

# Package ‘ggpmisc’

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**Type** Package

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**Description** Extensions to 'ggplot2' respecting the grammar of graphics paradigm. Specialization of method ggplot(): accept and convert on the fly time series data. Geom: ``table``, ``plot`` and ``grob`` add insets to plots using native data coordinates, while ``table\_npc``, ``plot\_npc`` and ``grob\_npc`` do the same using ``npc`` coordinates through new aesthetics ``npcx`` and ``npcy``. Statistics: locate and tag peaks and valleys; count observations in different quadrants of a plot; select observations based on 2D density; label with the equation of a polynomial fitted with lm() or other types of models; labels with P-value, R<sup>2</sup> or adjusted R<sup>2</sup> or information criteria for fitted models; label with ANOVA table for fitted models; label with summary for fitted models. Model fit classes for which suitable methods are provided by package 'broom' are supported. Scales and stats to build volcano and quadrant plots based on outcomes, fold changes, p-values and false discovery rates.

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<https://bitbucket.org/aphalo/ggpmisc>

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ggpmisc-package	<i>ggpmisc: Miscellaneous Extensions to 'ggplot2'</i>
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## Description

Extensions to 'ggplot2' respecting the grammar of graphics paradigm. Specialization of method `ggplot()`: accept and convert on the fly time series data. Geom: "table", "plot" and "grob" add insets to plots using native data coordinates, while "table\_npc", "plot\_npc" and "grob\_npc" do the same using "npc" coordinates through new aesthetics "npcx" and "npcy". Statistics: locate and tag peaks and valleys; count observations in different quadrants of a plot; select observations based on 2D density; label with the equation of a polynomial fitted with `lm()` or other types of models; labels with P-value,  $R^2$  or adjusted  $R^2$  or information criteria for fitted models; label with ANOVA table for fitted models; label with summary for fitted models. Model fit classes for which suitable methods are provided by package 'broom' are supported. Scales and stats to build volcano and quadrant plots based on outcomes, fold changes, p-values and false discovery rates.

## Details

The new facilities for cleanly defining new stats and geoms added to 'ggplot2' in version 2.0.0 and the support for nested tibbles and new syntax for mapping computed values to aesthetics added to 'ggplot2' in version 3.0.0 are used in this package's code. This means that 'ggpmisc' ( $\geq 0.3.0$ ) requires version 3.0.0 or later of ggplot2 while 'ggpmisc' ( $< 0.3.0$ ) requires version 2.0.0 or later of ggplot2.

Extensions provided:

- Function for conversion of time series data into tibbles that can be plotted with `ggplot`.
- `ggplot()` method for time series data.
- Stats for locating and tagging "peaks" and "valleys" (local or global maxima and minima).
- Stat for generating labels from a `lm()` model fit, including formatted equation. By default labels are expressions but tikz device is supported optionally with LaTeX formatted labels.
- Stats for extracting information from a any model fit supported by package 'broom'.
- Stats for filtering-out/filtering-in observations in regions of a panel or group where the density of observations is high.
- Geom for annotating plots with tables.

The stats for peaks and valleys are coded so as to work correctly both with numeric and POSIXct variables mapped to the x aesthetic. Special handling was needed as text labels are generated from the data.

**Warning!**

`geom_null()`, `stat_debug_group()`, `stat_debug_panel()`, `geom_debug()`, `append_layers()`, `bottom_layer()`, `delete_layers()`, `extract_layers()`, `move_layers()`, `num_layers()`, `shift_layers()`, `top_layer()` and `which_layers()` have been moved from package 'ggpmisc' into their own separate package '[gginnards-package](#)'.

**Acknowledgements**

We thank Kamil Slowikowski not only for contributing ideas and code examples to this package but also for adding new features to his package 'ggrepel' that allow new use cases for `stat_dens2d_labels` from this package.

**Note**

The signatures of `stat_peaks()` and `stat_valleys()` are identical to those of `stat_peaks` and `stat_valleys` from package `photobiology` but the variables returned are a subset as values related to light spectra are missing. Furthermore the stats from package `ggpmisc` work correctly when the `x` aesthetic uses a date or datetime scale, while those from package `photobiology` do not generate correct labels in this case.

**Author(s)**

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Other contributors:

- Kamil Slowikowski [contributor]

**References**

Package suite 'r4photobiology' web site at <https://www.r4photobiology.info/>

Package 'ggplot2' documentation at <https://ggplot2.tidyverse.org/>

Package 'ggplot2' source code at <https://github.com/tidyverse/ggplot2>

**See Also**

Useful links:

- <https://docs.r4photobiology.info/ggpmisc/>
- <https://bitbucket.org/aphalo/ggpmisc>
- Report bugs at <https://bitbucket.org/aphalo/ggpmisc/issues>

**Examples**

```
library(tibble)

ggplot(lynx, as.numeric = FALSE) + geom_line() +
  stat_peaks(colour = "red") +
  stat_peaks(geom = "text", colour = "red", angle = 66,
            hjust = -0.1, x.label.fmt = "%Y") +
  ylim(NA, 8000)
```

```
formula <- y ~ poly(x, 2, raw = TRUE)
ggplot(cars, aes(speed, dist)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(aes(label = stat(eq.label)), formula = formula,
               parse = TRUE)

formula <- y ~ x
ggplot(PlantGrowth, aes(group, weight)) +
  stat_summary(fun.data = "mean_se") +
  stat_fit_tb(method = "lm",
              method.args = list(formula = formula),
              tb.type = "fit.anova") +
  theme_classic()
```

---

annotate

*Annotations supporting NPC*

---

## Description

A revised version of `annotate()` from package 'ggplot2' adding support for `npcx` and `npcy` position aesthetics, allowing use of the geometries defined in the current package such as `geom_text_npc()`. It also has a parameter `label` that directly accepts data frames, ggplots and grobs as arguments in addition to objects of atomic classes like character. When package 'ggpmisc' is loaded this definition of `annotate()` overrides that in package 'ggplot2'.

## Usage

```
annotate(
  geom,
  x = NULL,
  y = NULL,
  xmin = NULL,
  xmax = NULL,
  ymin = NULL,
  ymax = NULL,
  xend = NULL,
  yend = NULL,
  npcx = NULL,
  npcy = NULL,
  label = NULL,
  ...,
  na.rm = FALSE
)
```

## Arguments

<code>geom</code>	character Name of geom to use for annotation.
<code>x, y, xmin, ymin, xmax, ymax, xend, yend, npcx, npcy</code>	numeric Positioning aesthetics - you must specify at least one of these.
<code>label</code>	character, data.frame, ggplot or grob.
<code>...</code>	Other named arguments passed on to <code>layer()</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
<code>na.rm</code>	logical If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

## Details

Note that all position aesthetics are scaled (i.e., they will expand the limits of the plot so they are visible), but all other aesthetics are set. This means that layers created with this function will never affect the legend.

## Note

To use the original definition of `annotate()` after loading package 'ggpmisc', use `ggplot2::annotate()`.

## Examples

```
p <- ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point()
p + annotate("text_npc", npcx = 0.9, npcy = 0.9, label = "Some text")
p + annotate("text_npc", npcx = "right", npcy = "top", label = "Some text")
p + annotate("label_npc", npcx = c(0.1, 0.9), npcy = c(0.1, 0.9),
            label = c("A", "B"))
p + annotate("label_npc", npcx = 0.9, npcy = c(0.1, 0.9),
            label = c("A", "B"))
p + annotate("table_npc", npcx = 0.9, npcy = 0.9,
            label = data.frame(A = 1:2, B = letters[1:2]))
p + annotate("plot_npc", npcx = 1, npcy = 1,
            label = p + theme_bw(9))
p + annotate("plot_npc", npcx = c(0, 1), npcy = c(0, 1),
            label = list(p + theme_bw(9), p + theme_grey(9)),
            vp.width = 0.3, vp.height = 0.4)
```

---

geom\_grob

*Inset graphical objects*

---

## Description

`geom_grob` and `geom_grob_npc` add a Grob as inset to the ggplot using syntax similar to that of [geom\\_label](#). In most respects they behave as any other ggplot geometry: a layer can contain multiple tables and faceting works as usual.

## Usage

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

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
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 <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.
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.
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. <a href="#">borders</a> .

## Details

The "width" and "height" of an inset as for a text element are 0, so stacking and dodging inset plots will not work by default, and axis limits are not automatically expanded to include all inset plots. Obviously, insets do have height and width, but they are physical units, not data units. The amount

of space they occupy on the main plot is not constant in data units of the base plot: when you modify scale limits, inset plots stay the same size relative to the physical size of the base plot.

### Alignment

You can modify table alignment with the `vjust` and `hjust` aesthetics. These can either be a number between 0 (right/bottom) and 1 (top/left) or a character ("left", "middle", "right", "bottom", "center", "top").

### Inset size

You can modify inset plot size with the `vp.width` and `vp.height` aesthetics. These can be a number between 0 (smallest possible inset) and 1 (whole plotting area width or height). The default value for both of these aesthetics is 1/3.

### Note

These geoms work only with tibbles as data, as they expect a list of graphics objects ("grob") to be mapped to the `label` aesthetic. Aesthetics mappings in the inset plot are independent of those in the base plot.

In the case of `geom_grob()`, `x` and `y` aesthetics determine the position of the whole inset grob, similarly to that of a text label, justification is interpreted as indicating the position of the grob with respect to the `$x` and `$y` coordinates in the data, and `angle` is used to rotate the plot as a whole.

In the case of `geom_grob_npc()`, `npcx` and `npcy` aesthetics determine the position of the whole inset plot, similarly to that of a text label, justification is interpreted as indicating the position of the grob with respect to the `$x` and `$y` coordinates in "npc" units, and `angle` is used to rotate the plot as a whole.

`annotate()` **cannot be used with** `geom = "grob"`. Use `annotation_custom` directly when adding inset plots as annotations.

### References

The idea of implementing a `geom_custom()` for grobs has been discussed as an issue at <https://github.com/tidyverse/ggplot2/issues/1399>.

### See Also

Other geometries for adding insets to ggplots: `geom_plot()`, `geom_table()`, `ttheme_gtdefault()`

### Examples

```
library(tibble)
df <- tibble(x = 2, y = 15, grob = list(grid::circleGrob(r = 0.2)))
ggplot(data = mtcars, aes(wt, mpg)) +
  geom_point(aes(colour = factor(cyl))) +
  geom_grob(data = df, aes(x, y, label = grob))
```



## Description

'geom\_text\_npc()' adds text directly to the plot. 'geom\_label\_npc()' draws a rectangle behind the text, making it easier to read. The difference is that x and y mappings are expected to be given in 'npc' graphic units. They are intended to be used for positioning text relative to the physical dimensions of a plot. This can be achieved with 'annotate()' except when faceting is used.

## Usage

```
geom_label_npc(  
  mapping = NULL,  
  data = NULL,  
  stat = "identity",  
  position = "identity",  
  ...,  
  parse = FALSE,  
  nudge_x = 0,  
  nudge_y = 0,  
  label.padding = unit(0.25, "lines"),  
  label.r = unit(0.15, "lines"),  
  label.size = 0.25,  
  na.rm = FALSE,  
  show.legend = FALSE,  
  inherit.aes = FALSE  
)
```

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

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
---------	--

<code>data</code>	A layer specific data set - only needed if you want to override the plot defaults.
<code>stat</code>	The statistical transformation to use on the data for this layer, as a string.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.
<code>parse</code>	If TRUE, the labels will be parsed into expressions and displayed as described in <code>?plotmath</code> .
<code>nudge_x, nudge_y</code>	Horizontal and vertical adjustment to nudge labels by. Useful for offsetting text from points, particularly on discrete scales.
<code>label.padding</code>	Amount of padding around label. Defaults to 0.25 lines.
<code>label.r</code>	Radius of rounded corners. Defaults to 0.15 lines.
<code>label.size</code>	Size of label border, in mm.
<code>na.rm</code>	If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .
<code>check_overlap</code>	If 'TRUE', text that overlaps previous text in the same layer will not be plotted.

## Details

Note that the "width" and "height" of a text element are 0, so stacking and dodging text will not work by default, and axis limits are not automatically expanded to include all text. Obviously, labels do have height and width, but they are physical units, not data units. The amount of space they occupy on the plot is not constant in data units: when you resize a plot, labels stay the same size, but the size of the axes changes.

'`geom_text_npc()`' and '`geom_label_npc()`' add labels for each row in the data, even if coordinates `x`, `y` are set to single values in the call to '`geom_label_npc()`' or '`geom_text_npc()`'. To add labels at specified points use `[annotate()]` with '`annotate(geom = "text_npc", ...)`' or '`annotate(geom = "label_npc", ...)`'.

## 'geom\_label\_npc()'

Currently '`geom_label_npc()`' does not support the '`angle`' aesthetic and is considerably slower than '`geom_text_npc()`'. The '`fill`' aesthetic controls the background colour of the label.

## Alignment

You can modify text alignment with the '`vjust`' and '`hjust`' aesthetics. These can either be a number between 0 (right/bottom) and 1 (top/left) or a character ("`left`", "`middle`", "`right`", "`bottom`", "`center`", "`top`"). There are two special alignments: "`inward`" and "`outward`". Inward always

aligns text towards the center, and outward aligns it away from the center. When using textual positions a shift is added based on grouping, however unused levels are not dropped. In plots with faceting so that not all groups appear in each panel, gaps will appear in between labels. To solve this pass numeric values for the npc coordinates of each label instead of character strings.

### Note

This geom is identical to 'ggplot2' `geom_text()` except that it interprets x and y positions in npc units. It translates x and y coordinates from npc units to native data units and calls functions from 'ggplot2's `GeomText()`.

### See Also

[geom\\_text](#)

### Examples

```
df <- data.frame(
  x = c(0, 0, 1, 1, 0.5),
  x.chr = c("left", "left", "right", "right", "center"),
  y = c(0, 1, 0, 1, 0.5),
  y.chr = c("bottom", "top", "bottom", "top", "middle"),
  text = c("bottom-left", "top-left", "bottom-right", "top-right", "center-middle")
)
ggplot(df) +
  geom_text_npc(aes(npcx = x, npcy = y, label = text))

ggplot(df) +
  geom_text_npc(aes(npcx = x.chr, npcy = y.chr, label = text))

ggplot(data = mtcars, mapping = aes(wt, mpg)) +
  geom_point() +
  geom_text_npc(data = df, aes(npcx = x, npcy = y, label = text))

ggplot(data = mtcars, mapping = aes(wt, mpg)) +
  geom_point() +
  geom_text_npc(data = df, aes(npcx = x, npcy = y, label = text)) +
  expand_limits(y = 40, x = 6)

ggplot(data = mtcars) +
  geom_point(mapping = aes(wt, mpg)) +
  geom_label_npc(data = df, aes(npcx = x, npcy = y, label = text))
```

## Description

`geom_plot` and `geom_plot_npc` add ggplot objects as insets to the base ggplot, using syntax similar to that of [geom\\_label](#). In most respects they behave as any other ggplot geometry: a layer can contain multiple tables and faceting works as usual.

