Package ‘ggpmisc’

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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.

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Description

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

Details

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

Extensions provided:

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

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

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

Acknowledgements

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

Note

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

Author(s)

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• Kamil Slowikowski [contributor]

References

Package suite 'r4photobiology' web site at https://www.r4photobiology.info/
Package 'ggplot2' documentation at https://ggplot2.tidyverse.org/
Package 'ggplot2' source code at https://github.com/tidyverse/ggplot2

See Also

Useful links:

• https://docs.r4photobiology.info/ggpmisc/
• https://bitbucket.org/aphalo/ggpmisc
• Report bugs at https://bitbucket.org/aphalo/ggpmisc/issues

Examples

library(tibble)

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

Annotate supporting NPC

Description

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

Usage

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

Arguments

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

Details

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

Note

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

Examples

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

**Inset graphical objects**

**Description**

`geom_grob` and `geom_grob_npc` add a Grob as inset to the ggplot using syntax similar to that of `geom_label`. In most respects they behave as any other ggplot geometry: a layer can contain multiple tables and faceting works as usual.

**Usage**

```r
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.

- **na.rm**
  - If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

- **...**
  - other arguments passed on to `layer`. This can include aesthetics whose values you want to set, not map. See `layer` for more details.
geom_grob

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

Note

These geoms work only with tibbles as data, as they 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(), npc.x and npc.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 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 adding layers with insets: geom_plot(), geom_table()
Examples

```r
library(tibble)
library(grid)
library(ggplot2)
library(gridExtra)

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

Description

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

Usage

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

```r
geom_text_npc(
  mapping = NULL,
  data = NULL,
  stat = \texttt{"identity"},
  position = \texttt{"identity"},
  ...,
  parse = \texttt{FALSE},
  nudge.x = 0,
  nudge.y = 0,
  check.overlap = \texttt{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", ...)'.

na.rm = FALSE,
show.legend = FALSE,
inherit.aes = FALSE
)
**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**

```r
def <- data.frame(
  x = c(0, 0, 1, 1, 0.5),
  x.chr = c("left", "left", "right", "right", "center"),
  y = c(0, 1, 1, 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_text_npc(aes(npcx = x, npcy = y, label = text))
```

---

**ncl**

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**

```r
def <- data.frame(
  x = c(0, 0, 1, 1, 0.5),
  x.chr = c("left", "left", "right", "right", "center"),
  y = c(0, 1, 1, 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_text_npc(aes(npcx = x, npcy = y, label = text))
```

---
**geom_plot**

```r
gem_label_npc(data = df, aes(npcx = x, npcy = y, label = text))
```

---

**Description**

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

**Usage**

```r
gem_plot(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...
)
```

```r
gem_plot_npc(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...
)
```

**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.
geomet_plot

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 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(), npc.x and npc.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 "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 adding layers with insets: `geom_grob()`, `geom_table()`

Examples

```r
# 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))
```

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

```r
geom_quadrant_lines(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  pool.along = "none",
  xintercept = 0,
)```


```r
geom_quadrant_lines

  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**

```r
# generate artificial data
set.seed(4321)
x <- 1:100
y <- rnorm(length(x), mean = 10)
my.data <- data.frame(x, y)
ggplot(my.data, aes(x, y)) +
  geom_quadrant_lines() +
  geom_point()
ggplot(my.data, aes(x, y)) +
  geom_quadrant_lines(linetype = "dotted") +
  geom_point()
ggplot(my.data, aes(x, y)) +
  geom_quadrant_lines(xintercept = 50, yintercept = 10, colour = "blue") +
  geom_point()
ggplot(my.data, aes(x, y)) +
  geom_quadrant_lines(xintercept = 50, pool.along = "y", colour = "blue") +
  geom_point()
ggplot(my.data, aes(x, y)) +
  geom_vhlines(xintercept = c(25, 50, 75), yintercept = 10, 
               linetype = "dotted", colour = "red") +
  geom_point() +
  theme_bw()
```

---

**geom_table**

**Inset tables**

**Description**

`geom_table` adds a textual table directly to the ggplot using syntax similar to that of `geom_label` while `geom_table_npc` is similar to `geom_label_npc` in that x and y coordinates are given in npc units. In most respects they behave as any other ggplot geometry: a layer can contain multiple tables and faceting works as usual.
Usage

```r
gemm_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
)
```

```r
gemm_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 theme definition, or a constructor for a theme or NULL for default.
- **table.rownames, table.colnames**: logical flag to enable or disable printing of row names and column names.
geom_table

- **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 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 be 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 `theme`.

