  outline.type = "upper"
```

```
)

geom_ysidedensity(
  mapping = NULL,
  data = NULL,
  stat = "density",
  position = "identity",
  ...,
  na.rm = FALSE,
  orientation = "y",
  show.legend = NA,
  inherit.aes = TRUE,
  outline.type = "upper"
)
```

## 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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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_density() and stat_density(). |
| 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. |
| orientation | The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the *Orientation* section for more detail. |
| 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(). |

`outline.type` Type of the outline of the area; `"both"` draws both the upper and lower lines, `"upper"`/`"lower"` draws the respective lines only. `"full"` draws a closed polygon around the area.

## Value

XLayer or YLayer object to be added to a ggplot object

## Examples

```
ggplot(mpg, aes(displ, hwy, colour = class)) +
 geom_point(size = 2) +
 geom_xsidedensity() +
 geom_ysidedensity() +
 theme(axis.text.x = element_text(angle = 90, vjust = .5))

ggplot(mpg, aes(displ, hwy, colour = class)) +
 geom_point(size = 2) +
 geom_xsidedensity(aes(y = after_stat(count)),position = "stack") +
 geom_ysidedensity(aes(x = after_stat(scaled))) +
 theme(axis.text.x = element_text(angle = 90, vjust = .5))
```

---

# geom_xsidefreqpoly *Side Frequency Polygons*

---

## Description

The xside and yside variants of geom_freqpoly is geom_xsidefreqpoly and geom_ysidefreqpoly.

## Usage

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

geom_ysidefreqpoly(
  mapping = NULL,
  data = NULL,
  stat = "bin",
```

```
  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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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_histogram()/geom_freqpoly() and stat_bin(). |
| 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(). |

## Value

XLayer or YLayer object to be added to a ggplot object

## Examples

```
ggplot(diamonds, aes(price, carat, colour = cut)) +
  geom_point() +
  geom_xsidefreqpoly(aes(y=after_stat(count)),binwidth = 500) +
  geom_ysidefreqpoly(aes(x=after_stat(count)),binwidth = .2)
```

`geom_xsidehistogram` *Side Histograms*

## Description

The xside and yside variants of geom_histogram is geom_xsidehistogram and geom_ysidehistogram. These variants both inherit from geom_histogram and only differ on where they plot data relative to main panels.

## Usage

```
geom_xsidehistogram(
  mapping = NULL,
  data = NULL,
  stat = "bin",
  position = "stack",
  ...,
  binwidth = NULL,
  bins = NULL,
  na.rm = FALSE,
  orientation = "x",
  show.legend = NA,
  inherit.aes = TRUE
)

geom_ysidehistogram(
  mapping = NULL,
  data = NULL,
  stat = "bin",
  position = "stack",
  ...,
  binwidth = NULL,
  bins = NULL,
  na.rm = FALSE,
  orientation = "y",
  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:<br>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.<br>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_histogram()/geom_freqpoly() and stat_bin(). |
| 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 | 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 the number of bins in bins, covering 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.<br>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. |
| na.rm | If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed. |
| orientation | The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the *Orientation* section for more detail. |
| 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(). |

## Value

XLayer or YLayer object to be added to a ggplot object

## Aesthetics

geom_*sidehistogram uses the same aesthetics as geom_*sidebar()

## Examples

```
p <-ggplot(iris, aes(Sepal.Width, Sepal.Length, color = Species, fill = Species)) +
geom_point()

#sidehistogram
p +
geom_xsidehistogram(binwidth = 0.1) +
geom_ysidehistogram(binwidth = 0.1)
p +
geom_xsidehistogram(aes(y = after_stat(density)), binwidth = 0.1) +
geom_ysidehistogram(aes(x = after_stat(density)), binwidth = 0.1)
```