## Usage

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

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

## Arguments

<code>mapping</code>	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
<code>data</code>	A layer specific data set - only needed if you want to override the plot defaults.
<code>stat</code>	The statistical transformation to use on the data for this layer, as a string.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.
<code>na.rm</code>	If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .

## Details

The "width" and "height" of an inset as for a text element are 0, so stacking and dodging inset plots will not work by default, and axis limits are not automatically expanded to include all inset plots. Obviously, insets do have height and width, but they are physical units, not data units. The amount of space they occupy on the main plot is not constant in data units of the base plot: when you modify scale limits, inset plots stay the same size relative to the physical size of the base plot.

## Inset alignment

You can modify inset plot alignment with the `vjust` and `hjust` aesthetics. These can either be a number between 0 (right/bottom) and 1 (top/left) or a character ("left", "middle", "right", "bottom", "center", "top"). The `angle` aesthetics can be used to rotate the inset plots.

## Inset size

You can modify inset plot size with the `vp.width` and `vp.height` aesthetics. These can be a number between 0 (smallest possible inset) and 1 (whole plotting area width or height). The default value for both of these aesthetics is 1/3.

## Known problem!

In some cases when explicit coordinates are added to the inner plot, it may be also necessary to add explicitly coordinates to the outer plots.

## Note

These geoms work only with tibbles as data, as they expects a list of ggplots ("gg" objects) to be mapped to the `label` aesthetic. Aesthetics mappings in the inset plot are independent of those in the base plot.

In the case of `geom_plot()`, `x` and `y` aesthetics determine the position of the whole inset plot, similarly to that of a text label, justification is interpreted as indicating the position of the plot with respect to the `$x` and `$y` coordinates in the data, and `angle` is used to rotate the plot as a whole.

In the case of `geom_plot_npc()`, `npcx` and `npcy` aesthetics determine the position of the whole inset plot, similarly to that of a text label, justification is interpreted as indicating the position of the plot with respect to the `$x` and `$y` coordinates in "npc" units, and `angle` is used to rotate the plot as a whole.

`annotate()` **cannot be used with** `geom = "plot"`. Use `annotation_custom` directly when adding inset plots as annotations.

## References

The idea of implementing a `geom_custom()` for grobs has been discussed as an issue at <https://github.com/tidyverse/ggplot2/issues/1399>.

## See Also

Other geometries for adding insets to ggplots: `geom_grob()`, `geom_table()`, `ttheme_gtdefault()`

**Examples**

```
# inset plot with enlarged detail from a region of the main plot
library(tibble)
p <-
  ggplot(data = mtcars, mapping = aes(wt, mpg)) +
  geom_point()

df <- tibble(x = 0.01, y = 0.01,
             plot = list(p +
                         coord_cartesian(xlim = c(3, 4),
                                         ylim = c(13, 16)) +
                         labs(x = NULL, y = NULL) +
                         theme_bw(10)))

p +
  expand_limits(x = 0, y = 0) +
  geom_plot_npc(data = df, aes(npcx = x, npcy = y, label = plot))
```

---

geom\_quadrant\_lines      *Reference lines: horizontal plus vertical, and quadrants*

---

**Description**

geom\_vhlines() adds in a single layer both vertical and horizontal guide lines. Can be thought of as a convenience function that helps with producing consistent vertical and horizontal guide lines. It behaves like geom\_vline() and geom\_hline(). geom\_quadrant\_lines() displays the boundaries of four quadrants with an arbitrary origin. The quadrants are specified in the same way as in stat\_quadrant\_counts() and is intended to be used to add guide lines consistent with the counts by quadrant computed by this stat.

**Usage**

```
geom_quadrant_lines(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  pool.along = "none",
  xintercept = 0,
  yintercept = 0,
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = FALSE,
  ...
)

geom_vhlines(
  mapping = NULL,
```

```

    data = NULL,
    stat = "identity",
    position = "identity",
    xintercept = NULL,
    yintercept = NULL,
    na.rm = FALSE,
    show.legend = FALSE,
    inherit.aes = FALSE,
    ...
  )

```

### Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific data set - only needed if you want to override the plot defaults.
stat	The statistic object to use display the data
position	The position adjustment to use for overlapping points on this layer
pool.along	character, one of "none", "x" or "y", indicating which quadrants to pool to calculate counts by pair of quadrants.
xintercept, yintercept	numeric vectors the coordinates of the origin of the quadrants.
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and should not inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

### Details

While [geom\\_vhlines\(\)](#) does not provide defaults for the intercepts and accept vectors of length > 1, [geom\\_quadrant\\_lines\(\)](#) sets by default the intercepts to zero producing the natural quadrants and only accepts vectors of length one per panel. That is [geom\\_vhlines\(\)](#) can be used to plot a grid while [geom\\_quadrant\\_lines\(\)](#) plots at most one vertical and one horizontal line. In the case of [geom\\_quadrant\\_lines\(\)](#) the pooling along axes can be specified in the same way as in [stat\\_quadrant\\_counts\(\)](#).

### See Also

[geom\\_abline](#), the topic where [geom\\_vline\(\)](#) and [geom\\_hline\(\)](#) are described.

Other Functions for quadrant and volcano plots: [FC\\_format\(\)](#), [outcome2factor\(\)](#), [scale\\_colour\\_outcome\(\)](#), [scale\\_shape\\_outcome\(\)](#), [scale\\_y\\_Pvalue\(\)](#), [stat\\_quadrant\\_counts\(\)](#), [xy\\_outcomes2factor\(\)](#)

## Examples

```
# generate artificial data
set.seed(4321)
x <- 1:100
y <- rnorm(length(x), mean = 10)
my.data <- data.frame(x, y)

ggplot(my.data, aes(x, y)) +
  geom_quadrant_lines() +
  geom_point()

ggplot(my.data, aes(x, y)) +
  geom_quadrant_lines(linetype = "dotted") +
  geom_point()

ggplot(my.data, aes(x, y)) +
  geom_quadrant_lines(xintercept = 50, yintercept = 10, colour = "blue") +
  geom_point()

ggplot(my.data, aes(x, y)) +
  geom_quadrant_lines(xintercept = 50, pool.along = "y", colour = "blue") +
  geom_point()

ggplot(my.data, aes(x, y)) +
  geom_vhlines(xintercept = c(25, 50, 75), yintercept = 10 ,
              linetype = "dotted", colour = "red") +
  geom_point() +
  theme_bw()
```

---

geom\_table

*Inset tables*

---

## Description

geom\_table adds a textual table directly to the ggplot using syntax similar to that of [geom\\_label](#) while geom\_table\_npc is similar to geom\_label\_npc in that x and y coordinates are given in npc units. In most respects they behave as any other ggplot geometry: a layer can contain multiple tables and faceting works as usual.

## Usage

```
geom_table(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  table.theme = NULL,
```



```

    table.rownames = FALSE,
    table.colnames = TRUE,
    table.hjust = 0.5,
    parse = FALSE,
    na.rm = FALSE,
    show.legend = FALSE,
    inherit.aes = FALSE
  )

  geom_table_npc(
    mapping = NULL,
    data = NULL,
    stat = "identity",
    position = "identity",
    ...,
    table.theme = NULL,
    table.rownames = FALSE,
    table.colnames = TRUE,
    table.hjust = 0.5,
    parse = FALSE,
    na.rm = FALSE,
    show.legend = FALSE,
    inherit.aes = FALSE
  )

```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific data set - only needed if you want to override the plot defaults.
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 <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.
table.theme	NULL, list or function A gridExtra ttheme definition, or a constructor for a ttheme or NULL for default.
table.rownames, table.colnames	logical flag to enable or disable printing of row names and column names.
table.hjust	numeric Horizontal justification for the core and column headings of the table.
parse	If TRUE, the labels will be parsed into expressions and displayed as described in <a href="#">?plotmath</a> .
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.

`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

These geoms work only with tibbles as data, as they expects a list of data frames or tibbles ("tb" objects) to be mapped to the `label` aesthetic. Aesthetics mappings in the inset plot are independent of those in the base plot.

In the case of `geom_table()`, `x` and `y` aesthetics determine the position of the whole inset table, similarly to that of a text label, justification is interpreted as indicating the position of the table with respect to the `$x` and `$y` coordinates in the data, and `angle` is used to rotate the table as a whole.

In the case of `geom_table_npc()`, `npcx` and `npcy` aesthetics determine the position of the whole inset table, similarly to that of a text label, justification is interpreted as indicating the position of the table with respect to the `$x` and `$y` coordinates in "npc" units, and `angle` is used to rotate the table as a whole.

The "width" and "height" of an inset as for a text element are 0, so stacking and dodging inset plots will not work by default, and axis limits are not automatically expanded to include all inset plots. Obviously, insets do have height and width, but they are physical units, not data units. The amount of space they occupy on the main plot is not constant in data units of the base plot: when you modify scale limits, inset plots stay the same size relative to the physical size of the base plot.

## Alignment

You can modify table alignment with the `vjust` and `hjust` aesthetics. These can either be a number between 0 (right/bottom) and 1 (top/left) or a character ("left", "middle", "right", "bottom", "center", "top").

## Inset size

You can modify inset table size with the `size` aesthetics, which determines the size of text within the table.

## Warning!

`annotate()` **cannot be used with** `geom = "table"`. Use [annotation\\_custom](#) directly when adding inset tables as annotations.

## Note

As all geoms, `geom_table()` and `geom_table_npc()` add a layer to a plot, and behave as expected in the grammar of graphics: ggplot themes do not affect how layers are rendered. The formatting of the inset table is done according to the the argument passed to `table.theme`.

As the table is built with function `gridExtra::gtable()`, for formatting details, please, consult [tableGrob](#). If the argument passed to `table.theme` is a constructor function, the values mapped to `size`, `color`, `fill`, `alpha`, and `family` aesthetics will the passed to the theme constructor for each table. In the case of `colour` and `fill`, the default mapping is to NA which triggers the use of the default `base_colour` of the `ttheme`.

The constructor `ttheme_gtdefault` is used by default, but others are available predefined or can be created by the user. If instead of a constructor a ready constructed `ttheme` as a list object is passed as argument, it will be used as is. In such a case mapped aesthetics normally mapped aesthetics are ignored if present.

Complex tables with annotations or different coloring of rows or cells can be constructed with functions in package 'gridExtra' or in any other way as long as they can be saved as grid graphical objects and added to a `ggplot` as a new layer with `geom_grob`.

## References

This geometry is inspired on answers to two questions in Stackoverflow. In contrast to these earlier examples, the current `geom` obeys the grammar of graphics, and attempts to be consistent with the behaviour of 'ggplot2' geometries. <https://stackoverflow.com/questions/12318120/adding-table-within-the-plotting-region-of-a-ggplot-in-r> <https://stackoverflow.com/questions/25554548/adding-sub-tables-on-each-panel-of-a-facet-ggplot-in-r?>

## See Also

function `tableGrob` as it is used to construct the table.

Other geometries for adding insets to `ggplots`: `geom_grob()`, `geom_plot()`, `ttheme_gtdefault()`

## Examples

```
library(dplyr)
library(tibble)

mtcars %>%
  group_by(cyl) %>%
  summarize(wt = mean(wt), mpg = mean(mpg)) %>%
  ungroup() %>%
  mutate(wt = sprintf("%.2f", wt),
         mpg = sprintf("%.1f", mpg)) -> tb

df <- tibble(x = 5.45, y = 34, tb = list(tb))

# using defaults
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb))

ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.rownames = TRUE, table.theme = ttheme_gtstripes)

# settings aesthetics to constants
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            color = "red", fill = "#FFCCCC", family = "serif", size = 5,
            angle = 90, vjust = 0)
```

```
# passing a theme constructor as argument
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtminimal) +
  theme_classic()

df2 <- tibble(x = 5.45, y = c(34, 29, 24), cyl = c(4, 6, 8),
             tb = list(tb[1, 1:3], tb[2, 1:3], tb[3, 1:3]))

# mapped aesthetics
ggplot(data = mtcars, mapping = aes(wt, mpg, color = factor(cyl))) +
  geom_point() +
  geom_table(data = df2,
            inherit.aes = TRUE,
            mapping = aes(x = x, y = y, label = tb))

# Using native plot coordinates instead of data coordinates
dfnpc <- tibble(x = 0.95, y = 0.95, tb = list(tb))

ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table_npc(data = dfnpc, aes(npcx = x, npcy = y, label = tb))
```

---

geom\_x\_margin\_arrow      *Reference arrows on the margins*

---

## Description

Small arrows on plot margins can supplement a 2d display with annotations. Arrows can be used to highlight specific values along a margin. The geometries `geom_x_margin_arrow()` and `geom_y_margin_arrow()` behave similarly `geom_vline()` and `geom_hline()` and share their "double personality" as both annotations and geometries.

## Usage

```
geom_x_margin_arrow(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  xintercept,
  sides = "b",
  arrow.length = 0.03,
  na.rm = FALSE,
  show.legend = FALSE,
```

```

    inherit.aes = FALSE
  )

  geom_y_margin_arrow(
    mapping = NULL,
    data = NULL,
    stat = "identity",
    position = "identity",
    ...,
    yintercept,
    sides = "l",
    arrow.length = 0.03,
    na.rm = FALSE,
    show.legend = FALSE,
    inherit.aes = FALSE
  )

```

### Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
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 <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.
xintercept, yintercept	numeric Parameters that control the position of the marginal points. If these are set, data, mapping and show.legend are overridden.
sides	A string that controls which sides of the plot the rugs appear on. It can be set to a string containing any of "trbl", for top, right, bottom, and left.
arrow.length	numeric value expressed in npc units for the length of the arrows inwards from the edge of the plotting area.
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.
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. <a href="#">borders</a> .