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 theme 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/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?](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 adding layers with insets: `geom_grob()`, `geom_plot()`

Examples

```r
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))
```
geom_x_margin_arrow

Reference arrows on the margins

Description

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

Usage

`geom_x_margin_arrow()`
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(x = wt, y = mpg)) + geom_point()
p
p + geom_x_margin_grob(xintercept = 3.5)
p + geom_x_margin_grob(xintercept = 3.5)
p + geom_y_margin_grob(yintercept = c(18, 28, 15))
p + geom_x_margin_grob(data = data.frame(x = c(2.5, 4.5)), mapping = aes(xintercept = x))
p + geom_x_margin_grob(data = data.frame(x = c(2.5, 4.5)), mapping = aes(xintercept = x), sides = "tb")
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

## 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_point()` and `geom_y_margin_point()` behave similarly to `geom_vline()` and `geom_hline()` and share their "double personality" as both annotations and geometries.

## Usage

```r
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 = "1",
  point.shift = 0.017,
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = FALSE
)
```
Arguments

mapping  The aesthetic mapping, usually constructed with \texttt{aes} or \texttt{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 \texttt{layer}. This can include aesthetics whose values you want to set, not map. See \texttt{layer} for more details.
xintercept, yintercept numeric Parameters that control the position of the marginal points. If these are set, data, mapping and \texttt{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 \texttt{npc} units for the shift of the rug points inwards from the edge of the plotting area.
na.rm If \texttt{FALSE} (the default), removes missing values with a warning. If \texttt{TRUE} silently removes missing values.
show.legend logical. Should this layer be included in the legends? \texttt{NA}, the default, includes if any aesthetics are mapped. \texttt{FALSE} never includes, and \texttt{TRUE} always includes.
inherit.aes If \texttt{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. \texttt{borders}.

See Also

Other Geometries for marginal annotations in \texttt{ggplots}: \texttt{geom_x_margin_arrow()}, \texttt{geom_x_margin_grob()}

Examples

```r
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**

```r
## 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 supplied 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.
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**

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

---

**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 default by scales `scale_colour_outcome`, `scale_fill_outcome` and `scale_shape_outcome`. When n.levels = 2 both -1 and +1 are merged to the same level of the factor with label "de".

Note

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

See Also

Other Functions for quadrant and volcano plots: `FC_format()`, `geom_quadrant_lines()`, `scale_colour_outcome()`, `scale_shape_outcome()`, `scale_y_Pvalue()`, `stat_quadrant_counts()`, `xy_outcomes2factor()`

Other scales for omics data: `scale_shape_outcome()`, `scale_x_logFC()`, `xy_outcomes2factor()`

Examples

outcome2factor(c(-1, 1, 0, 1))
outcome2factor(c(-1, 1, 0, 1), n.levels = 2L)
threshold2factor(c(-0.1, -2, 0, +5))
threshold2factor(c(-0.1, -2, 0, +5), n.levels = 2L)
threshold2factor(c(-0.1, -2, 0, +5), threshold = c(-1, 1))
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

```r
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(....)
scale_shape_outcome

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

```r
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.
n.a.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

```r
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

```r
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,
  ...
)
```

```r
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 a possibly different log transformation (default is fold-change with no transformation).

