Package 'ggpmisc'

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Type Package

Title Miscellaneous Extensions to 'ggplot2'

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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.

License GPL (>= 2)

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ByteCompile TRUE

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(>= 0.8.3), xts (>= 0.12-0), zoo (>= 1.8-7), broom (>= 0.5.5),
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URL https://docs.r4photobiology.info/ggpmisc/,
https://bitbucket.org/aphalo/ggpmisc

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

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ggpmisc-package   *ggpmisc: Miscellaneous Extensions to 'ggplot2'*

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' (>= 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_layesr(), shift_layers(), top_layer() and which_layers() have been moved from package 'ggpmisc' into their own seperate 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/hadley/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()
```

---

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 con contain multi-
ple 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 aes or aes_. 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 layer. This can include aesthetics whose values you want to set, not map. See layer 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. borders.

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 posisble inset) and 1 (whole plotting area width or height). The default value for for both of these aesthetics is 1/3.

Note

These geoms work only with tibbles as data, as they expects 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))
```

---

geom_label_npc   *Text with Normalised Parent Coordinates*

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 [aes](#) or [aes_](#). 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 [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) for more details.
parse	If TRUE, the labels will be parsed into expressions and displayed as described in ?plotmath.
nudge_x, nudge_y	
	Horizontal and vertical adjustment to nudge labels by. Useful for offsetting text from points, particularly on discrete scales.
label.padding	Amount of padding around label. Defaults to 0.25 lines.
label.r	Radius of rounded corners. Defaults to 0.15 lines.
label.size	Size of label border, in mm.
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](#).
check_overlap	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))
```

---

geom_plot   *Inset plots*

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 con
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

mapping	The aesthetic mapping, usually constructed with [aes](#) or [aes_](#). 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 [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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. [borders](#).

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 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 [aes](#) or [aes_](#). 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. [borders](#).

...   other arguments passed on to layer. This can include aesthetics whose values
                          you want to set, not map. See layer 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 con 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 [aes](#) or [aes_](#). 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 [layer](). This can include aesthetics whose values you want to set, not map. See [layer]() for more details.
table.theme	NULL, list or function A gridExtra ttheme defintion, 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 ?plotmath.
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 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 highligth 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 [aes](#) or [aes_](#). 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 [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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 arows 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. borders.

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   *Add Grobs on the margins*

Description

Marging points can supplement a 2d display with annotations. Marging points can highligth 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 [aes](#) or [aes_](#). 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 [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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. `borders`.

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 highligth individ-
ual 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 an-
notations 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 [aes](#) or [aes_](#). 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 [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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.
point.shift	numeric value expressed in npc units for the shift of the rug points 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. [borders](#).

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

data   Default spectrum dataset to use for plot. If not a spectrum, the methods used
            will be those defined in package ggplot2. See [ggplot](). If not specified, must be
            suppled in each layer added to the plot.

mapping   Default list of aesthetic mappings to use for plot. If not specified, in the case of
            spectral objects, a default mapping will be used.

`...`	Other arguments passed on to methods. Not currently used.
`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.
`environment`	If an variable defined in the aesthetic mapping is not found in the data, ggplot will look for it in this environment. It defaults to using the environment in which `ggplot()` 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 'ggpmisc' 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   *Convert numeric ternary outcomes into a factor*

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 de-
fault 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   *Example gene expression data*

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   *Colour and fill scales for ternary outcomes*

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

`...`	other named arguments passed to `scale_manual`.
`name`	The name of the scale, used for the axis-label.
`ns.colour, down.colour, up.colour, de.colour`	
	The colour definitions to use for each of the three possible outcomes.
`na.colour`	colour definition used for NA.
`aesthetics`	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 aesthetics = c("colour", "fill").

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 & npcy)*

Description

'scale_npcx_continuous()' and 'scale_npcy_continuous()' are scales for continuous npcx and npcy
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 npcy.

Usage

```
scale_npcx_continuous(...)

scale_npcy_continuous(...)
```

Arguments

...   Other arguments passed on to 'continuous_scale()'

---

scale_shape_outcome   *Shape scale for ternary outcomes*

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 `log.base.labels`. if supplied as a numeric vector they should be given using the data as passed to parameter `data`.
labels	The tick labels or a function to generate them from the tick positions. The default is function that uses the arguments passed to `log.base.data` and `log.base.labels` to generate suitable labels.
limits	limits One of: NULL to use the default scale range from ggplot2. A numeric vector of length two providing limits of the scale, using NA to refer to the existing minimum or maximum. A function that accepts the existing (automatic) limits and returns new limits. The default is function `symmetric_limits()` 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 apossibly 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   *Covenience scale for P-values*

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 `scale_y_continuous`.
`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 NULL for the default.
`breaks`	The positions of ticks or a function to generate them. Default varies depending on argument passed to `log.base.labels`.
`labels`	The tick labels or a function to generate them from the tick positions. The default is function that uses the arguments passed to `log.base.data` and `log.base.labels` to generate suitable labels.
`limits`	Use one of: NULL 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   *Apply a function to x or y values*

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 cumu-
lative 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 = NULL,
  .fun.x.args = list(),
  .fun.y = NULL,
  .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 = NULL,
  .fun.x.args = list(),
  .fun.y = NULL,
  .fun.y.args = list(),
  position = "identity",
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  ...
)
```