### See Also

Other Geometries for marginal annotations in ggplots: [geom\\_x\\_margin\\_grob\(\)](#), [geom\\_x\\_margin\\_point\(\)](#)

## Examples

```
p <- ggplot(mtcars, aes(wt, mpg)) +
  geom_point()
p
p + geom_x_margin_arrow(xintercept = 3.5)
p + geom_y_margin_arrow(yintercept = c(18, 28, 15))
p + geom_x_margin_arrow(data = data.frame(x = c(2.5, 4.5)),
  mapping = aes(xintercept = x))
p + geom_x_margin_arrow(data = data.frame(x = c(2.5, 4.5)),
  mapping = aes(xintercept = x),
  sides="tb")
```

---

geom_x_margin_grob	<i>Add Grobs on the margins</i>
--------------------	---------------------------------

---

## Description

Marging points can supplement a 2d display with annotations. Marging points can highlight individual cases or values along a margin. The geometries `geom_x_margin_grob()` and `geom_y_margin_grob()` behave similarly `geom_vline()` and `geom_hline()` and share their "double personality" as both annotations and geometries.

## Usage

```
geom_x_margin_grob(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  xintercept,
  sides = "b",
  grob.shift = 0,
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = FALSE
)
```

```
geom_y_margin_grob(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  yintercept,
  sides = "l",
```

```

  grob.shift = 0,
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = FALSE
)

```

### Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
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 <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.
xintercept, yintercept	numeric Parameters that control the position of the marginal points. If these are set, data, mapping and show.legend are overridden.
sides	A character string of length one that controls on which side of the plot the grob annotations appear on. It can be set to a string containing one of "t", "r", "b" or "l", for top, right, bottom, and left.
grob.shift	numeric value expressed in npc units for the shift of the marginal grob inwards from the edge of the plotting area.
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.
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. <a href="#">borders</a> .

### See Also

Other Geometries for marginal annotations in ggplots: [geom\\_x\\_margin\\_arrow\(\)](#), [geom\\_x\\_margin\\_point\(\)](#)

### Examples

```
# We can add icons to the margin of a plot to signal events
```

---

geom\_x\_margin\_point      *Reference points on the margins*

---

## Description

Marging points can supplement a 2d display with annotations. Marging points can highlight individual cases or values along a margin. The geometries `geom_x_margin_point()` and `geom_y_margin_point()` behave similarly `geom_vline()` and `geom_hline()` and share their "double personality" as both annotations and geometries.

## Usage

```
geom_x_margin_point(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  xintercept,
  sides = "b",
  point.shift = 0.017,
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = FALSE
)
```

```
geom_y_margin_point(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  yintercept,
  sides = "l",
  point.shift = 0.017,
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = FALSE
)
```

## Arguments

mapping	The aesthetic mapping, usually constructed with <code>aes</code> or <code>aes_</code> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
stat	The statistical transformation to use on the data for this layer, as a string.



<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.
<code>xintercept, yintercept</code>	numeric Parameters that control the position of the marginal points. If these are set, <code>data</code> , <code>mapping</code> and <code>show.legend</code> are overridden.
<code>sides</code>	A string that controls which sides of the plot the rugs appear on. It can be set to a string containing any of "trbl", for top, right, bottom, and left.
<code>point.shift</code>	numeric value expressed in npc units for the shift of the rug points inwards from the edge of the plotting area.
<code>na.rm</code>	If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .

### See Also

Other Geometries for marginal annotations in ggplots: [geom\\_x\\_margin\\_arrow\(\)](#), [geom\\_x\\_margin\\_grob\(\)](#)

### Examples

```
p <- ggplot(mtcars, aes(wt, mpg)) +
  geom_point()
p
p + geom_x_margin_point(xintercept = 3.5)
p + geom_y_margin_point(yintercept = c(18, 28, 15))
p + geom_x_margin_point(data = data.frame(x = c(2.5, 4.5)),
  mapping = aes(xintercept = x))
p + geom_x_margin_point(data = data.frame(x = c(2.5, 4.5)),
  mapping = aes(xintercept = x),
  sides="tb")
```

---

ggplot

---

Create a new ggplot plot from time series data

---

### Description

`ggplot()` initializes a ggplot object. It can be used to declare the input spectral object for a graphic and to optionally specify the set of plot aesthetics intended to be common throughout all subsequent layers unless specifically overridden.

**Usage**

```
## S3 method for class 'ts'
ggplot(
  data,
  mapping = NULL,
  ...,
  time.resolution = "day",
  as.numeric = TRUE,
  environment = parent.frame()
)

## S3 method for class 'xts'
ggplot(
  data,
  mapping = NULL,
  ...,
  time.resolution = "day",
  as.numeric = TRUE,
  environment = parent.frame()
)
```

**Arguments**

<code>data</code>	Default spectrum dataset to use for plot. If not a spectrum, the methods used will be those defined in package <code>ggplot2</code> . See <a href="#">ggplot</a> . If not specified, must be supplied in each layer added to the plot.
<code>mapping</code>	Default list of aesthetic mappings to use for plot. If not specified, in the case of spectral objects, a default mapping will be used.
<code>...</code>	Other arguments passed on to methods. Not currently used.
<code>time.resolution</code>	character The time unit to which the returned time values will be rounded.
<code>as.numeric</code>	logical If TRUE convert time to numeric, expressed as fractional calendar years.
<code>environment</code>	If an variable defined in the aesthetic mapping is not found in the data, <code>ggplot</code> will look for it in this environment. It defaults to using the environment in which <code>ggplot()</code> is called.

**Details**

`ggplot()` is typically used to construct a plot incrementally, using the `+` operator to add layers to the existing `ggplot` object. This is advantageous in that the code is explicit about which layers are added and the order in which they are added. For complex graphics with multiple layers, initialization with `ggplot` is recommended.

There are three common ways to invoke `ggplot`:

- `ggplot(ts, aes(x, y, <other aesthetics>))`
- `ggplot(ts)`

The first method is recommended if all layers use the same data and the same set of aesthetics, although this method can also be used to add a layer using data from another data frame. See the first example below. The second method specifies the default spectrum object to use for the plot, and the units to be used for y in the plot, but no aesthetics are defined up front. This is useful when one data frame is used predominantly as layers are added, but the aesthetics may vary from one layer to another. The third method specifies the default spectrum object to use for the plot, but no aesthetics are defined up front. This is useful when one spectrum is used predominantly as layers are added, but the aesthetics may vary from one layer to another.

### Note

Current implementation does not merge default mapping with user supplied mapping. If user supplies a mapping, it is used as is. To add to the default mapping, `aes()` can be used by itself to compose the `ggplot`.

### Examples

```
library(ggplot2)
ggplot(lynx) + geom_line()
```

---

Moved

*Moved to package 'gginnards'*

---

### Description

Some stats, geoms and the plot layer manipulation functions have been moved from package 'ggp-misc' to a separate new package called 'gginnards'.

### Details

To continue using any of these functions and methods, simply run at the R prompt or add to your script `library(gginnards)`, after installing package 'gginnards'.

### See Also

[gginnards-package](#), [geom\\_null](#), [stat\\_debug\\_group](#), [stat\\_debug\\_panel](#), [geom\\_debug](#) and [delete\\_layers](#).

---

outcome2factor	<i>Convert numeric ternary outcomes into a factor</i>
----------------	---

---

## Description

Convert numeric ternary outcomes into a factor

## Usage

```
outcome2factor(x, n.levels = 3L)
```

```
threshold2factor(x, n.levels = 3L, threshold = 0)
```

## Arguments

x	a numeric vector of -1, 0, and +1 values, indicating down-regulation, uncertain response or up-regulation, or a numeric vector that can be converted into such values using a pair of thresholds.
n.levels	numeric Number of levels to create, either 3 or 2.
threshold	numeric vector Range enclosing the values to be considered uncertain.

## Details

These functions convert the numerically encoded values into a factor with the three levels "down", "uncertain" and "up", or into a factor with two levels de and uncertain as expected by default by scales [scale\\_colour\\_outcome](#), [scale\\_fill\\_outcome](#) and [scale\\_shape\\_outcome](#). When n.levels = 2 both -1 and +1 are merged to the same level of the factor with label "de".

## Note

These are convenience functions that only save some typing. The same result can be achieved by a direct call to [factor](#) and comparisons. These functions aim at making it easier to draw volcano and quadrant plots.

## See Also

Other Functions for quadrant and volcano plots: [FC\\_format\(\)](#), [geom\\_quadrant\\_lines\(\)](#), [scale\\_colour\\_outcome\(\)](#), [scale\\_shape\\_outcome\(\)](#), [scale\\_y\\_Pvalue\(\)](#), [stat\\_quadrant\\_counts\(\)](#), [xy\\_outcomes2factor\(\)](#)

Other scales for omics data: [scale\\_shape\\_outcome\(\)](#), [scale\\_x\\_logFC\(\)](#), [xy\\_outcomes2factor\(\)](#)

## Examples

```
outcome2factor(c(-1, 1, 0, 1))
outcome2factor(c(-1, 1, 0, 1), n.levels = 2L)

threshold2factor(c(-0.1, -2, 0, +5))
```

```
threshold2factor(c(-0.1, -2, 0, +5), n.levels = 2L)
threshold2factor(c(-0.1, -2, 0, +5), threshold = c(-1, 1))
```

---

quadrant_example.df	<i>Example gene expression data</i>
---------------------	-------------------------------------

---

### Description

A dataset containing reshaped and simplified output from an analysis of data from RNAseq done with package edgeR. Original data from gene expression in the plant species *Arabidopsis thaliana*.

### Usage

```
quadrant_example.df
```

### Format

A data.frame object with 6088 rows and 6 variables

### See Also

Other Transcriptomics data examples: [volcano\\_example.df](#)

### Examples

```
names(quadrant_example.df)
head(quadrant_example.df)
```

---

scale_colour_outcome	<i>Colour and fill scales for ternary outcomes</i>
----------------------	--

---

### Description

Manual scales for colour and fill aesthetics with defaults suitable for the three way outcome from some statistical tests.

**Usage**

```

scale_colour_outcome(
  ...,
  name = "Outcome",
  ns.colour = "grey80",
  up.colour = "red",
  down.colour = "dodgerblue2",
  de.colour = "goldenrod",
  na.colour = "black",
  aesthetics = "colour"
)

scale_color_outcome(
  ...,
  name = "Outcome",
  ns.colour = "grey80",
  up.colour = "red",
  down.colour = "dodgerblue2",
  de.colour = "goldenrod",
  na.colour = "black",
  aesthetics = "colour"
)

scale_fill_outcome(
  ...,
  name = "Outcome",
  ns.colour = "grey80",
  up.colour = "red",
  down.colour = "dodgerblue2",
  de.colour = "goldenrod",
  na.colour = "black",
  aesthetics = "fill"
)

```

**Arguments**

<code>...</code>	other named arguments passed to <code>scale_manual</code> .
<code>name</code>	The name of the scale, used for the axis-label.
<code>ns.colour</code> , <code>down.colour</code> , <code>up.colour</code> , <code>de.colour</code>	The colour definitions to use for each of the three possible outcomes.
<code>na.colour</code>	colour definition used for NA.
<code>aesthetics</code>	Character string or vector of character strings listing the name(s) of the aesthetic(s) that this scale works with. This can be useful, for example, to apply colour settings to the colour and fill aesthetics at the same time, via <code>aesthetics = c("colour", "fill")</code> .

## Details

These scales only alter the breaks, values, and na.value default arguments of `scale_colour_manual()` and `scale_fill_manual()`. Please, see documentation for [scale\\_manual](#) for details.

## See Also

Other Functions for quadrant and volcano plots: [FC\\_format\(\)](#), [geom\\_quadrant\\_lines\(\)](#), [outcome2factor\(\)](#), [scale\\_shape\\_outcome\(\)](#), [scale\\_y\\_Pvalue\(\)](#), [stat\\_quadrant\\_counts\(\)](#), [xy\\_outcomes2factor\(\)](#)

## Examples

```
set.seed(12346)
outcome <- sample(c(-1, 0, +1), 50, replace = TRUE)
my.df <- data.frame(x = rnorm(50),
                    y = rnorm(50),
                    outcome2 = outcome2factor(outcome, n.levels = 2),
                    outcome3 = outcome2factor(outcome))

ggplot(my.df, aes(x, y, colour = outcome3)) +
  geom_point() +
  scale_colour_outcome() +
  theme_bw()

ggplot(my.df, aes(x, y, colour = outcome2)) +
  geom_point() +
  scale_colour_outcome() +
  theme_bw()

ggplot(my.df, aes(x, y, fill = outcome3)) +
  geom_point(shape = 21) +
  scale_fill_outcome() +
  theme_bw()
```

---

scale\_continuous\_npc    *Position scales for continuous data (npcx & npcyl)*

---

## Description

'scale\_npcx\_continuous()' and 'scale\_npcyl\_continuous()' are scales for continuous npcx and npcyl aesthetics expressed in "npc" units. There are no variants. Obviously limits are always the full range of "npc" units and transformations meaningless. These scales are used by the newly defined aesthetics npcx and npcyl.

## Usage

```
scale_npcx_continuous(...)

scale_npcyl_continuous(...)
```

**Arguments**

... Other arguments passed on to 'continuous\_scale()'

---

scale_shape_outcome	<i>Shape scale for ternary outcomes</i>
---------------------	---

---

**Description**

Manual scales for colour and fill aesthetics with defaults suitable for the three way outcome from some statistical tests.

**Usage**

```
scale_shape_outcome(
  ...,
  name = "Outcome",
  ns.shape = "circle filled",
  up.shape = "triangle filled",
  down.shape = "triangle down filled",
  de.shape = "square filled",
  na.shape = "cross"
)
```

**Arguments**

... other named arguments passed to scale\_manual.

name The name of the scale, used for the axis-label.

ns.shape, down.shape, up.shape, de.shape  
The shapes to use for each of the three possible outcomes.

na.shape Shape used for NA.

**Details**

These scales only alter the values, and na.value default arguments of scale\_shape\_manual(). Please, see documentation for [scale\\_manual](#) for details.