See Also
Other scales for omics data: outcome2factor(), scale_shape_outcome(), xy_outcomes2factor()

Examples

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

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

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

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

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

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

# taking into account that data are expressed as log2 FC.
ggplot(my.df, aes(x, y)) +
  geom_point() +
  scale_x_logFC("A concentration%unit", breaks = log2(c(1/100, 1, 100))) +
  scale_y_logFC("B concentration%unit", breaks = log2(c(1/100, 1, 100)))

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

# override "special" default arguments.

# 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  

### Convenience 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_Pvalue

`

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()`, `scale_colour_outcome()`, `stat_quadrant_counts()`, `xy_outcomes2factor()`

**Examples**

```r
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 cumulative sums or running medians, and for normalizations it can be convenient to apply such functions.
on-the-fly to ensure that grouping is consistent between computations and aesthetics. One particularity of these statistics is that they can apply simultaneously different functions to \textit{x} values and to \textit{y} values when needed. In contrast \texttt{geom_smooth} applies a function that takes both \textit{x} and \textit{y} values as arguments.

\textbf{Usage}

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

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

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

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

Arguments

- **mapping**: The aesthetic mapping, usually constructed with `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**, **.fun.x**, **.fun.y**, **.fun**: function to be applied or the name of the function to be applied as a character string. One and only one of these parameters should be passed a non-null argument.

- **.fun.x.args**, **.fun.y.args**, **.fun.args**: additional arguments to be passed to the function as a named list.

- **position**: The position adjustment to use for overlapping points on this layer

- **na.rm**: a logical value indicating whether NA values should be stripped before the computation proceeds.

- **show.legend**: logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.

- **inherit.aes**: If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `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


Examples

```r
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
```


```r
stat_dens1d_filter

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

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

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

---

### `stat_dens1d_filter`

Filter observations by local 1D density

#### Description

`stat_dens1d_filter` Filters-out/filters-in observations in regions of a plot panel with high density of observations, based on the values mapped to one of x and y aesthetics. `stat_dens1d_filter_g` does the same 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

```r
stat_dens1d_filter(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  ..., 
  keep.fraction = 0.1,
  keep.number = Inf,
  keep.sparse = TRUE,
  invert.selection = FALSE,
  bw = "SJ",
  kernel = "gaussian",
  adjust = 1,
  n = 512,
  orientation = "x",
  na.rm = TRUE,
  show.legend = FALSE,
  inherit.aes = TRUE
)
```

`stat_dens1d_filter_g`
stat_dens1d_filter

mapping = NULL,
data = NULL,
geom = "point",
position = "identity",
keep.fraction = 0.1,
keep.number = Inf,
keep.sparse = TRUE,
invert.selection = FALSE,
na.rm = TRUE,
show.legend = FALSE,
inherit.aes = TRUE,
bw = "SJ",
adjust = 1,
kernel = "gaussian",
n = 512,
orientation = "x",
...
}

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.
keep.fraction numeric [0..1]. The fraction of the observations (or rows) in data to be retained.
keep.number integer Set the maximum number of observations to retain, effective only if obeying keep.fraction would result in a larger number.
keep.sparse logical If TRUE, the default, observations from the more sparse regions are retained, if FALSE those from the densest regions.
invert.selection logical If TRUE, the complement of the selected rows are returned.
bw numeric or character The smoothing bandwidth to be used. If numeric, the standard deviation of the smoothing kernel. If character, a rule to choose the bandwidth, as listed in bw.nrd.
kernel character See density for details.
adjust numeric A multiplicative bandwidth adjustment. This makes it possible to adjust the bandwidth while still using the a bandwidth estimator through an argument passed to bw. The larger the value passed to adjust the stronger the smoothing, hence decreasing sensitivity to local changes in density.
n numeric Number of equally spaced points at which the density is to be estimated for applying the cut point. See density for details.
orientation  character  The aesthetic along which density is computed. Given explicitly by setting orientation to either "x" or "y".

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.

Value
A copy of data with a subset of the rows retained based on the filtering criterion.

See Also
density used internally.