Arguments

mapping	The aesthetic mapping, usually constructed with [aes](#). 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	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	
	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. borders.
...	other arguments passed on to layer. This can include aesthetics whose values you want to set, not map. See layer 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))})
```

---

stat_dens2d_filter   *Filter observations by local density*

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 [aes](#) or [aes_](#). 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. [borders](#).
h	vector of bandwidths for x and y directions. Defaults to normal reference bandwidth (see bandwidth.nrd). 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 [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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 off 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   *Reset labels of observations in high density regions*

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 [aes](#) or [aes_](#). 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 bandwidth.nrd). 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.
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. borders.
...	other arguments passed on to layer. This can include aesthetics whose values you want to set, not map. See layer 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 [aes](#) or [aes_](#). 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.
augment.args	list of arguments to pass to broom:augment.
level	numeric Level of confidence interval to use (0.95 by default)
y.out	character (or numeric) index to column to return as y.
position	The position adjustment to use for overlapping points on this layer
na.rm	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. [borders](#).
...	other arguments passed on to [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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](#) wich 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 intead 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   *Residuals from model fit as segments*

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 [aes](#) or [aes_](#). 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.
`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. borders.
`...`	other arguments passed on to layer. This can include aesthetics whose values you want to set, not map. See layer 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 intead 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 [aes](#) or [aes_](#). 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 geom_text_npc() or geom_label_npc(). If using geom_text() or geom_label() 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. [borders](#).
...	other arguments passed on to [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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](#) wich 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 intead 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 AN-COVA. In such cases use the `stat_fit_tb()` statistic which applie 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 consitent 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   *Residuals from a model fit*

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 [aes] or [aes_]. 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.
resid.type	character passed to residuals() as argument for type.
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 should not inherit behaviour from the default plot specification, e.g. [borders].
...	other arguments passed on to [layer]. This can include aesthetics whose values you want to set, not map. See [layer] 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 intead 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   *Model-fit summary or ANOVA*

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 [aes](#) or [aes_](#). 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 defintion, 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 ?plotmath.
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. [borders](#).
...	other arguments passed on to [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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 orverridden.

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_gtdefault.

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 [aes](#) or [aes_](#). 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. [borders](#).
...	other arguments passed on to [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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](#) wich 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 intead 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 AN-COVA. 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 separatately 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 tible 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 [aes](#) or [aes_](#). 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 gridExtra ttheme defintion, 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 ?plotmath.
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. [borders](#).
...	other arguments passed on to [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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 list 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 [aes](#) or [aes_](#). 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 [sprintf](#) or [strptime](#), its use is deprecated.
`x.label.fmt`	character string giving a format definition for converting x-values into character strings by means of function [sprintf](#) or [strftime](#). 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 [sprintf](#).
`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. [borders](#).
`...`	other arguments passed on to [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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   *Equation, p-value, R^2, AIC or BIC of fitted polynomial*

Description

`stat_poly_eq` fits a polynomial and generates several labels including the equation, p-value, coefficient of determination (R^2), '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 [aes](#) or [aes_](#). 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 [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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^2, 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 geom_text_npc() or geom_label_npc(). If using geom_text() or geom_label() 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 label.x and label.y instead; together with a geom using npcx and npcy 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" or "text", 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. [borders](#).

Details

This stat can be used to automatically annotate a plot with R^2, adjusted R^2 or the fitted model equation. It supports only linear models fitted with function lm(). The R^2 and adjusted R^2 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^2 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 undertood 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 numric 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(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   *Number of observations in quadrants*

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 en 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

mapping	The aesthetic mapping, usually constructed with [aes](#) or [aes_](#). 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
quadrants	integer vector indicating which quadrants are of interest, with a 0L indicating the whole plot.
pool.along	character, one of "none", "x" or "y", indicating which quadrants to pool to calculate counts by pair of quadrants.
xintercept, yintercept	
	numeric the coordinates of the origin of the quadrants.
label.x, label.y	
	numeric Coordinates (in npc units) to be used for absolute positioning of the labels.
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. [borders](#).
...	other arguments passed on to [layer](#). This can include aesthetics whose values you want to set, not map. See [layer](#) 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 positve 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`. Alsoby 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   *Expand limits to be symetric*

Description

A simple function to expand scale limits to be symetric 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	*Convert an R object into a tibble*

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   *Table themes*

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

base_size	numeric, default font size.
base_colour	default font colour.
base_family	default font family.
parse	logical, default behaviour for parsing text as plotmath.
padding	length-2 unit vector specifying the horizontal and vertical padding of text within each cell.
...	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 defintion, or a constructor for a
               ttheme 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   *Example gene expression data*

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 | *Convert two numeric ternary outcomes into a factor*

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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