**See Also**

Other Functions for quadrant and volcano plots: [FC\\_format\(\)](#), [geom\\_quadrant\\_lines\(\)](#), [outcome2factor\(\)](#), [scale\\_colour\\_outcome\(\)](#), [scale\\_y\\_Pvalue\(\)](#), [stat\\_quadrant\\_counts\(\)](#), [xy\\_outcomes2factor\(\)](#)

Other scales for omics data: [outcome2factor\(\)](#), [scale\\_x\\_logFC\(\)](#), [xy\\_outcomes2factor\(\)](#)



**Examples**

```

set.seed(12346)
outcome <- sample(c(-1, 0, +1), 50, replace = TRUE)
my.df <- data.frame(x = rnorm(50),
                    y = rnorm(50),
                    outcome2 = outcome2factor(outcome, n.levels = 2),
                    outcome3 = outcome2factor(outcome))

ggplot(my.df, aes(x, y, shape = outcome3)) +
  geom_point() +
  scale_shape_outcome() +
  theme_bw()

ggplot(my.df, aes(x, y, shape = outcome3)) +
  geom_point() +
  scale_shape_outcome(guide = FALSE) +
  theme_bw()

ggplot(my.df, aes(x, y, shape = outcome2)) +
  geom_point(size = 2) +
  scale_shape_outcome() +
  theme_bw()

ggplot(my.df, aes(x, y, shape = outcome3, fill = outcome2)) +
  geom_point() +
  scale_shape_outcome() +
  scale_fill_outcome() +
  theme_bw()

ggplot(my.df, aes(x, y, shape = outcome3, fill = outcome2)) +
  geom_point() +
  scale_shape_outcome(name = "direction") +
  scale_fill_outcome(name = "significance") +
  theme_bw()

```

---

scale\_x\_logFC

*Position scales for log fold change data*


---

**Description**

Continuous scales for x and y aesthetics with defaults suitable for values expressed as log2 fold change in data and fold-change in tick labels. Supports tick labels and data expressed in any combination of fold-change, log2 fold-change and log10 fold-change. Supports addition of units to axis labels passed as argument to the name formal parameter.

**Usage**

```

scale_x_logFC(
  name = "Abundance of x%unit",
  breaks = NULL,
  labels = NULL,
  limits = symmetric_limits,
  oob = scales::squish,
  expand = expansion(mult = 0.15, add = 0),
  log.base.labels = FALSE,
  log.base.data = 2L,
  ...
)

scale_y_logFC(
  name = "Abundance of y%unit",
  breaks = NULL,
  labels = NULL,
  limits = symmetric_limits,
  oob = scales::squish,
  expand = expansion(mult = 0.15, add = 0),
  log.base.labels = FALSE,
  log.base.data = 2L,
  ...
)

```

**Arguments**

name	The name of the scale without units, used for the axis-label.
breaks	The positions of ticks or a function to generate them. Default varies depending on argument passed to <code>log.base.labels</code> . if supplied as a numeric vector they should be given using the data as passed to parameter <code>data</code> .
labels	The tick labels or a function to generate them from the tick positions. The default is function that uses the arguments passed to <code>log.base.data</code> and <code>log.base.labels</code> to generate suitable labels.
limits	limits One of: <code>NULL</code> to use the default scale range from <code>ggplot2</code> . A numeric vector of length two providing limits of the scale, using <code>NA</code> to refer to the existing minimum or maximum. A function that accepts the existing (automatic) limits and returns new limits. The default is function <code>symmetric_limits()</code> which keep 1 at the middle of the axis..
oob	Function that handles limits outside of the scale limits (out of bounds). The default squishes out-of-bounds values to the boundary.
expand	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. The default is to expand the scale by 15% on each end for log-fold-data, so as to leave space for counts annotations.

```
log.base.labels, log.base.data
      integer or logical Base of logarithms used to express fold-change values in tick
      labels and in data. Use FALSE for no logarithm transformation.
...
      other named arguments passed to scale_y_continuous.
```

## Details

These scales only alter default arguments of `scale_x_continuous()` and `scale_y_continuous()`. Please, see documentation for [scale\\_continuous](#) for details. The `name` argument supports the use of `"%unit"` at the end of the string to automatically add a units string, otherwise user-supplied values for names, breaks, and labels work as usual. Tick labels are built based on the transformation already applied to the data (log2 by default) and a possibly different log transformation (default is fold-change with no transformation).

## See Also

Other scales for omics data: [outcome2factor\(\)](#), [scale\\_shape\\_outcome\(\)](#), [xy\\_outcomes2factor\(\)](#)

## Examples

```
set.seed(12346)
my.df <- data.frame(x = rnorm(50, sd = 4), y = rnorm(50, sd = 4))

ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC() +
  scale_y_logFC()

ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC(labels = scales::trans_format(function(x) {log10(2^x)},
      scales::math_format())) +
  scale_y_logFC(labels = scales::trans_format(function(x) {log10(2^x)},
      scales::math_format()))

ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC(log.base.labels = 2) +
  scale_y_logFC(log.base.labels = 2)

ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC("A concentration%unit", log.base.labels = 10) +
  scale_y_logFC("B concentration%unit", log.base.labels = 10)

ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC("A concentration%unit", breaks = NULL) +
  scale_y_logFC("B concentration%unit", breaks = NULL)

# taking into account that data are expressed as log2 FC.
```

```

ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC("A concentration%unit", breaks = log2(c(1/100, 1, 100))) +
  scale_y_logFC("B concentration%unit", breaks = log2(c(1/100, 1, 100)))

ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC(labels = scales::trans_format(function(x) {log10(2^x)}),
                scales::math_format()) +
  scale_y_logFC(labels = scales::trans_format(function(x) {log10(2^x)}),
                scales::math_format())

# override "special" default arguments.
ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC("A concentration",
                breaks = waiver(),
                labels = waiver()) +
  scale_y_logFC("B concentration",
                breaks = waiver(),
                labels = waiver())

ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC() +
  scale_y_logFC() +
  geom_quadrant_lines() +
  stat_quadrant_counts(size = 3.5)

```

---

scale_y_Pvalue	<i>Covenience scale for P-values</i>
----------------	--------------------------------------

---

## Description

Scales for y aesthetic mapped to P-values as used in volcano plots with transcriptomics and metabolomics data.

## Usage

```

scale_y_Pvalue(
  ...,
  name = expression(italic(P) - plain(value)),
  trans = NULL,
  breaks = NULL,
  labels = NULL,
  limits = c(1, 1e-20),
  oob = NULL,
  expand = NULL

```

```

)

scale_y_FDR(
  ...,
  name = "False discovery rate",
  trans = NULL,
  breaks = NULL,
  labels = NULL,
  limits = c(1, 1e-10),
  oob = NULL,
  expand = NULL
)

scale_x_Pvalue(
  ...,
  name = expression(italic(P) - plain(value)),
  trans = NULL,
  breaks = NULL,
  labels = NULL,
  limits = c(1, 1e-20),
  oob = NULL,
  expand = NULL
)

scale_x_FDR(
  ...,
  name = "False discovery rate",
  trans = NULL,
  breaks = NULL,
  labels = NULL,
  limits = c(1, 1e-10),
  oob = NULL,
  expand = NULL
)

```

## Arguments

...	other named arguments passed to <code>scale_y_continuous</code> .
name	The name of the scale without units, used for the axis-label.
trans	Either the name of a transformation object, or the object itself. Use <code>NULL</code> for the default.
breaks	The positions of ticks or a function to generate them. Default varies depending on argument passed to <code>log.base.labels</code> .
labels	The tick labels or a function to generate them from the tick positions. The default is function that uses the arguments passed to <code>log.base.data</code> and <code>log.base.labels</code> to generate suitable labels.
limits	Use one of: <code>NULL</code> to use the default scale range, a numeric vector of length two

	providing limits of the scale; NA to refer to the existing minimum or maximum; a function that accepts the existing (automatic) limits and returns new limits.
oob	Function that handles limits outside of the scale limits (out of bounds). The default squishes out-of-bounds values to the boundary.
expand	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. The default is to expand the scale by 15% on each end for log-fold-data, so as to leave space for counts annotations.

## Details

These scales only alter default arguments of `scale_x_continuous()` and `scale_y_continuous()`. Please, see documentation for [scale\\_continuous](#) for details.

## See Also

Other Functions for quadrant and volcano plots: [FC\\_format\(\)](#), [geom\\_quadrant\\_lines\(\)](#), [outcome2factor\(\)](#), [scale\\_colour\\_outcome\(\)](#), [scale\\_shape\\_outcome\(\)](#), [stat\\_quadrant\\_counts\(\)](#), [xy\\_outcomes2factor\(\)](#)

## Examples

```
set.seed(12346)
my.df <- data.frame(x = rnorm(50, sd = 4),
                    y = 10^-runif(50, min = 0, max = 20))

ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC() +
  scale_y_Pvalue()

ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC() +
  scale_y_FDR(limits = c(NA, 1e-20))
```

---

stat_apply_group	<i>Apply a function to x or y values</i>
------------------	--

---

## Description

`stat_apply_group` and `stat_apply_panel` apply functions to data. In most cases one should simply use transformations through scales or summary functions through `stat_summary()`. There are some computations that are not scale transformations but are not usual summaries either, the number of data values does not decrease. It is always possible to precompute quantities like cumulative sums or running medians, and for normalizations it can be convenient to apply such functions

on-the-fly to ensure that grouping is consistent between computations and aesthetics. One particularity of these statistics is that they can apply simultaneously different functions to x values and to y values when needed. In contrast `geom_smooth` applies a function that takes both x and y values as arguments.

## Usage

```
stat_apply_group(  
  mapping = NULL,  
  data = NULL,  
  geom = "line",  
  .fun.x = function(x) {    x },  
  .fun.x.args = list(),  
  .fun.y = function(y) {    y },  
  .fun.y.args = list(),  
  position = "identity",  
  na.rm = FALSE,  
  show.legend = FALSE,  
  inherit.aes = TRUE,  
  ...  
)
```

```
stat_apply_panel(  
  mapping = NULL,  
  data = NULL,  
  geom = "line",  
  .fun.x = function(x) {    x },  
  .fun.x.args = list(),  
  .fun.y = function(y) {    y },  
  .fun.y.args = list(),  
  position = "identity",  
  na.rm = FALSE,  
  show.legend = FALSE,  
  inherit.aes = TRUE,  
  ...  
)
```

```
stat_summary_xy(  
  mapping = NULL,  
  data = NULL,  
  geom = "point",  
  .fun.x = function(x) {    x },  
  .fun.x.args = list(),  
  .fun.y = function(y) {    y },  
  .fun.y.args = list(),  
  position = "identity",  
  na.rm = FALSE,  
  show.legend = FALSE,  
  inherit.aes = TRUE,
```

```

    ...
  )

  stat_centroid(
    mapping = NULL,
    data = NULL,
    geom = "point",
    .fun = mean,
    .fun.args = list(),
    position = "identity",
    na.rm = FALSE,
    show.legend = FALSE,
    inherit.aes = TRUE,
    ...
  )

```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
.fun.x, .fun.y, .fun	function to be applied or the name of the function to be applied as a character string. One and only one of these parameters should be passed a non-null argument.
.fun.x.args, .fun.y.args, .fun.args	additional arguments to be passed to the function as a named list.
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. 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. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Details

The function(s) to be applied is expected to be vectorized and to return a vector of (almost) the same length. The vector mapped to the x or y aesthetic is passed as the first positional argument to the call. The function must accept as first argument a vector or list that matches the data.



### Computed variables

One of x or y or both x and y replaced by the vector returned by the corresponding applied function.

**x** x-value as returned by .fun.x

**y** y-value as returned by .fun.y

### Note

This stat is at early stages of development and its interface may change at any time.

### References

Answers question "R ggplot on-the-fly calculation by grouping variable" at <https://stackoverflow.com/questions/51412522>.

### Examples

```
library(gginnards)
set.seed(123456)
my.df <- data.frame(X = rep(1:20,2),
                    Y = runif(40),
                    category = rep(c("A","B"), each = 20))

# make sure row are ordered for X as we will use functions that rely on this
my.df <- my.df[order(my.df[["X"]]), ]

ggplot(my.df, aes(x = X, y = Y, colour = category)) +
  stat_apply_group(.fun.y = cumsum)

# Use of geom_debug() to inspect the computed values
ggplot(my.df, aes(x = X, y = Y, colour = category)) +
  stat_apply_group(.fun.y = cumsum, geom = "debug")

ggplot(my.df, aes(x = X, y = Y, colour = category)) +
  stat_apply_group(.fun.y = cummax)

ggplot(my.df, aes(x = X, y = Y, colour = category)) +
  stat_apply_group(.fun.x = cumsum, .fun.y = cumsum)

# diff returns a shorter vector by 1 for each group
ggplot(my.df, aes(x = X, y = Y, colour = category)) +
  stat_apply_group(.fun.y = diff, na.rm = TRUE)

ggplot(my.df, aes(x = X, y = Y, colour = category)) +
  geom_point() +
  stat_apply_group(.fun.y = runmed, .fun.y.args = list(k = 5))

# Rescaling per group
ggplot(my.df, aes(x = X, y = Y, colour = category)) +
  stat_apply_group(.fun.y = function(x) {(x - min(x)) / (max(x) - min(x))})

# Joint rescaling for whole panel
```

```

ggplot(my.df, aes(x = X, y = Y, colour = category)) +
  stat_apply_panel(.fun.y = function(x) {(x - min(x)) / (max(x) - min(x))})

# Centroid
ggplot(my.df, aes(x = X, y = Y, colour = category)) +
  stat_centroid(shape = "cross", size = 6) +
  geom_point()

# Centroid
ggplot(my.df, aes(x = X, y = Y, colour = category)) +
  stat_centroid(geom = "text", aes(label = category)) +
  geom_point()

```

---

stat_dens2d_filter	<i>Filter observations by local density</i>
--------------------	---

---

## Description

stat\_dens2d\_filter Filters-out/filters-in observations in regions of a plot panel with high density of observations. stat\_dens2d\_filter\_g does the filtering by group instead of by panel. This second stat is useful for highlighting observations, while the first one tends to be most useful when the aim is to prevent clashes among text labels.

## Usage

```

stat_dens2d_filter(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  keep.fraction = 0.1,
  keep.number = Inf,
  keep.sparse = TRUE,
  na.rm = TRUE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  h = NULL,
  n = NULL,
  ...
)

```

```

stat_dens2d_filter_g(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  keep.fraction = 0.1,

```

```

    keep.number = Inf,
    keep.sparse = TRUE,
    na.rm = TRUE,
    show.legend = FALSE,
    inherit.aes = TRUE,
    h = NULL,
    n = NULL,
    ...
  )

```

### Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data.
position	The position adjustment to use for overlapping points on this layer
keep.fraction	numeric [0..1].
keep.number	integer number of labels to keep.
keep.sparse	logical If false the observations from the densest regions are kept.
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. 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. <a href="#">borders</a> .
h	vector of bandwidths for x and y directions. Defaults to normal reference bandwidth (see <a href="#">bandwidth.nrd</a> ). A scalar value will be taken to apply to both directions.
n	Number of grid points in each direction. Can be scalar or a length-2 integer vector
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

### Computed variables

**labels** x at centre of range

### See Also

[kde2d](#) used internally.