Other statistics returning a subset of data: stat_dens1d_labels(), stat_dens2d_filter(), stat_dens2d_labels()

Examples

library(ggrepel)

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() })
)
d$xg <- d$x
d$xg[51:100] <- d$xg[51:100] + 1

# highlight the 1/10 of observations in sparsest regions of the plot
ggplot(data = d, aes(x, y)) +
  geom_point() +
  geom_rug(sides = "b") +
  stat_dens1d_filter(colour = "red") +
  stat_dens1d_filter(geom = "rug", colour = "red", sides = "b")

# highlight the 1/4 of observations in densest regions of the plot
ggplot(data = d, aes(x, y)) +
  geom_point() +
  geom_rug(sides = "b") +
```r
stat_dens1d_filter(colour = "blue", keep.fraction = 1/4, keep.sparse = FALSE) +
stat_dens1d_filter(geom = "rug", colour = "blue", keep.fraction = 1/4, keep.sparse = FALSE, sides = "b")

# switching axes
ggplot(data = d, aes(x, y)) +
  geom_point() +
  geom_rug(sides = "l") +
  stat_dens1d_filter(colour = "red", orientation = "y") +
  stat_dens1d_filter(geom = "rug", colour = "red", orientation = "y", sides = "l")

# highlight 1/10 plus 1/10 observations in high and low density regions
ggplot(data = d, aes(x, y)) +
  geom_point() +
  geom_rug(sides = "b") +
  stat_dens1d_filter(colour = "red") +
  stat_dens1d_filter(geom = "rug", colour = "red", sides = "b") +
  stat_dens1d_filter(colour = "blue", keep.sparse = FALSE) +
  stat_dens1d_filter(geom = "rug", colour = "blue", keep.sparse = FALSE, sides = "b")

# selecting the 1/10 observations in sparsest regions and their complement
ggplot(data = d, aes(x, y)) +
  stat_dens1d_filter(colour = "red") +
  stat_dens1d_filter(geom = "rug", colour = "red", sides = "b") +
  stat_dens1d_filter(colour = "blue", invert.selection = TRUE) +
  stat_dens1d_filter(geom = "rug", colour = "blue", invert.selection = TRUE, sides = "b")

# density filtering done jointly across groups
ggplot(data = d, aes(xg, y, colour = group)) +
  geom_point() +
  geom_rug(sides = "b", colour = "black") +
  stat_dens1d_filter(shape = 1, size = 3, keep.fraction = 1/4, adjust = 2)

# density filtering done independently for each group
ggplot(data = d, aes(xg, y, colour = group)) +
  geom_point() +
  geom_rug(sides = "b") +
  stat_dens1d_filter_g(shape = 1, size = 3, keep.fraction = 1/4, adjust = 2)

# density filtering done jointly across groups by overriding grouping
ggplot(data = d, aes(xg, y, colour = group)) +
  geom_point() +
  geom_rug(sides = "b") +
  stat_dens1d_filter_g(colour = "black", shape = 1, size = 3, keep.fraction = 1/4, adjust = 2)

# label observations
ggplot(data = d, aes(x, y, label = lab, colour = group)) +
```
geom_point() +
stat_dens1d_filter(geom = "text", hjust = "outward")

# repulsive labels with ggrepel::geom_text_repel()
ggplot(data = d, aes(x, y, label = lab, colour = group)) +
geom_point() +
stat_dens1d_filter(geom = "text_repel")

stat_dens1d_labels

Replace labels in data based on 1D density

Description

stat_dens1d_labels() Sets values mapped to the label aesthetic to "" or a user provided character string based on the local density in regions of a plot panel. Its main use is together with repulsive geoms from package ggrepel. If there is no mapping to label in data, the mapping is set to rownames(data), with a message.

Usage

stat_dens1d_labels(
  mapping = NULL,
  data = NULL,
  geom = "text",
  position = "identity",
  ...,
  keep.fraction = 0.1,
  keep.number = Inf,
  keep.sparse = TRUE,
  invert.selection = FALSE,
  bw = "SJ",
  kernel = "gaussian",
  adjust = 1,
  n = 512,
  orientation = "x",
  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.
stat_dens1d_labels

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.

keep.fraction
numeric [0.1]. The fraction of the observations (or rows) in data to be retained.

keep.number
integer Set the maximum number of observations to retain, effective only if
obeying keep.fraction would result in a larger number.