---

# geom_xsideline *Side line plot*

---

## Description

The xside and yside of geom_line. The xside and yside variants of geom_path

## Usage

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

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

geom_xsidepath(
```

```
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
  arrow = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_ysidepath(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
  arrow = 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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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. |
| na.rm | If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed. |

| | |
|---|---|
| orientation | The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the *Orientation* section for more detail. |
| 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. |
| lineend | Line end style (round, butt, square). |
| linejoin | Line join style (round, mitre, bevel). |
| linemitre | Line mitre limit (number greater than 1). |
| arrow | Arrow specification, as created by grid::arrow(). |

## Value

XLayer or YLayer object to be added to a ggplot object

## Examples

```
#sideline
ggplot(economics, aes(date, pop)) +
  geom_xsideline(aes(y = unemploy)) +
  geom_col()
```

---

# geom_xsidepoint *Side Points*

---

## Description

The ggside variants of geom_point is geom_xsidepoint() and geom_ysidepoint(). Both variants inherit from geom_point, thus the only difference is where the data is plotted. The xside variant will plot data along the x-axis, while the yside variant will plot data along the y-axis.

## Usage

```
geom_xsidepoint(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
```

```
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_ysidepoint(
  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() 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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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(). |

## Value

XLayer or YLayer object to be added to a ggplot object

## Examples

```
ggplot(diamonds, aes(depth, table, alpha = .2)) +
  geom_point() +
  geom_ysidepoint(aes(x = price)) +
  geom_xsidepoint(aes(y = price)) +
  theme(
        ggside.panel.scale = .3
    )
```

---

geom_xsidesegment *Side line Segments*

---

## Description

The xside and yside of geom_segment.

## Usage

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

geom_ysidesegment(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  arrow = NULL,
  arrow.fill = NULL,
  lineend = "butt",
  linejoin = "round",
  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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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. |
| arrow | specification for arrow heads, as created by arrow(). |
| arrow.fill | fill colour to use for the arrow head (if closed). NULL means use colour aesthetic. |
| 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(). |

## Value

XLayer or YLayer object to be added to a ggplot object

## Examples

```
library(dplyr)
library(tidyr)
library(ggdendro)
#dendrogram with geom_*sidesegment
df0 <- mutate(diamonds,
colclar = interaction(color, clarity,
```

```
                      sep = "_", drop = TRUE))
df1 <- df0 %>%
  group_by(color, clarity, colclar, cut) %>%
  summarise(m_price = mean(price))
df <- df1 %>%
  pivot_wider(id_cols = colclar,
              names_from = cut,
              values_from = m_price,
              values_fill = 0L)

mat <- as.matrix(df[,2:6])
rownames(mat) <- df[["colclar"]]
dst <- dist(mat)
hc_x <- hclust(dst)
lvls <- rownames(mat)[hc_x$order]
df1[["colclar"]] <- factor(df1[["colclar"]], levels = lvls)
dendrox <- dendro_data(hc_x)

p <- ggplot(df1, aes(x = colclar, cut)) +
  geom_tile(aes(fill = m_price)) +
  viridis::scale_fill_viridis(option = "magma") +
  theme(axis.text.x = element_text(angle = 90, vjust = .5))
p +
  geom_xsidesegment(data = dendrox$segments,aes(x = x, y = y, xend = xend, yend = yend))
```

---

geom_xsidetext *Side text*

---

## Description

The xside and yside variants of geom_text.

## Usage

```
geom_xsidetext(
  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
)
```

```
geom_ysidetext(
  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() 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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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. 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 | Horizontal and vertical adjustment to nudge labels by. Useful for offsetting text from points, particularly on discrete scales. Cannot be jointly specified with position. |
| nudge_y | Horizontal and vertical adjustment to nudge labels by. Useful for offsetting text from points, particularly on discrete scales. Cannot be jointly specified with position. |
| 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(). |

## Value

XLayer or YLayer object to be added to a ggplot object

---

# geom_xsidetile *Side tile plot*

---

## Description

The xside and yside variants of geom_tile

## Usage

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

geom_ysidetile(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  linejoin = "mitre",
  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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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. |
| 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(). |