Other statistics for selection of observations based on local density: [stat\\_dens2d\\_labels\(\)](#)

**Examples**

```

library(ggrepel)
library(gginnards)

random_string <- function(len = 6) {
  paste(sample(letters, len, replace = TRUE), collapse = "")
}

# Make random data.
set.seed(1001)
d <- tibble::tibble(
  x = rnorm(100),
  y = rnorm(100),
  group = rep(c("A", "B"), c(50, 50)),
  lab = replicate(100, { random_string() })
)

ggplot(data = d, aes(x, y)) +
  geom_point() +
  stat_dens2d_filter(colour = "red")

# Using geom_debug() we can see that only 10 out of 100 rows in \code{d} are
# returned. Those highlighted in red in the previous example.
ggplot(data = d, aes(x, y)) +
  geom_point() +
  stat_dens2d_filter(geom = "debug")

ggplot(data = d, aes(x, y)) +
  geom_point() +
  stat_dens2d_filter(colour = "red", keep.fraction = 0.5)

ggplot(data = d, aes(x, y)) +
  geom_point() +
  stat_dens2d_filter(colour = "red",
                    keep.fraction = 0.5,
                    keep.number = 12)

ggplot(data = d, aes(x, y, colour = group)) +
  geom_point() +
  stat_dens2d_filter(shape = 1, size = 3, keep.fraction = 1/4)

ggplot(data = d, aes(x, y, colour = group)) +
  geom_point() +
  stat_dens2d_filter_g(shape = 1, size = 3, keep.fraction = 1/4)

ggplot(data = d, aes(x, y, label = lab, colour = group)) +
  geom_point() +
  stat_dens2d_filter(geom = "text")

ggplot(data = d, aes(x, y, label = lab, colour = group)) +
  geom_point() +

```

```
stat_dens2d_filter(geom = "text_repel")
```

---

stat_dens2d_labels	<i>Reset labels of observations in high density regions</i>
--------------------	---

---

## Description

stat\_low\_dens Sets values ampped to label to "" in regions of a plot panel with high density of observations.

## Usage

```
stat_dens2d_labels(
  mapping = NULL,
  data = NULL,
  geom = "text",
  position = "identity",
  keep.fraction = 0.1,
  keep.number = Inf,
  h = NULL,
  n = NULL,
  label.fill = "",
  na.rm = TRUE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  ...
)
```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data.
position	The position adjustment to use for overlapping points on this layer
keep.fraction	numeric [0..1].
keep.number	integer number of labels to keep.
h	vector of bandwidths for x and y directions. Defaults to normal reference bandwidth (see <code>bandwidth.nrd</code> ). A scalar value will be taken to apply to both directions.
n	Number of grid points in each direction. Can be scalar or a length-2 integer vector
label.fill	character.

<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Details

`stat_dens2d_labels()` is designed to work together with statistics from package 'ggrepel'. To avoid text labels being plotted over unlabelled points the corresponding rows in data need to be retained but labels replaced with the empty character string, `""`. `stat_dens2d_labels()` replaces labels by `""` based on the local density of observations.

## Computed variables

**labels** x at centre of range

## See Also

[kde2d](#) used internally.

Other statistics for selection of observations based on local density: [stat\\_dens2d\\_filter\(\)](#)

## Examples

```
library(ggrepel)
library(gginnards)

random_string <- function(len = 6) {
  paste(sample(letters, len, replace = TRUE), collapse = "")
}

# Make random data.
set.seed(1001)
d <- tibble::tibble(
  x = rnorm(100),
  y = rnorm(100),
  group = rep(c("A", "B"), c(50, 50)),
  lab = replicate(100, { random_string() })
)

ggplot(data = d, aes(x, y, label = lab)) +
  geom_point() +
  stat_dens2d_labels()

# Using geom_debug() we can see that all 100 rows in \code{d} are
```

```

# returned. But only those labelled in the previous example still contain
# the original labels.
ggplot(data = d, aes(x, y, label = lab)) +
  geom_point() +
  stat_dens2d_labels(geom = "debug")

ggplot(data = d, aes(x, y, label = lab, colour = group)) +
  geom_point() +
  stat_dens2d_labels()

ggplot(data = d, aes(x, y, label = lab, colour = group)) +
  geom_point() +
  stat_dens2d_labels(geom = "text_repel")

ggplot(data = d, aes(x, y, label = lab, colour = group)) +
  geom_point() +
  stat_dens2d_labels(geom = "text_repel", label.fill = NA)

```

stat\_fit\_augment

*Augment data with fitted values and statistics*

## Description

stat\_fit\_augment fits a model and returns the data augmented with information from the fitted model, using package 'broom'.

## Usage

```

stat_fit_augment(
  mapping = NULL,
  data = NULL,
  geom = "smooth",
  method = "lm",
  method.args = list(formula = y ~ x),
  augment.args = list(),
  level = 0.95,
  y.out = ".fitted",
  position = "identity",
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  ...
)

```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
---------	--

<code>data</code>	A layer specific dataset - only needed if you want to override the plot defaults.
<code>geom</code>	The geometric object to use display the data
<code>method</code>	character.
<code>method.args</code>	list of arguments to pass to <code>method</code> .
<code>augment.args</code>	list of arguments to pass to <code>broom::augment</code> .
<code>level</code>	numeric Level of confidence interval to use (0.95 by default)
<code>y.out</code>	character (or numeric) index to column to return as y.
<code>position</code>	The position adjustment to use for overlapping points on this layer
<code>na.rm</code>	logical indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	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.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders</code> .
<code>...</code>	other arguments passed on to <code>layer</code> . This can include aesthetics whose values you want to set, not map. See <code>layer</code> for more details.

## Details

`stat_fit_augment` together with `stat_fit_glance` and `stat_fit_tidy`, based on package 'broom' can be used with a broad range of model fitting functions as supported at any given time by 'broom'. In contrast to `stat_poly_eq` which can generate text or expression labels automatically, for these functions the mapping of aesthetic `label` needs to be explicitly supplied in the call, and labels built on the fly.

A ggplot statistic receives as data a data frame that is not the one passed as argument by the user, but instead a data frame with the variables mapped to aesthetics. In other words, it respects the grammar of graphics and consequently within arguments passed through `method.args` names of aesthetics like `$x$` and `$y$` should be used instead of the original variable names, while data is automatically passed the data frame. This helps ensure that the model is fitted to the same data as plotted in other layers.

## Handling of grouping

`stat_fit_augment` applies the function given by `method` separately to each group of observations; in ggplot2 factors mapped to aesthetics generate a separate group for each level. Because of this, `stat_fit_augment` is not useful for annotating plots with results from `t.test()` or ANOVA or ANCOVA. In such cases use instead `stat_fit_tb()` which applies the model fitting per panel.

## Computed variables

The output of `augment()` is returned as is, except for `y` which is set based on `y.out` and `y.observed` which preserves the `y` returned by the `broom::augment` methods. This renaming is needed so that the `geom` works as expected.

To explore the values returned by this statistic, which vary depending on the model fitting function and model formula we suggest the use of `geom_debug`. An example is shown below.



**Note**

The statistic `stat_fit_augment` can be used only with methods that accept formulas under any formal parameter name and a data argument. Use `ggplot2::stat_smooth()` instead of `stat_fit_augment` in production code if the additional features are not needed.

**See Also**

[broom](#)

Other ggplot2 statistics based on 'broom': [stat\\_fit\\_glance\(\)](#), [stat\\_fit\\_tb\(\)](#), [stat\\_fit\\_tidy\(\)](#)

**Examples**

```
library(gginnards)
# Regression by panel, using geom_debug() to explore computed variables
ggplot(mtcars, aes(x = disp, y = mpg)) +
  geom_point(aes(colour = factor(cyl))) +
  stat_fit_augment(method = "lm",
                  method.args = list(formula = y ~ x),
                  geom = "debug",
                  summary.fun = colnames)

# Regression by panel example
ggplot(mtcars, aes(x = disp, y = mpg)) +
  geom_point(aes(colour = factor(cyl))) +
  stat_fit_augment(method = "lm",
                  method.args = list(formula = y ~ x))

# Residuals from regression by panel example
ggplot(mtcars, aes(x = disp, y = mpg)) +
  geom_hline(yintercept = 0, linetype = "dotted") +
  stat_fit_augment(geom = "point",
                  method = "lm",
                  method.args = list(formula = y ~ x),
                  y.out = ".resid")

# Regression by group example
ggplot(mtcars, aes(x = disp, y = mpg, colour = factor(cyl))) +
  geom_point() +
  stat_fit_augment(method = "lm",
                  method.args = list(formula = y ~ x))

# Residuals from regression by group example
ggplot(mtcars, aes(x = disp, y = mpg, colour = factor(cyl))) +
  geom_hline(yintercept = 0, linetype = "dotted") +
  stat_fit_augment(geom = "point",
                  method.args = list(formula = y ~ x),
                  y.out = ".resid")

# Weighted regression example
ggplot(mtcars, aes(x = disp, y = mpg, weight = cyl)) +
  geom_point(aes(colour = factor(cyl))) +
```

```

stat_fit_augment(method = "lm",
                 method.args = list(formula = y ~ x,
                                    weights = quote(weight)))

# Residuals from weighted regression example
ggplot(mtcars, aes(x = disp, y = mpg, weight = cyl)) +
  geom_hline(yintercept = 0, linetype = "dotted") +
  stat_fit_augment(geom = "point",
                  method.args = list(formula = y ~ x,
                                     weights = quote(weight)),
                  y.out = ".resid")

```

---

stat_fit_deviations	<i>Residuals from model fit as segments</i>
---------------------	---

---

## Description

stat\_fit\_deviations fits a linear model and returns fitted values and residuals ready to be plotted as segments.

## Usage

```

stat_fit_deviations(
  mapping = NULL,
  data = NULL,
  geom = "segment",
  method = "lm",
  formula = NULL,
  position = "identity",
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  ...
)

```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
method	character Currently only "lm" is implemented.
formula	a "formula" object. Using aesthetic names instead of original variable names.
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.

<code>show.legend</code>	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.
<code>inherit.aes</code>	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 should not inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Details

This stat can be used to automatically highlight residuals as segments in a plot of a fitted model equation. At the moment it supports only linear models fitted with function `lm()`. This stat only generates the residuals, the predicted values need to be separately added to the plot, so to make sure that the same model formula is used in all steps it is best to save the formula as an object and supply this object as argument to the different statistics.

A ggplot statistic receives as data a data frame that is not the one passed as argument by the user, but instead a data frame with the variables mapped to aesthetics. In other words, it respects the grammar of graphics and consequently within the model formula names of aesthetics like `$x$` and `$y$` should be used instead of the original variable names, while data is automatically passed the data frame. This helps ensure that the model is fitted to the same data as plotted in other layers.

## Computed variables

Data frame with same nrow as data as subset for each group containing five numeric variables.

**x** x coordinates of observations

**y.fitted** x coordinates of fitted values

**y** y coordinates of observations

**y.fitted** y coordinates of fitted values

To explore the values returned by this statistic we suggest the use of [geom\\_debug](#). An example is shown below, where one can also see in addition to the computed values the default mapping of the fitted values to aesthetics `xend` and `yend`.

## Note

For linear models `x1` is equal to `x2`.

## See Also

Other statistics for linear model fits: [stat\\_fit\\_residuals\(\)](#), [stat\\_poly\\_eq\(\)](#)

## Examples

```
library(gginnards) # needed for geom_debug()
# generate artificial data
set.seed(4321)
x <- 1:100
y <- (x + x^2 + x^3) + rnorm(length(x), mean = 0, sd = mean(x^3) / 4)
```

```

my.data <- data.frame(x, y, group = c("A", "B"), y2 = y * c(0.5,2))

# give a name to a formula
my.formula <- y ~ poly(x, 3, raw = TRUE)

# plot
ggplot(my.data, aes(x, y)) +
  geom_smooth(method = "lm", formula = my.formula) +
  stat_fit_deviations(formula = my.formula, colour = "red") +
  geom_point()

# plot, using geom_debug()
ggplot(my.data, aes(x, y)) +
  geom_smooth(method = "lm", formula = my.formula) +
  stat_fit_deviations(formula = my.formula, colour = "red",
    geom = "debug") +
  geom_point()

```

---

stat\_fit\_glance

*One row summary data frame for a fitted model*


---

## Description

stat\_fit\_glance fits a model and returns a summary "glance" of the model's statistics, using package 'broom'.

## Usage

```

stat_fit_glance(
  mapping = NULL,
  data = NULL,
  geom = "text_npc",
  method = "lm",
  method.args = list(formula = y ~ x),
  label.x = "left",
  label.y = "top",
  hstep = 0,
  vstep = 0.075,
  position = "identity",
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  ...
)

```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific data set - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
method	character.
method.args	list of arguments to pass to method.
label.x, label.y	numeric with range 0..1 "normalized parent coordinates" (npc units) or character if using <code>geom_text_npc()</code> or <code>geom_label_npc()</code> . If using <code>geom_text()</code> or <code>geom_label()</code> numeric in native data units. If too short they will be recycled.
hstep, vstep	numeric in npc units, the horizontal and vertical step used between labels for different groups.
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. 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. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Details

`stat_fit_glance` together with [stat\\_fit\\_tidy](#) and [stat\\_fit\\_augment](#), based on package 'broom' can be used with a broad range of model fitting functions as supported at any given time by package 'broom'. In contrast to [stat\\_poly\\_eq](#) which can generate text or expression labels automatically, for these functions the mapping of aesthetic `label` needs to be explicitly supplied in the callm, and labels built on the fly.

A ggplot statistic receives as data a data frame that is not the one passed as argument by the user, but instead a data frame with the variables mapped to aesthetics. In other words, it respects the grammar of graphics and consequently within arguments passed through `method.args` names of aesthetics like `$x$` and `$y$` should be used instead of the original variable names, while data is automatically passed the data frame. This helps ensure that the model is fitted to the same data as plotted in other layers.

## Handling of grouping

`stat_fit_glance` applies the function given by `method` separately to each group of observations, and factors mapped to aesthetics generate a separate group for each factor level. Because of this, `stat_fit_glance` is not useful for annotating plots with results from `t.test()`, ANOVA or ANCOVA. In such cases use the `stat_fit_tb()` statistic which applies the model fitting per panel.

### Model formula required

The current implementation works only with methods that accept a formula as argument and which have a data parameter through which a data frame can be passed. For example, `lm()` should be used with the formula interface, as the evaluation of `x` and `y` needs to be delayed until the internal object of the `ggplot` is available. With some methods like `cor.test()` the data embedded in the "ggplot" object cannot be automatically passed as argument for the data parameter of the test or model fit function.

### Computed variables

The output of `glance()` is returned almost as is in the data object. The names of the columns in the returned data are consistent with those returned by method `glance()` from package 'broom', that will frequently differ from the name of values returned by the print methods corresponding to the fit or test function used. To explore the values returned by this statistic, which vary depending on the model fitting function and model formula we suggest the use of `geom_debug`. An example is shown below.