keep.sparse
logical If TRUE, the default, observations from the more sparse regions are re-
tained, if FALSE those from the densest regions.

invert.selection
logical If TRUE, the complement of the selected rows are returned.

bw
numeric or character The smoothing bandwidth to be used. If numeric, the
standard deviation of the smoothing kernel. If character, a rule to choose the
bandwidth, as listed in bw.nrd.

kernel
character See density for details.

adjust
numeric A multiplicative bandwidth adjustment. This makes it possible to adjust
the bandwidth while still using the a bandwidth estimator through an argument
passed to bw. The larger the value passed to adjust the stronger the smoothing,
and so decreasing sensitivity to local changes in density.

n
numeric Number of equally spaced points at which the density is to be estimated
for applying the cut point. See density for details.

orientation
character The aesthetic along which density is computed. Given explicitly by
setting orientation to either "x" or "y".

label.fill
character vector of length 1 or a function.

na.rm
a logical value indicating whether NA values should be stripped before the com-
putation 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

stat_dens1d_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, "". This makes stat_dens1d_filter
unsuitable for the task. Non-the-less stat_dens1d_labels() could be useful in some other cases,
as the substitution character string can be set by the user.

Value

A copy of data with a subset of the rows retained based on the filtering criterion.
See Also

density used internally. Other statistics returning a subset of data: stat_dens1d_filter(), stat_dens2d_filter(), 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() })
)

# using defaults
ggplot(data = d, aes(x, y, label = lab)) +
  geom_point() +
  stat_dens1d_labels()

# using defaults
  geom_point() +
  stat_dens1d_labels(geom = "text_repel")

# if no mapping to label is found, it is set row names
  geom_point() +
  stat_dens1d_labels(geom = "text_repel")

# using defaults, along y-axis
  geom_point() +
  stat_dens1d_labels(orientation = "y", geom = "text_repel")

# example labelling with coordinates
  geom_point() +
  stat_dens1d_filter(colour = "red") +
  stat_dens1d_labels(geom = "text_repel", colour = "red", size = 3)

# 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_dens1d_labels(geom = "debug")

ggplot(data = d, aes(x, y, label = lab, colour = group)) +
  geom_point() +
  stat_dens1d_labels(geom = "text_repel")

# we keep labels starting with "a" across the whole plot, but all in sparse
# regions. To achieve this we pass as argument to label.fill a function
# instead of a character string.
label.fun <- function(x) {ifelse(grepl("^a", x), x, "")}

stat_dens2d_filter(data = d, aes(x, y, label = lab, colour = group)) +
  geom_point() +
  stat_dens1d_labels(geom = "text_repel", label.fill = label.fun)

---

**stat_dens2d_filter**  
*Filter observations by local 2D density*

**Description**

*stat_dens2d_filter* Filters-out/filters-in observations in regions of a plot panel with high density of observations, based on the values mapped to both x and y aesthetics. *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**

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

Arguments

mapping  The aesthetic mapping, usually constructed with \texttt{aes} or \texttt{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 \([0..1]\). The fraction of the observations (or rows) in \texttt{data} to be retained.
keep.number  integer Set the maximum number of observations to retain, effective only if obeying keep.fraction would result in a larger number.
keep.sparse  logical If TRUE, the default, observations from the more sparse regions are retained, if FALSE those from the densest regions.
invert.selection  logical If TRUE, the complement of the selected rows are returned.
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? \texttt{NA}, the default, includes if any aesthetics are mapped. \texttt{FALSE} never includes, and \texttt{TRUE} always includes.
inherit.aes  If \texttt{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. \texttt{borders}.
h  vector of bandwidths for x and y directions. Defaults to normal reference bandwidth (see \texttt{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 \texttt{layer}. This can include aesthetics whose values you want to set, not map. See \texttt{layer} for more details.
Value

A copy of data with a subset of the rows retained based on a 2D-density-based filtering criterion.