## Value

XLayer or YLayer object to be added to a ggplot object

## Examples

```
library(dplyr)
library(tidyr)
df <- mutate(diamonds,
             colclar = interaction(color, clarity, sep = "_", drop = TRUE)) %>%
      group_by(color, clarity, colclar, cut) %>%
      summarise(m_price = mean(price))

xside_data <- df %>%
  ungroup() %>%
  select(colclar, clarity, color) %>%
  mutate_all(~factor(as.character(.x), levels = levels(.x))) %>%
```

```
  pivot_longer(cols = c(clarity, color)) %>% distinct()


p <- ggplot(df, aes(x = colclar, cut)) +
  geom_tile(aes(fill = m_price)) +
  viridis::scale_fill_viridis(option = "magma") +
  theme(axis.text.x = element_blank())

p + geom_xsidetile(data = xside_data, aes(y = name, xfill = value)) +
   guides(xfill = guide_legend(nrow = 8))
```

---

`geom_xsideviolin` *Side Violin plots*

---

## Description

The xside and yside variants of geom_violin

## Usage

```
geom_xsideviolin(
  mapping = NULL,
  data = NULL,
  stat = "ydensity",
  position = "dodge",
  ...,
  draw_quantiles = NULL,
  trim = TRUE,
  scale = "area",
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_ysideviolin(
  mapping = NULL,
  data = NULL,
  stat = "ydensity",
  position = "dodge",
  ...,
  draw_quantiles = NULL,
  trim = TRUE,
  scale = "area",
  na.rm = FALSE,
  orientation = "y",
  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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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. |
| 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. |
| orientation | The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the *Orientation* section for more detail. |
| 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(). |

## Value

XLayer or YLayer object to be added to a ggplot object

## See Also

geom_*sideboxplot

## Examples

```
df <- expand.grid(UpperCase = LETTERS, LowerCase = letters)
df$Combo_Index <- as.integer(df$UpperCase)*as.integer(df$LowerCase)

p1 <- ggplot(df, aes(UpperCase, LowerCase)) +
geom_tile(aes(fill = Combo_Index))

#sideviolins
#Note - Mixing discrete and continuous axis scales
#using xsideviolins when the y aesthetic was previously
#mapped with a continuous varialbe will prevent
#any labels from being plotted. This is a feature that
#will hopefully be added to ggside in the future.

p1 + geom_xsideviolin(aes(y = Combo_Index)) +
   geom_ysideviolin(aes(x = Combo_Index))

#sideviolins with swapped orientation
#Note - Discrete before Continuous
#If you are to mix Discrete and Continuous variables on
#one axis, ggplot2 prefers the discrete variable to be mapped
#BEFORE the continuous.
ggplot(iris, aes(Sepal.Width, Sepal.Length, color = Species)) +
    geom_xsideviolin(aes(y = Species), orientation = "y") +
    geom_point()

#Alternatively, you can recast the value as a factor and then
# a numeric

ggplot(iris, aes(Sepal.Width, Sepal.Length, color = Species))+
    geom_point() +
    geom_xsideviolin(aes(y = as.numeric(Species)), orientation = "y") +
    geom_ysideviolin(aes(x = as.numeric(Species)), orientation = "x")
```

---

`ggside` *ggside options*

---

## Description

Set characteristics of side panels

## Usage