### See Also

[broom](#)

Other `ggplot2` statistics based on 'broom': [stat\\_fit\\_augment\(\)](#), [stat\\_fit\\_tb\(\)](#), [stat\\_fit\\_tidy\(\)](#)

### Examples

```
library(gginnards)
# Regression by panel example, using geom_debug.
ggplot(mtcars, aes(x = disp, y = mpg)) +
  stat_smooth(method = "lm") +
  geom_point(aes(colour = factor(cyl))) +
  stat_fit_glance(method = "lm",
                  method.args = list(formula = y ~ x),
                  geom = "debug")

# Regression by panel example
ggplot(mtcars, aes(x = disp, y = mpg)) +
  stat_smooth(method = "lm") +
  geom_point(aes(colour = factor(cyl))) +
  stat_fit_glance(method = "lm",
                  label.y = "bottom",
                  method.args = list(formula = y ~ x),
                  mapping = aes(label = sprintf('r^2~"~%.3f~italic(P)~"~"~%.2g',
                                                stat(r.squared), stat(p.value))),
                  parse = TRUE)

# Regression by group example
ggplot(mtcars, aes(x = disp, y = mpg, colour = factor(cyl))) +
  stat_smooth(method = "lm") +
  geom_point() +
  stat_fit_glance(method = "lm",
                  label.y = "bottom",
```

```

method.args = list(formula = y ~ x),
mapping = aes(label = sprintf('r^2~'="%%.3f~italic(P)~'="%%.2g',
                             stat(r.squared), stat(p.value))),
parse = TRUE)

# Weighted regression example
ggplot(mtcars, aes(x = disp, y = mpg, weight = cyl)) +
  stat_smooth(method = "lm") +
  geom_point(aes(colour = factor(cyl))) +
  stat_fit_glance(method = "lm",
                  label.y = "bottom",
                  method.args = list(formula = y ~ x, weights = quote(weight)),
                  mapping = aes(label = sprintf('r^2~'="%%.3f~italic(P)~'="%%.2g',
                                                  stat(r.squared), stat(p.value))),
                  parse = TRUE)

```

---

stat_fit_residuals	<i>Residuals from a model fit</i>
--------------------	-----------------------------------

---

## Description

stat\_fit\_residuals fits a linear model and returns residuals ready to be plotted as points.

## Usage

```

stat_fit_residuals(
  mapping = NULL,
  data = NULL,
  geom = "point",
  method = "lm",
  formula = NULL,
  resid.type = NULL,
  position = "identity",
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  ...
)

```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
method	character Currently only "lm" is implemented.

<code>formula</code>	a "formula" object. Using aesthetic names instead of original variable names.
<code>resid.type</code>	character passed to <code>residuals()</code> as argument for type.
<code>position</code>	The position adjustment to use for overlapping points on this layer
<code>na.rm</code>	a logical indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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 should not inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Details

This stat can be used to automatically plot residuals as points in a plot. At the moment it supports only linear models fitted with function `lm()`. This stat only generates the residuals.

A ggplot statistic receives as data a data frame that is not the one passed as argument by the user, but instead a data frame with the variables mapped to aesthetics. In other words, it respects the grammar of graphics and consequently within the model formula names of aesthetics like `$x$` and `$y$` should be used instead of the original variable names, while data is automatically passed the data frame. This helps ensure that the model is fitted to the same data as plotted in other layers.

## Computed variables

Data frame with same nrow as data as subset for each group containing five numeric variables.

**x** x coordinates of observations

**y.resid** residuals from fitted values

**y.resid.abs** absolute residuals from the fit

.

By default `stat(y.resid)` is mapped to the y aesthetic.

## See Also

Other statistics for linear model fits: [stat\\_fit\\_deviations\(\)](#), [stat\\_poly\\_eq\(\)](#)

## Examples

```
# generate artificial data
set.seed(4321)
x <- 1:100
y <- (x + x^2 + x^3) + rnorm(length(x), mean = 0, sd = mean(x^3) / 4)
my.data <- data.frame(x, y, group = c("A", "B"), y2 = y * c(0.5, 2))

# give a name to a formula
my.formula <- y ~ poly(x, 3, raw = TRUE)
```



```
# plot
ggplot(my.data, aes(x, y)) +
  stat_fit_residuals(formula = my.formula, resid.type = "working")

library(gginnards) # needed for geom_debug()
# print to the console the returned data
ggplot(my.data, aes(x, y)) +
  stat_fit_residuals(formula = my.formula, resid.type = "working",
                    geom = "debug")
```

---

stat_fit_tb	<i>Model-fit summary or ANOVA</i>
-------------	-----------------------------------

---

## Description

stat\_fit\_tb fits a model and returns a "tidy" version of the model's summary or ANOVA table, using package 'broom'. The annotation is added to the plots in tabular form.

## Usage

```
stat_fit_tb(
  mapping = NULL,
  data = NULL,
  geom = "table_npc",
  method = "lm",
  method.args = list(formula = y ~ x),
  tb.type = "fit.summary",
  tb.vars = NULL,
  digits = 3,
  label.x = "center",
  label.y = "top",
  label.x.npc = NULL,
  label.y.npc = NULL,
  position = "identity",
  table.theme = NULL,
  table.rownames = FALSE,
  table.colnames = TRUE,
  table.hjust = 1,
  parse = FALSE,
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  ...
)
```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset, only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
method	character.
method.args	list of arguments to pass to method.
tb.type	character One of "fit.summary", "fit.anova" or "fit.coefs".
tb.vars	character vector, optionally named, used to select and or rename the columns of the table returned.
digits	integer indicating the number of significant digits to be used.
label.x, label.y	numeric Coordinates (in data units) to be used for absolute positioning of the output. If too short they will be recycled.
label.x.npc, label.y.npc	numeric with range 0..1 or character. Coordinates to be used for positioning the output, expressed in "normalized parent coordinates" or character string. If too short they will be recycled.
position	The position adjustment to use for overlapping points on this layer
table.theme	NULL, list or function A gridExtra ttheme definition, or a constructor for a ttheme or NULL for default.
table.rownames, table.colnames	logical flag to enable or disabling printing of row names and column names.
table.hjust	numeric Horizontal justification for the core and column headings of the table.
parse	If TRUE, the labels will be parsed into expressions and displayed as described in <a href="#">?plotmath</a> .
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. 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. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Details

`stat_fit_tb` Applies a model fitting function per panel, using the grouping factors from easthetic mappings in the fitted model. This is suitable, for example for analysis of variance used to test for differences among groups.

The argument to `method` can be any fit method for which a suitable `tidy()` method is available, including non-linear regression. Fit methods retain their default arguments unless overridden.

A ggplot statistic receives as data a data frame that is not the one passed as argument by the user, but instead a data frame with the variables mapped to aesthetics. In other words, it respects the grammar of graphics and consequently within arguments passed through `method.args` names of aesthetics like `$x$` and `$y$` should be used instead of the original variable names, while data is automatically passed the data frame. This helps ensure that the model is fitted to the same data as plotted in other layers.

### Computed variables

The output of `tidy()` is returned as a single "cell" in a tibble (i.e. a tibble nested within a tibble). The returned data object contains a single, containing the result from a single model fit to all data in a panel. If grouping is present, it is ignored.

To explore the values returned by this statistic, which vary depending on the model fitting function and model formula we suggest the use of [geom\\_debug](#). An example is shown below.

### See Also

[broom](#) for details on how the tidying of the result of model fits is done. See [geom\\_table](#) for details on how inset tables respond to mapped aesthetics and table themes. For details on predefined table themes see [ttheme\\_gtddefault](#).

Other ggplot2 statistics based on 'broom': [stat\\_fit\\_augment\(\)](#), [stat\\_fit\\_glance\(\)](#), [stat\\_fit\\_tidy\(\)](#)

### Examples

```
# data for examples
x <- c(44.4, 45.9, 41.9, 53.3, 44.7, 44.1, 50.7, 45.2, 60.1)
covariate <- sqrt(x) + rnorm(9)
group <- factor(c(rep("A", 4), rep("B", 5)))
my.df <- data.frame(x, group, covariate)

# Linear regression
ggplot(my.df, aes(covariate, x)) +
  geom_point() +
  stat_fit_tb() +
  expand_limits(y = 70)

# Linear regression using a table theme
ggplot(my.df, aes(covariate, x)) +
  geom_point() +
  stat_fit_tb(table.theme = ttheme_gtlight) +
  expand_limits(y = 70)

# Polynomial regression
ggplot(my.df, aes(covariate, x)) +
  geom_point() +
  stat_fit_tb(method.args = list(formula = y ~ poly(x, 2))) +
  expand_limits(y = 70)

# ANOVA
ggplot(my.df, aes(group, x)) +
  geom_point() +
```

```

stat_fit_tb() +
  expand_limits(y = 70)

# ANOVA with renamed and selected columns
ggplot(my.df, aes(group, x)) +
  geom_point() +
  stat_fit_tb(tb.vars = c(Effect = "term", "italic(F)" = "statistic", "italic(P)" = "p.value"),
    parse = TRUE)

# ANCOVA (covariate not plotted)
ggplot(my.df, aes(group, x, z = covariate)) +
  geom_point() +
  stat_fit_tb(method.args = list(formula = y ~ x + z),
    tb.vars = c(Effect = "term", "italic(F)" = "statistic", "italic(P)" = "p.value"),
    parse = TRUE)

# t-test
ggplot(my.df, aes(group, x)) +
  geom_point() +
  stat_fit_tb(method = "t.test",
    tb.vars = c("italic(t)" = "statistic", "italic(P)" = "p.value"),
    parse = TRUE)

# t-test (equal variances assumed)
ggplot(my.df, aes(group, x)) +
  geom_point() +
  stat_fit_tb(method = "t.test",
    method.args = list(formula = y ~ x, var.equal = TRUE),
    tb.vars = c("italic(t)" = "statistic", "italic(P)" = "p.value"),
    parse = TRUE)

```

---

stat\_fit\_tidy

---

*One row data frame with fitted parameter estimates*


---

## Description

stat\_fit\_tidy fits a model and returns a "tidy" version of the model's summary, using package 'broom'. To add the summary in tabular form use [stat\\_fit\\_tb](#). When using stat\_fit\_tidy() you will most likely want to change the default mapping for label.

## Usage

```

stat_fit_tidy(
  mapping = NULL,
  data = NULL,
  geom = "text_npc",
  method = "lm",
  method.args = list(formula = y ~ x),

```

```

    label.x = "left",
    label.y = "top",
    hstep = 0,
    vstep = NULL,
    position = "identity",
    na.rm = FALSE,
    show.legend = FALSE,
    inherit.aes = TRUE,
    ...
  )

```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
method	character.
method.args	list of arguments to pass to method.
label.x, label.y	numeric with range 0..1 or character. Coordinates to be used for positioning the output, expressed in "normalized parent coordinates" or character string. If too short they will be recycled.
hstep, vstep	numeric in npc units, the horizontal and vertical step used between labels for different groups.
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. 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. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Details

`stat_fit_tidy` together with [stat\\_fit\\_glance](#) and [stat\\_fit\\_augment](#), based on package 'broom' can be used with a broad range of model fitting functions as supported at any given time by 'broom'. In contrast to [stat\\_poly\\_eq](#) which can generate text or expression labels automatically, for these functions the mapping of aesthetic `label` needs to be explicitly supplied in the call, and labels built on the fly.

A ggplot statistic receives as data a data frame that is not the one passed as argument by the user, but instead a data frame with the variables mapped to aesthetics. In other words, it respects the grammar

of graphics and consequently within arguments passed through `method.args` names of aesthetics like `$x$` and `$y$` should be used instead of the original variable names, while data is automatically passed the data frame. This helps ensure that the model is fitted to the same data as plotted in other layers.

### Handling of grouping

`stat_fit_tidy` applies the function given by `method` separately to each group of observations; in `ggplot2` factors mapped to aesthetics generate a separate group for each level. Because of this, `stat_fit_tidy` is not useful for annotating plots with results from `t.test()` or ANOVA or ANCOVA. In such cases use instead `stat_fit_tb()` which applies the model fitting per panel.

### Computed variables

The output of `tidy()` is returned after reshaping it into a single row. Grouping is respected, and the model fit separately to each group of data. The returned data object has one row for each group within a panel. To use the intercept, note that output of `tidy()` is renamed from `(Intercept)` to `Intercept`.

To explore the values returned by this statistic, which vary depending on the model fitting function and model formula we suggest the use of [geom\\_debug](#). An example is shown below.

### Note

The statistic `stat_fit_augment` can be used only with methods that accept formulas under any formal parameter name and a data argument. Use `ggplot2::stat_smooth()` instead of `stat_fit_augment` in production code if the additional features are not needed.

### See Also

[broom](#)

Other `ggplot2` statistics based on 'broom': [stat\\_fit\\_augment\(\)](#), [stat\\_fit\\_glance\(\)](#), [stat\\_fit\\_tb\(\)](#)

### Examples

```
library(gginnards)
# Regression by panel, exploring computed variables with geom_debug()
ggplot(mtcars, aes(x = disp, y = mpg)) +
  stat_smooth(method = "lm") +
  geom_point(aes(colour = factor(cyl))) +
  stat_fit_tidy(method = "lm",
               method.args = list(formula = y ~ x),
               geom = "debug")

# Regression by panel example
ggplot(mtcars, aes(x = disp, y = mpg)) +
  stat_smooth(method = "lm") +
  geom_point(aes(colour = factor(cyl))) +
  stat_fit_tidy(method = "lm",
               label.x = "right",
               method.args = list(formula = y ~ x),
```

```

        mapping = aes(label = sprintf("Slope = %.3g\np-value = %.3g",
                                      stat(x_estimate),
                                      stat(x_p.value))))

# Regression by group example
ggplot(mtcars, aes(x = disp, y = mpg, colour = factor(cyl))) +
  stat_smooth(method = "lm") +
  geom_point() +
  stat_fit_tidy(method = "lm",
               label.x = "right",
               method.args = list(formula = y ~ x),
               mapping = aes(label = sprintf("Slope = %.3g, p-value = %.3g",
                                             stat(x_estimate),
                                             stat(x_p.value))))

# Weighted regression example
ggplot(mtcars, aes(x = disp, y = mpg, weight = cyl)) +
  stat_smooth(method = "lm") +
  geom_point(aes(colour = factor(cyl))) +
  stat_fit_tidy(method = "lm",
               label.x = "right",
               method.args = list(formula = y ~ x, weights = quote(weight)),
               mapping = aes(label = sprintf("Slope = %.3g\np-value = %.3g",
                                             stat(x_estimate),
                                             stat(x_p.value))))

```

---

stat\_fmt\_tb

---

*Select and slice a tibble nested in data*


---

## Description

stat\_partial\_tb selects columns and/or remanes them and/or slices rows from a tibble nested in data. This stat is designed to be used to pre-process tibble objects mapped to the label aesthetic before adding them to a plot with geom\_table.