```
ggside(x.pos = "top", y.pos = "right", scales = "fixed", collapse = NULL)
```

## Arguments

| | |
|---|---|
| `x.pos` | x side panel can either take "top" or "bottom" |

| | |
|---|---|
| y.pos | y side panel can either take "right" or "left" |
| scales | Determines side panel's unaligned axis scale. Inputs are similar to facet_* scales function. Default is set to "fixed", but "free_x", "free_y" and "free" are acceptable inputs. For example, xside panels are aligned to the x axis of the main panel. Setting "free" or "free_y" will cause all y scales of the x side Panels to be independent. |
| collapse | Determines if side panels should be collapsed into a single panel. Set "x" to collapse all x side panels, set "y" to collapse all y side panels, set "all" to collapse both x and y side panels. |

## Value

a object of class 'ggside_options' or to be added to a ggplot

## See Also

For more information regarding the ggside api: see xside or yside

---

`ggside-scales-continuous`

*Position scales for continuous data ggside scales*

---

## Description

The xside and yside variants of scale_x_continuous/scale_y_continuous. scale_xsidey_continuous enables better control on how the y-axis is rendered on the xside panel and scale_ysidex_continuous enables better control on how the x-axis is rendered on the yside panel.

## Arguments

| | |
|---|---|
| name | The name of the scale. Used as the axis or legend title. If `waiver()`, the default, the name of the scale is taken from the first mapping used for that aesthetic. If `NULL`, the legend title will be omitted. |
| breaks | One of:<br>• `NULL` for no breaks<br>• `waiver()` for the default breaks computed by the transformation object<br>• A numeric vector of positions<br>• A function that takes the limits as input and returns breaks as output (e.g., a function returned by `scales::extended_breaks()`). Also accepts rlang lambda function notation. |
| minor_breaks | One of:<br>• `NULL` for no minor breaks<br>• `waiver()` for the default breaks (one minor break between each major break)<br>• A numeric vector of positions |

- A function that given the limits returns a vector of minor breaks. Also accepts rlang lambda function notation.

`n.breaks` An integer guiding the number of major breaks. The algorithm may choose a slightly different number to ensure nice break labels. Will only have an effect if `breaks = waiver()`. Use `NULL` to use the default number of breaks given by the transformation.

`labels` One of:

- `NULL` for no labels
- `waiver()` for the default labels computed by the transformation object
- A character vector giving labels (must be same length as `breaks`)
- A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

`limits` One of:

- `NULL` to use the default scale range
- A numeric vector of length two providing limits of the scale. Use `NA` to refer to the existing minimum or maximum
- A function that accepts the existing (automatic) limits and returns new limits. Also accepts rlang lambda function notation. Note that setting limits on positional scales will **remove** data outside of the limits. If the purpose is to zoom, use the limit argument in the coordinate system (see `coord_cartesian()`).

`expand` For position scales, a vector of range expansion constants used to add some padding around the data to ensure that they are placed some distance away from the axes. Use the convenience function `expansion()` to generate the values for the `expand` argument. The defaults are to expand the scale by 5% on each side for continuous variables, and by 0.6 units on each side for discrete variables.

`oob` One of:

- Function that handles limits outside of the scale limits (out of bounds). Also accepts rlang lambda function notation.
- The default (`scales::censor()`) replaces out of bounds values with `NA`.
- `scales::squish()` for squishing out of bounds values into range.
- `scales::squish_infinite()` for squishing infinite values into range.

`na.value` Missing values will be replaced with this value.

`trans` For continuous scales, the name of a transformation object or the object itself. Built-in transformations include "asn", "atanh", "boxcox", "date", "exp", "hms", "identity", "log", "log10", "log1p", "log2", "logit", "modulus", "probability", "probit", "pseudo_log", "reciprocal", "reverse", "sqrt" and "time".

A transformation object bundles together a transform, its inverse, and methods for generating breaks and labels. Transformation objects are defined in the scales package, and are called <name>_trans (e.g., `scales::boxcox_trans()`). You can create your own transformation with `scales::trans_new()`.

`guide` A function used to create a guide or its name. See `guides()` for more information.

`position` For position scales, The position of the axis. `left` or `right` for y axes, `top` or `bottom` for x axes.

## Value

ggside_scale object inheriting from ggplot2::ScaleContinuousPosition

## Examples

```
library(ggside)
library(ggplot2)
# adding continuous y-scale to the x-side panel, when main panel mapped to discrete data
ggplot(mpg, aes(hwy, class, colour = class)) +
  geom_boxplot() +
  geom_xsidedensity(position = "stack") +
  theme(ggside.panel.scale = .3) +
  scale_xsidey_continuous(minor_breaks = NULL, limits = c(NA,1))