## Usage

```

stat_fmt_tb(
  mapping = NULL,
  data = NULL,
  geom = "table",
  tb.vars = NULL,
  tb.rows = NULL,
  digits = 3,
  position = "identity",
  table.theme = NULL,
  table.rownames = FALSE,
  table.colnames = TRUE,

```

```

    table.hjust = 0.5,
    parse = FALSE,
    na.rm = FALSE,
    show.legend = FALSE,
    inherit.aes = TRUE,
    ...
  )

```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
tb.vars	character vector, optionally named, used to select and or rename the columns of the table returned.
tb.rows	integer vector of row indexes of rows to be retained.
digits	integer indicating the number of significant digits to be retained in data.
position	The position adjustment to use for overlapping points on this layer
table.theme	NULL, list or function A <code>gridExtra</code> ttheme definition, or a constructor for a theme or NULL for default.
table.rownames, table.colnames	logical flag to enable or disabling printing of row names and column names.
table.hjust	numeric Horizontal justification for the core and column headings of the table.
parse	If TRUE, the labels will be parsed into expressions and displayed as described in <code>?plotmath</code> .
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. 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. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Computed variables

The output of sequentially applying [slice](#) with `tb.rows` as argument and [select](#) with `tb.vars` to a list variable mapped to `label` and containing a single tibble per row in data.

## See Also

See [geom\\_table](#) for details on how tables respond to mapped aesthetics and table themes. For details on predefined table themes see [ttheme\\_gtdefault](#).



## Examples

```
my.df <-
  tibble::tibble(
    x = c(1, 2),
    y = c(0, 4),
    group = c("A", "B"),
    tbs = list(a = tibble::tibble(X = 1:6, Y = rep(c("x", "y"), 3)),
              b = tibble::tibble(X = 1:3, Y = "x"))
  )

ggplot(my.df, aes(x, y, label = tbs)) +
  stat_fmt_tb() +
  expand_limits(x = c(0,3), y = c(-2, 6))

ggplot(my.df, aes(x, y, label = tbs)) +
  stat_fmt_tb(table.theme = ttheme_gtlight) +
  expand_limits(x = c(0,3), y = c(-2, 6))

ggplot(my.df, aes(x, y, label = tbs)) +
  stat_fmt_tb(tb.vars = c(value = "X", group = "Y"),
             tb.rows = 1:3) +
  expand_limits(x = c(0,3), y = c(-2, 6))
```

stat\_peaks

*Local maxima (peaks) or minima (valleys)*

## Description

stat\_peaks finds at which x positions local y maxima are located and stat\_valleys finds at which x positions local y minima are located. Both stats return x and y numeric values for peaks or valleys and formatted character labels. The formatting is determined by a format string suitable for sprintf().

## Usage

```
stat_peaks(
  mapping = NULL,
  data = NULL,
  geom = "point",
  span = 5,
  ignore_threshold = 0,
  strict = FALSE,
  label.fmt = NULL,
  x.label.fmt = NULL,
  y.label.fmt = NULL,
  position = "identity",
  na.rm = FALSE,
```

```

    show.legend = FALSE,
    inherit.aes = TRUE,
    ...
)

stat_valleys(
  mapping = NULL,
  data = NULL,
  geom = "point",
  span = 5,
  ignore_threshold = 0,
  strict = FALSE,
  label.fmt = NULL,
  x.label.fmt = NULL,
  y.label.fmt = NULL,
  position = "identity",
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  ...
)

```

### Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data.
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element. The default value is 5, meaning that a peak is bigger than two consecutive neighbors on each side. A NULL value for span is taken as a span covering the whole of the data range.
ignore_threshold	numeric value between 0.0 and 1.0 indicating the size threshold below which peaks will be ignored.
strict	logical flag: if TRUE, an element must be strictly greater than all other values in its window to be considered a peak. Default: FALSE.
label.fmt	character string giving a format definition for converting values into character strings by means of function <a href="#">sprintf</a> or <a href="#">strptime</a> , its use is deprecated.
x.label.fmt	character string giving a format definition for converting $x$ -values into character strings by means of function <a href="#">sprintf</a> or <a href="#">strftime</a> . The default argument varies depending on the scale in use.
y.label.fmt	character string giving a format definition for converting $y$ -values into character strings by means of function <a href="#">sprintf</a> .
position	The position adjustment to use for overlapping points on this layer.

<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

### Details

These stats use `geom_point` by default as it is the geom most likely to work well in almost any situation without need of tweaking. The default aesthetics set by these stats allow their direct use with `geom_text`, `geom_label`, `geom_line`, `geom_rug`, `geom_hline` and `geom_vline`. The formatting of the labels returned can be controlled by the user.

### Computed variables

**x** x-value at the peak (or valley) as numeric  
**y** y-value at the peak (or valley) as numeric  
**x.label** x-value at the peak (or valley) as character  
**y.label** y-value at the peak (or valley) as character

### Note

These stats check the scale of the x aesthetic and if it is Date or Datetime they correctly generate the labels by transforming the numeric x values to POSIXct objects, in which case the `x.label.fmt` must be suitable for `strftime()` rather than for `sprintf()`. These stats work nicely together with geoms [geom\\_text\\_repel](#) and [geom\\_label\\_repel](#) from package [ggrepel](#) to solve the problem of overlapping labels by displacing them. Alternatively, to discard overlapping labels use `check_overlap = TRUE` as argument to `geom_text`. By default the labels are character values suitable to be plotted as is, but with a suitable `label.fmt` labels suitable for parsing by the geoms (e.g. into expressions containing Greek letters, super- or subscripts, maths symbols or maths constructs) can be also easily obtained.

### See Also

Other peaks and valleys functions: [find\\_peaks\(\)](#)

### Examples

```
library(ggplot2)
lynx.df <- data.frame(year = as.numeric(time(lynx)), lynx = as.matrix(lynx))
ggplot(lynx.df, aes(year, lynx)) + geom_line() +
  stat_peaks(colour = "red") +
  stat_valleys(colour = "blue")
ggplot(lynx.df, aes(year, lynx)) + geom_line() +
```

```
stat_peaks(colour = "red") +
stat_peaks(colour = "red", geom = "rug")
```

---

stat_poly_eq	<i>Equation, p-value, R<sup>2</sup>, AIC or BIC of fitted polynomial</i>
--------------	--

---

## Description

stat\_poly\_eq fits a polynomial and generates several labels including the equation, p-value, coefficient of determination (R<sup>2</sup>), 'AIC' and 'BIC'.

## Usage

```
stat_poly_eq(
  mapping = NULL,
  data = NULL,
  geom = "text_npc",
  position = "identity",
  ...,
  formula = NULL,
  eq.with.lhs = TRUE,
  eq.x.rhs = NULL,
  coef.digits = 3,
  rr.digits = 2,
  f.digits = 3,
  p.digits = 3,
  label.x = "left",
  label.y = "top",
  label.x.npc = NULL,
  label.y.npc = NULL,
  hstep = 0,
  vstep = NULL,
  output.type = "expression",
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE
)
```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset, only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
position	The position adjustment to use for overlapping points on this layer

...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.
formula	a formula object. Using aesthetic names instead of original variable names.
eq.with.lhs	If character the string is pasted to the front of the equation label before parsing or a logical (see note).
eq.x.rhs	character this string will be used as replacement for "x" in the model equation when generating the label before parsing it.
coef.digits, rr.digits, f.digits, p.digits	integer Number of significant digits to use for the fitted coefficients, R <sup>2</sup> , F-value and P-value in labels.
label.x, label.y	numeric with range 0..1 "normalized parent coordinates" (npc units) or character if using <code>geom_text_npc()</code> or <code>geom_label_npc()</code> . If using <code>geom_text()</code> or <code>geom_label()</code> numeric in native data units. If too short they will be recycled.
label.x.npc, label.y.npc	numeric with range 0..1 (npc units) DEPRECATED, use <code>label.x</code> and <code>label.y</code> instead; together with a geom using <code>npcx</code> and <code>npcy</code> aesthetics.
hstep, vstep	numeric in npc units, the horizontal and vertical step used between labels for different groups.
output.type	character One of "expression", "LaTeX", "text", "markdown" or "numeric".
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. 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. <a href="#">borders</a> .

## Details

This stat can be used to automatically annotate a plot with R<sup>2</sup>, adjusted R<sup>2</sup> or the fitted model equation. It supports only linear models fitted with function `lm()`. The R<sup>2</sup> and adjusted R<sup>2</sup> annotations can be used with any linear model formula. The fitted equation label is correctly generated for polynomials or quasi-polynomials through the origin. Model formulas can use `poly()` or be defined algebraically with terms of powers of increasing magnitude with no missing intermediate terms, except possibly for the intercept indicated by "- 1" or "-1" in the formula. The validity of the formula is not checked in the current implementation, and for this reason the default aesthetics sets R<sup>2</sup> as label for the annotation. This stat only generates labels, the predicted values need to be separately added to the plot, so to make sure that the same model formula is used in all steps it is best to save the formula as an object and supply this object as argument to the different statistics.

A ggplot statistic receives as data a data frame that is not the one passed as argument by the user, but instead a data frame with the variables mapped to aesthetics. `stat_poly_eq()` mimics how `stat_smooth()` works, except that only polynomials can be fitted. In other words, it respects the grammar of graphics. This helps ensure that the model is fitted to the same data as plotted in other layers.

## Aesthetics

stat\_poly\_eq understands x and y, to be referenced in the formula and weight passed as argument to parameter weights of lm(). All three must be mapped to numeric variables. In addition, the aesthetics understood by the geom used ("text" by default) are understood and grouping respected.

## Computed variables

If output.type different from "numeric" the returned tibble contains columns:

**x, npcx** x position

**y, npcy** y position

**coef.ls, r.squared, adj.r.squared, AIC, BIC** as numeric values extracted from fit object

**eq.label** equation for the fitted polynomial as a character string to be parsed

**rr.label**  $R^2$  of the fitted model as a character string to be parsed

**adj.rr.label** Adjusted  $R^2$  of the fitted model as a character string to be parsed

**f.value.label** F value and degrees of freedom for the fitted model as a whole.

**p.value..label** P-value for the F-value above.

**AIC.label** AIC for the fitted model.

**BIC.label** BIC for the fitted model.

**hjust, vjust** Set to "inward" to override the default of the "text" geom.

If output.type is "numeric" the returned tibble contains columns:

**x, npcx** x position

**y, npcy** y position

**coef.ls** list containing the "coefficients" matrix from the summary of the fit object

**r.squared, adj.r.squared, f.value, f.df1, f.df2, p.value, AIC, BIC** numeric values extracted or computed from fit object

**hjust, vjust** Set to "inward" to override the default of the "text" geom.

To explore the computed values returned for a given input we suggest the use of [geom\\_debug](#) as shown in the example below.

## Parsing may be required

if using the computed labels with output.type = "expression", then parse = TRUE is needed, while if using output.type = "LaTeX" parse = FALSE is needed.

## Note

For backward compatibility a logical is accepted as argument for eq.with.lhs, giving the same output than the current default character value. By default "x" is retained as independent variable as this is the name of the aesthetic. However, it can be substituted by providing a suitable replacement character string through eq.x.rhs.

## References

Written as an answer to a question at Stackoverflow. <https://stackoverflow.com/questions/7549694/adding-regression-line-equation-and-r2-on-graph>

## See Also

This `stat_poly_eq` statistic can return ready formatted labels depending on the argument passed to `output.type`. This is possible because only polynomial models are supported. For other types of models, statistics `stat_fit_glance`, `stat_fit_tidy` and `stat_fit_glance` should be used instead and the code for construction of character strings from numeric values and their mapping to aesthetic label needs to be explicitly supplied in the call.

Other statistics for linear model fits: `stat_fit_deviations()`, `stat_fit_residuals()`

## Examples

```
# generate artificial data
set.seed(4321)
x <- 1:100
y <- (x + x^2 + x^3) + rnorm(length(x), mean = 0, sd = mean(x^3) / 4)
my.data <- data.frame(x = x, y = y,
                      group = c("A", "B"),
                      y2 = y * c(0.5, 2),
                      w = sqrt(x))

# give a name to a formula
formula <- y ~ poly(x, 3, raw = TRUE)

# no weights
ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula, parse = TRUE)

ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula, parse = TRUE,
               label.y = "bottom", label.x = "right")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula, parse = TRUE,
               label.y = 0.1, label.x = 0.9)

# using weights
ggplot(my.data, aes(x, y, weight = w)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula, parse = TRUE)
```

```

# no weights, digits for R square
ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula, rr.digits = 4, parse = TRUE)

# user specified label
ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(aes(label = paste(stat(eq.label),
                                stat(adj.rr.label), sep = "*\\", \\"*")),
              formula = formula, parse = TRUE)

ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(aes(label = paste(stat(f.value.label),
                                stat(p.value.label), sep = "*\\", \\"*")),
              formula = formula, parse = TRUE)

# user specified label and digits
ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(aes(label = paste(stat(eq.label),
                                stat(adj.rr.label), sep = "*\\", \\"*")),
              formula = formula, rr.digits = 3, coef.digits = 4,
              parse = TRUE)

# geom = "text"
ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(geom = "text", label.x = 100, label.y = 0, hjust = 1,
              formula = formula, parse = TRUE)

# using numeric values
# Here we use column "Estimate" from the matrix.
# Other available columns are "Std. Error", "t value" and "Pr(>|t|)".
my.format <-
  "b[0]~`=~%.3g*\\", \\"*b[1]~`=~%.3g*\\", \\"*b[2]~`=~%.3g*\\", \\"*b[3]~`=~%.3g"
ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula,
              output.type = "numeric",
              parse = TRUE,
              mapping =
                aes(label = sprintf(my.format,
                                    stat(coef.ls)[[1]][[1], "Estimate"]],
                    stat(coef.ls)[[1]][[2], "Estimate"]],
                    stat(coef.ls)[[1]][[3], "Estimate"]],

```



```

        stat(coef.ls)[[1]][[4, "Estimate"]])
    )

# Examples using geom_debug() to show computed values
#
# This provides a quick way of finding out which variables are available for
# use in mapping of aesthetics when using other geoms as in the examples
# above.

library(gginnards)

ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula, geom = "debug")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(aes(label = stat(eq.label)),
               formula = formula, geom = "debug",
               output.type = "markdown")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula, geom = "debug", output.type = "text")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula, geom = "debug", output.type = "numeric")

# show the content of a list column
ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula, geom = "debug", output.type = "numeric",
               summary.fun = function(x) {x[["coef.ls"]][[1]]})

```

---

stat_quadrant_counts	<i>Number of observations in quadrants</i>
----------------------	--

---

## Description

`stat_quadrant_counts()` counts the number of observations in each quadrant of a plot panel. By default it adds a text label to the far corner of each quadrant. It can also be used to obtain the total number of observations in each of two pairs of quadrants or in the whole panel. Grouping is ignored, so in every case a single count is computed for each quadrant in a plot panel.

**Usage**

```
stat_quadrant_counts(
  mapping = NULL,
  data = NULL,
  geom = "text_npc",
  position = "identity",
  quadrants = NULL,
  pool.along = "none",
  xintercept = 0,
  yintercept = 0,
  label.x = NULL,
  label.y = NULL,
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  ...
)
```

**Arguments**

<code>mapping</code>	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
<code>data</code>	A layer specific dataset - only needed if you want to override the plot defaults.
<code>geom</code>	The geometric object to use display the data
<code>position</code>	The position adjustment to use for overlapping points on this layer
<code>quadrants</code>	integer vector indicating which quadrants are of interest, with a 0L indicating the whole plot.
<code>pool.along</code>	character, one of "none", "x" or "y", indicating which quadrants to pool to calculate counts by pair of quadrants.
<code>xintercept, yintercept</code>	numeric the coordinates of the origin of the quadrants.
<code>label.x, label.y</code>	numeric Coordinates (in npc units) to be used for absolute positioning of the labels.
<code>na.rm</code>	a logical indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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 should not inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Details

This stat can be used to automatically count observations in each of the four quadrants of a plot, and by default add these counts as text labels. Values exactly equal to zero are counted as belonging to the positive quadrant. An argument value of zero, passed to formal parameter `quadrants` is interpreted as a request for the count of all observations in each plot panel.

The default origin of quadrants is at `xintercept = 0`, `yintercept = 0`. Also by default, counts are computed for all quadrants within the `$x$` and `$y$` scale limits, but ignoring any marginal scale expansion. The default positions of the labels is in the farthest corner or edge of each quadrant using npc coordinates. Consequently, when using facets even with free limits for `$x$` and `$y$` axes, the location of the labels is consistent across panels. This is achieved by use of `geom = "text_npc"` or `geom = "label_npc"`. To pass the positions in native data units, pass `geom = "text"` explicitly as argument.

## Computed variables

Data frame with one to four rows, one for each quadrant for which counts are counted in data.

**quadrant** integer, one of 0:4  
**x** x value of label position in data units  
**y** y value of label position in data units  
**npcx** x value of label position in npc units  
**npcy** y value of label position in npc units  
**count** number of observations

.

As shown in one example below [geom\\_debug](#) can be used to print the computed values returned by any statistic. The output shown includes also values mapped to aesthetics, like `label` in the example.

## See Also

Other Functions for quadrant and volcano plots: [FC\\_format\(\)](#), [geom\\_quadrant\\_lines\(\)](#), [outcome2factor\(\)](#), [scale\\_colour\\_outcome\(\)](#), [scale\\_shape\\_outcome\(\)](#), [scale\\_y\\_Pvalue\(\)](#), [xy\\_outcomes2factor\(\)](#)

## Examples

```
library(gginnards)
# generate artificial data
set.seed(4321)
x <- 1:100
y <- rnorm(length(x), mean = 10)
my.data <- data.frame(x, y)

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quadrant_counts()

# We use geom_debug() to see the computed values
```

```

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quadrant_counts(geom = "debug")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quadrant_counts(aes(label = sprintf("%i observations", stat(count)))) +
  expand_limits(y = 12.7)

ggplot(my.data, aes(x, y)) +
  geom_quadrant_lines(colour = "blue", xintercept = 50, yintercept = 10) +
  stat_quadrant_counts(colour = "blue", xintercept = 50, yintercept = 10) +
  geom_point() +
  scale_y_continuous(expand = expansion(mult = 0.15, add = 0))

ggplot(my.data, aes(x, y)) +
  geom_quadrant_lines(colour = "blue",
                      pool.along = "x", yintercept = 10) +
  stat_quadrant_counts(colour = "blue", label.x = "right",
                      pool.along = "x", yintercept = 10) +
  geom_point() +
  expand_limits(y = c(7, 13))

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quadrant_counts(quadrants = 0, label.x = "left", label.y = "bottom")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quadrant_counts(geom = "text") # use "tex" instead

```

---

symmetric_limits	<i>Expand limits to be symmetric</i>
------------------	--------------------------------------

---

## Description

A simple function to expand scale limits to be symmetric around zero. Can be passed as argument to parameter limits of continuous scales from packages 'ggplot2' or 'scales'.

## Usage

```
symmetric_limits(x)
```

## Arguments

x                      numeric The automatic limits

## Value

A numeric vector of length two with the new limits.

**Examples**

```
symmetric_limits(c(-1, 1.8))
```

---

try_data_frame	<i>Convert an R object into a tibble</i>
----------------	--

---

**Description**

This functions tries to convert any R object into a data.frame object. If x is already a data.frame, it is returned as is. If it is a list or a vector it is converted by means of as.data.frame(). If of any other type, a conversion into an object of class xts is attempted by means of try.xts() and if successful the xts object is converted into a data frame with a variable time containing times as POSIXct and the remaining data columns with the time series data. In this conversion row names are stripped.

**Usage**

```
try_data_frame(
  x,
  time.resolution = "month",
  as.numeric = FALSE,
  col.names = NULL
)

try_tibble(x, time.resolution = "month", as.numeric = FALSE, col.names = NULL)
```

**Arguments**

x	An R object
time.resolution	character The time unit to which the returned time values will be rounded.
as.numeric	logical If TRUE convert time to numeric, expressed as fractional calendar years.
col.names	character vector

**Value**

A tibble::tibble object, derived from data.frame.

**Warning!**

The time zone was set to "UTC" by try.xts() in the test cases I used. Setting TZ to "UTC" can cause some trouble as several frequently used functions have as default the local or system TZ and will apply a conversion before printing or plotting time data, which in addition is affected by summer/winter time transitions. This should be taken into account as even for yearly data when conversion is to POSIXct a day (1st of January) will be set, but then shifted some hours if printed on a TZ

different from "UTC". I recommend reading the documentation of package [lubridate](#)-package where the irregularities of time data and the difficulties they cause are very well described. In many cases when working with time series with yearly observations it is best to work with numeric values for years.

### Note

This function can be used to easily convert time series data into a format that can be easily plotted with package `ggplot2`. `try_tibble` is another name for `try_data_frame` which tracks the separation and re-naming of `data_frame` into `tibble::tibble` in the imported packages.

### Examples

```
library(xts)
class(lynx)
try_data_frame(lynx)
try_data_frame(lynx, "year")
class(austres)
try_data_frame(austres)
try_data_frame(austres, "quarter")
class(cars)
try_data_frame(cars)
```

---

ttheme_gtdefault	<i>Table themes</i>
------------------	---------------------

---

### Description

Additional theme constructors for use with [geom\\_table](#).

### Usage

```
ttheme_gtdefault(
  base_size = 10,
  base_colour = "black",
  base_family = "",
  parse = FALSE,
  padding = unit(c(0.8, 0.6), "char"),
  ...
)

ttheme_gtminimal(
  base_size = 10,
  base_colour = "black",
  base_family = "",
  parse = FALSE,
  padding = unit(c(0.5, 0.4), "char"),
```

```
    ...
)

ttheme_gtbw(
  base_size = 10,
  base_colour = "black",
  base_family = "",
  parse = FALSE,
  padding = unit(c(0.8, 0.6), "char"),
  ...
)

ttheme_gtplain(
  base_size = 10,
  base_colour = "black",
  base_family = "",
  parse = FALSE,
  padding = unit(c(0.8, 0.6), "char"),
  ...
)

ttheme_gtdark(
  base_size = 10,
  base_colour = "grey90",
  base_family = "",
  parse = FALSE,
  padding = unit(c(0.8, 0.6), "char"),
  ...
)

ttheme_gtlight(
  base_size = 10,
  base_colour = "grey10",
  base_family = "",
  parse = FALSE,
  padding = unit(c(0.8, 0.6), "char"),
  ...
)

ttheme_gtsimple(
  base_size = 10,
  base_colour = "grey10",
  base_family = "",
  parse = FALSE,
  padding = unit(c(0.5, 0.4), "char"),
  ...
)
```

```
ttheme_gtstripes(
  base_size = 10,
  base_colour = "grey10",
  base_family = "",
  parse = FALSE,
  padding = unit(c(0.8, 0.6), "char"),
  ...
)
```

### Arguments

<code>base_size</code>	numeric, default font size.
<code>base_colour</code>	default font colour.
<code>base_family</code>	default font family.
<code>parse</code>	logical, default behaviour for parsing text as plotmath.
<code>padding</code>	length-2 unit vector specifying the horizontal and vertical padding of text within each cell.
<code>...</code>	further arguments to control the gtable.

### Details

Depending on the theme, the `base_colour`, which is mapped to the `colour` aesthetic if present, is applied to only the text elements, or to the text elements and rules. The difference is exemplified below.

### Value

A list object that can be used as `ttheme` in the construction of tables with functions from package 'gridExtra'.

### Note

These theme constructors are wrappers on `gridExtra::ttheme_default()` and `gridExtra::ttheme_minimal()`. They can also be used with [grid.table](#) if desired.

### See Also

Other geometries for adding insets to ggplots: [geom\\_grob\(\)](#), [geom\\_plot\(\)](#), [geom\\_table\(\)](#)

### Examples

```
library(dplyr)
library(tibble)

mtcars %>%
  group_by(cyl) %>%
  summarize(wt = mean(wt), mpg = mean(mpg)) %>%
  ungroup() %>%
  mutate(wt = sprintf("%.2f", wt),
```



```

mpg = sprintf("%.1f", mpg)) -> tb

df <- tibble(x = 5.45, y = 34, tb = list(tb))

# Same as the default theme constructor
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtdefault) +
  theme_classic()

# Minimal theme constructor
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtminimal) +
  theme_classic()

# A theme with white background
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtbw) +
  theme_bw()

# Default colour of theme superceded by aesthetic constant
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtbw, colour = "darkblue") +
  theme_bw()

# A theme with dark background
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtdark) +
  theme_dark()

# Default colour of theme superceded by aesthetic constant
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtdark, colour = "yellow") +
  theme_dark()

# A theme with light background
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtlight)

# Default colour of theme superceded by aesthetic constant

```

```

ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtlight, colour = "darkred")

# Default colour of theme superceded by aesthetic constant
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtsimple)

# Default colour of theme superceded by aesthetic constant
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb),
            table.theme = ttheme_gtstripes) +
  theme_dark()

```

---

ttheme\_set

*Set default table theme*


---

## Description

Set R option to the theme to use as current default. This function is implemented differently but is used in the same way as `ggplot2::theme_set()` but affects the default table-theme instead of the plot theme.

## Usage

```
ttheme_set(table.theme = NULL)
```

## Arguments

`table.theme` NULL, list or function A gridExtra ttheme definition, or a constructor for a theme or NULL for default.

## Value

A named list with the previous value of the option.

## Note

The ttheme is set when a plot object is constructed, and consequently the option setting does not affect rendering of ready built plot objects.

**Examples**

```
library(dplyr)
library(tibble)

mtcars %>%
  group_by(cyl) %>%
  summarize(wt = mean(wt), mpg = mean(mpg)) %>%
  ungroup() %>%
  mutate(wt = sprintf("%.2f", wt),
         mpg = sprintf("%.1f", mpg)) -> tb

df <- tibble(x = 5.45, y = 34, tb = list(tb))

# Same as the default theme constructor
ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb))

# set a new default
old_ttheme <- ttheme_set(ttheme_gtstripes)

ggplot(mtcars, aes(wt, mpg, colour = factor(cyl))) +
  geom_point() +
  geom_table(data = df, aes(x = x, y = y, label = tb))

# restore previous setting
ttheme_set(old_ttheme)
```

---

volcano_example.df	<i>Example gene expression data</i>
--------------------	-------------------------------------

---

**Description**

A dataset containing reshaped and simplified output from an analysis of data from RNAseq done with package edgeR. Original data from gene expression in the plant species *Arabidopsis thaliana*.

**Usage**

```
volcano_example.df
```

**Format**

A data.frame object with 1218 rows and 5 variables

**See Also**

Other Transcriptomics data examples: [quadrant\\_example.df](#)

**Examples**

```
colnames(volcano_example.df)
head(volcano_example.df)
```

---

xy_outcomes2factor	<i>Convert two numeric ternary outcomes into a factor</i>
--------------------	---

---

**Description**

Convert two numeric ternary outcomes into a factor

**Usage**

```
xy_outcomes2factor(x, y)

xy_thresholds2factor(x, y, x_threshold = 0, y_threshold = 0)
```

**Arguments**

x, y	numeric vectors of -1, 0, and +1 values, indicating down regulation, uncertain response or up-regulation, or numeric vectors that can be converted into such values using a pair of thresholds.
x_threshold, y_threshold	numeric vector Ranges enclosing the values to be considered uncertain for each of the two vectors..

**Details**

This function converts the numerically encoded values into a factor with the four levels "xy", "x", "y" and "none". The factor created can be used for faceting or can be mapped to aesthetics.

**Note**

This is an utility function that only saves some typing. The same result can be achieved by a direct call to [factor](#). This function aims at making it easier to draw quadrant plots with facets based on the combined outcomes.

**See Also**

Other Functions for quadrant and volcano plots: [FC\\_format\(\)](#), [geom\\_quadrant\\_lines\(\)](#), [outcome2factor\(\)](#), [scale\\_colour\\_outcome\(\)](#), [scale\\_shape\\_outcome\(\)](#), [scale\\_y\\_Pvalue\(\)](#), [stat\\_quadrant\\_counts\(\)](#)

Other scales for omics data: [outcome2factor\(\)](#), [scale\\_shape\\_outcome\(\)](#), [scale\\_x\\_logFC\(\)](#)

**Examples**

```
xy_outcomes2factor(c(-1, 0, 0, 1, -1), c(0, 1, 0, 1, -1))  
xy_thresholds2factor(c(-1, 0, 0, 1, -1), c(0, 1, 0, 1, -1))  
xy_thresholds2factor(c(-1, 0, 0, 0.1, -5), c(0, 2, 0, 1, -1))
```

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