#If you need to specify the main scale, but need to prevent this from
#affecting the side scale. Simply add the appropriate `scale_*side*_*()` function.
ggplot(mtcars, aes(wt, mpg)) +
  geom_point() +
  geom_xsidehistogram() +
  geom_ysidehistogram()  +
  scale_x_continuous(
      breaks = seq(1, 6, 1),
      #would otherwise remove the histogram
      #as they have a lower value of 0.
      limits = (c(1, 6))
      ) +
  scale_ysidex_continuous() #ensures the x-axis of the y-side panel has its own scale.
```

---

# ggside-scales-discrete

*Position scales for discrete data ggside scales*

---

## Description

The xside and yside variants of scale_x_discrete/scale_y_discrete. scale_xsidey_discrete enables better control on how the y-axis is rendered on the xside panel and scale_ysidex_discrete enables better control on how the x-axis is rendered on the yside panel.

## Arguments

| | |
|---|---|
| expand | For position scales, a vector of range expansion constants used to add some padding around the data to ensure that they are placed some distance away from the axes. Use the convenience function `expansion()` to generate the values for the expand argument. The defaults are to expand the scale by 5% on each side for continuous variables, and by 0.6 units on each side for discrete variables. |
| guide | A function used to create a guide or its name. See `guides()` for more information. |

position For position scales, The position of the axis. `left` or `right` for y axes, `top` or `bottom` for x axes.

## Value

ggside_scale object inheriting from ggplot2::ScaleDiscretePosition

## Examples

```
library(ggside)
library(ggplot2)
# adding discrete y-scale to the x-side panel, when main panel mapped to continuous data
ggplot(mpg, aes(displ, hwy, colour = class)) +
  geom_point() +
  geom_xsideboxplot(aes(y=class), orientation = "y") +
  theme(ggside.panel.scale = .3) +
  scale_xsidey_discrete(guide = guide_axis(angle = 45))

#If you need to specify the main scale, but need to prevent this from
#affecting the side scale. Simply add the appropriate `scale_*side*_*()` function.
ggplot(mpg, aes(class, displ)) +
  geom_boxplot() +
  geom_ysideboxplot(aes(x = "all"), orientation = "x") +
  scale_x_discrete(guide = guide_axis(angle = 90)) + #rotate the main panel text
  scale_ysidex_discrete() #leave side panel as default
```

---

# ggside-theme *ggside custom themes*

---

## Description

the following are the theme elements defined in ggside.

## Elements

- ggside.panel.scale - sets the scaling of side panels relative to the plotting width of the main panels. Default is set to 0.1, i.e. 0.1/1
- ggside.panel.scale.x - same as ggside.panel.scale except only for the xside panel.
- ggside.panel.scale.y - same as ggside.panel.scale except only for the yside panel.
- ggside.panel.spacing - sets how much spacing should be used between the main panels and the side panels. default is unit(2,"pt")
- ggside.panel.spacing.x - same as ggside.panel.spacing except only for the space between the main panel and the yside panel.
- ggside.panel.spacing.y - same as ggside.panel.spacing except only for the space between the main panel and the xside panel.

## is.ggside *Check ggside objects*

### Description

Check ggside objects

### Usage

```
is.ggside(x)

is.ggside_layer(x)

is.ggside_options(x)

is.ggside_scale(x)
```

### Arguments

| | |
|---|---|
| x | Object to test |

### Value

A logical value

## position_rescale *Rescale x or y onto new range in margin*

### Description

Take the range of the specified axis and rescale it to a new range about a midpoint. By default the range will be calculated from the associated main plot axis mapping. The range will either be the resolution or 5% of the axis range, depending if original data is discrete or continuous respectively. Each layer called with position_rescale will possess an instance value that indexes with axis rescale. By default, each position_rescale will dodge the previous call unless instance is specified to a previous layer.

### Usage

```
position_rescale(
  rescale = "y",
  midpoint = NULL,
  range = NULL,
  location = NULL,
  instance = NULL
)
```

```
position_yrescale(
  rescale = "y",
  midpoint = NULL,
  range = NULL,
  location = NULL,
  instance = NULL
)

position_xrescale(
  rescale = "x",
  midpoint = NULL,
  range = NULL,
  location = NULL,
  instance = NULL
)
```

## Arguments

| | |
|---|---|
| rescale | character value of "x" or "y". specifies which mapping data will be rescaled |
| midpoint | default set to NULL. Center point about which the rescaled x/y values will reside. |
| range | default set to NULL and auto generates from main mapping range. Specifies the size of the rescaled range. |
| location | specifies where position_rescale should try to place midpoint. If midpoint is specified, location is ignored and placed at the specified location. |
| instance | integer that indexes rescaled axis calls. instance may be specified and if a previous layer with the same instance exists, then the same midpoint and range are used for rescaling. x and y are indexed independently. |

## Format

An object of class `PositionRescale` (inherits from `Position`, `ggproto`, `gg`) of length 10.

## Value

a ggproto object inheriting from 'Position' and can be added to a ggplot

---

`scale_xcolour` *Scales for the *colour aesthetics*

---

## Description

These are the various scales that can be applied to the xsidebar or ysidebar colour aesthetics, such as xcolour and ycolour. They have the same usage as existing standard ggplot2 scales.

### Value

returns a ggproto object to be added to a ggplot

### Related Functions

- scale_xcolour_hue
- scale_ycolour_hue
- scale_xcolour_discrete
- scale_ycolour_discrete
- scale_xcolour_continuous
- scale_ycolour_continuous
- scale_xcolour_manual
- scale_ycolour_manual
- scale_xcolour_gradient
- scale_ycolour_gradient
- scale_xcolour_gradientn
- scale_ycolour_gradientn

---

## scale_xfill *Scales for the *fill aesthetics*

---

### Description

These are the various scales that can be applied to the xsidebar or ysidebar fill aesthetics, such as xfill and yfill. They have the same usage as existing standard ggplot2 scales.

### Value

returns a ggproto object to be added to a ggplot

### Related Functions

- scale_xfill_hue
- scale_yfill_hue
- scale_xfill_discrete
- scale_yfill_discrete
- scale_xfill_continuous
- scale_yfill_continuous
- scale_xfill_manual
- scale_yfill_manual
- scale_xfill_gradient
- scale_yfill_gradient
- scale_xfill_gradientn
- scale_yfill_gradientn

`scale_ycolour_hue` *scale_ycolour_hue*

## Description

scale_ycolour_hue

scale_ycolour_manual

scale_ycolour_gradient

scale_ycolour_discrete

scale_ycolour_discrete

scale_ycolour_continuous

scale_ycolour_continuous

`scale_yfill_hue` *scale_yfill_hue*

## Description

scale_yfill_hue

scale_yfill_manual

scale_yfill_gradient

scale_yfill_discrete

scale_yfill_continuous

`stat_summarise` *Summarise by grouping variable*

## Description

Applies a function to a specified grouping variable

## Usage

```
stat_summarise(
  mapping = NULL,
  data = NULL,
  geom = "bar",
  position = "identity",
  ...,
  fun = NULL,
  args = list(),
  show.legend = NA,
  inherit.aes = TRUE
)

stat_summarize(
  mapping = NULL,
  data = NULL,
  geom = "bar",
  position = "identity",
  ...,
  fun = NULL,
  args = list(),
  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:<br>If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().<br>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.<br>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 | The geometric object to use display the data |
| position | Position adjustment, either as a string, or the result of a call to a position adjustment function. |
| ... | additional arguments to pass to layer. |
| fun | Summarising function to use. If no function provided it will default to length. |
| args | List of additional arguments passed to the function. |

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().

## Format

An object of class StatSummarise (inherits from Stat, ggproto, gg) of length 5.

An object of class StatSummarize (inherits from Stat, ggproto, gg) of length 5.

## Value

A Layer object to be added to a ggplot

## Aesthetics

Using stat_summarise requires that you use domain as an aesthetic mapping. This allows you to summarise other data instead of assuming that x is the function's domain.

## Examples

```
library(tidyr)
i <- gather(iris,"key","value",-Species)
ggplot(i, aes(Species, fill = key, domain = value)) +
   geom_bar(aes(y = after_stat(summarise)), stat = "summarise", fun = mean) +
   stat_summarise(aes(y = after_stat(summarise),
                  label = after_stat(summarise)),
                  position = position_stack(vjust = .5), geom = "text", fun = mean)
```

---

# use_xside_aes *Extending base ggproto classes for ggside*

---

## Description

These ggproto classes are slightly modified from their respective inherited ggproto class. The biggest difference is exposing 'x/yfill', 'x/ycolour', and 'x/ycolor' as viable aesthetic mappings.

## Usage

```
use_xside_aes(data)

use_yside_aes(data)

parse_side_aes(data, params)
```

### Arguments

| | |
|---|---|
| `data` | data passed internally |
| `params` | params available to ggproto object |

### Value

ggproto object that is usually passed to layer

---

## `xside` *The xside geometries*

---

### Description

`xside` refers to the api of ggside. Any `geom_` with `xside` will plot its respective geometry along the x-axis per facet panel. By default the xside panel will plot above the main panel. This xside panel will always share the same scale as it's main panel, but is expected to have a separate y-axis scaling.

### Value

geom_xside* return a XLayer object to be added to a ggplot

### New Aesthetics

All `xside` Geometries have `xfill`, `xcolour`/`xcolor` available for aesthetic mappings. These mappings behave exactly like the default counterparts except that they are considered separate scales. All `xside` geometries will use `xfill` over `fill`, but will default to `fill` if `xfill` is not provided. The same goes for `xcolour` in respects to `colour`. This comes in handy if you wish to map both `fill` to one geometry as continuous, you can still map `xfill` for a separate `xside` geometry without conflicts. See more information in `vignette("ggside")`.

### Exported Geometries

The following are the `xside` variants of the ggplot2 Geometries

- geom_xsidebar
- geom_xsideboxplot
- geom_xsidecol
- geom_xsidedensity
- geom_xsidefreqpoly
- geom_xsidehistogram
- geom_xsideline
- geom_xsidepath
- geom_xsidepoint
- geom_xsidetext
- geom_xsidetile
- geom_xsideviolin

## See Also

yside

---

`yside` *The yside geometries*

---

## Description

`yside` refers to the api of ggside. Any `geom_` with `yside` will plot its respective geometry along the y-axis per facet panel. The yside panel will plot to the right of the main panel by default. This yside panel will always share the same scale as it's main panel, but is expected to have a separate x-axis scaling.

## Value

geom_yside* return a YLayer object to be added to a ggplot

## New Aesthetics

All `yside` Geometries have `yfill`, `ycolour`/`ycolor` available for aesthetic mappings. These mappings behave exactly like the default counterparts except that they are considered separate scales. All `yside` geometries will use `yfill` over `fill`, but will default to `fill` if `yfill` is not provided. The same goes for `ycolour` in respects to `colour`. This comes in handy if you wish to map both `fill` to one geometry as continuous, you can still map `yfill` for a separate `yside` geometry without conflicts. See more information in `vignette("ggside")`.

#' @section Exported Geometries:

The following are the `yside` variants of the ggplot2 Geometries

- geom_ysidebar
- geom_ysideboxplot
- geom_ysidecol
- geom_ysidedensity
- geom_ysidefreqpoly
- geom_ysidehistogram
- geom_ysideline
- geom_ysidepath
- geom_ysidepoint
- geom_ysidetext
- geom_ysidetile
- geom_ysideviolin

## See Also

xside

# Index