See Also

kde2d used internally.
Other statistics returning a subset of data: `stat_dens1d_filter()`, `stat_dens1d_labels()`, `stat_dens2d_labels()`

Examples

```r
library(ggrepel)

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() })
)

# filter (and here highlight) 1/10 observations in sparsest regions
ggplot(data = d, aes(x, y)) +
  geom_point() +
  stat_dens2d_filter(colour = "red")

# filter observations not in the sparsest regions
ggplot(data = d, aes(x, y)) +
  geom_point() +
  stat_dens2d_filter(colour = "blue", invert.selection = TRUE)

# filter observations in dense regions of the plot
ggplot(data = d, aes(x, y)) +
  geom_point() +
  stat_dens2d_filter(colour = "blue", keep.sparse = FALSE)

# filter 1/2 the observations
ggplot(data = d, aes(x, y)) +
  geom_point() +
  stat_dens2d_filter(colour = "red", keep.fraction = 0.5)

# filter 1/2 the observations but cap their number to maximum 12 observations
ggplot(data = d, aes(x, y)) +
  geom_point() +
  stat_dens2d_filter(colour = "red",
                    keep.fraction = 0.5,
                    keep.number = 12)
```
# density filtering done jointly across groups
ggplot(data = d, aes(x, y, colour = group)) +
  geom_point() +
  stat_dens2d_filter(shape = 1, size = 3, keep.fraction = 1/4)

# density filtering done independently for each group
ggplot(data = d, aes(x, y, colour = group)) +
  geom_point() +
  stat_dens2d_filter_g(shape = 1, size = 3, keep.fraction = 1/4)

# density filtering done jointly across groups by overriding grouping
ggplot(data = d, aes(x, y, colour = group)) +
  geom_point() +
  stat_dens2d_filter_g(colour = "black",
                      shape = 1, size = 3, keep.fraction = 1/4)

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

# repulsive labels with ggrepel::geom_text_repel()
ggplot(data = d, aes(x, y, label = lab, colour = group)) +
  geom_point() +
  stat_dens2d_filter(geom = "text_repel")

---

**stat_dens2d_labels**

Replace labels in data based on 2D density

---

**Description**

`stat_dens2d_labels()` sets values mapped to the `label` aesthetic to "" or a user provided character string based on the local density in regions of a plot panel. Its main use is together with repulsive geoms from package `ggrepel`. If there is no mapping to `label` in `data`, the mapping is set to `rownames(data)`, with a message.

**Usage**

```r
stat_dens2d_labels(
  mapping = NULL,
  data = NULL,
  geom = "text",
  position = "identity",
  ..., 
  keep.fraction = 0.1,
  keep.number = Inf,
  keep.sparse = TRUE,
)```
stat_dens2d_labels

invert.selection = FALSE,
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
...  other arguments passed on to layer. This can include aesthetics whose values you want to set, not map. See layer for more details.
keep.fraction  numeric [0..1]. The fraction of the observations (or rows) in data to be retained.
keep.number  integer Set the maximum number of observations to retain, effective only if obeying keep.fraction would result in a larger number.
keep.sparse  logical If TRUE, the default, observations from the more sparse regions are retained, if FALSE those from the densest regions.
invert.selection  logical If TRUE, the complement of the selected rows are returned.
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 vector of length 1 or a function.
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.

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, "". This makes stat_dens2d_filter unsuitable for the task. Non-the-less stat_dens2d_labels() could be useful in some other cases, as the substitution character string can be set by the user.
**stat_dens2d_labels**

**Value**

A copy of data with none, some or possibly all values for aesthetic label replaced by the value of label.fill based on a 2D-density-based filtering criterion.

**See Also**

`kde2d` used internally.

Other statistics returning a subset of data: `stat_dens1d_filter()`, `stat_dens1d_labels()`, `stat_dens2d_filter()`

**Examples**

```r
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() })
)

# using defaults
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(geom = "text_repel")

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

# we keep labels starting with "a" across the whole plot, but all in sparse
# regions. To achieve this we pass as argument to label.fill a function
# instead of a character string.
```
stat_fit_augment

label.fun <- function(x) {ifelse(grepl("^a", x), x, "")}

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

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 which can generate text or expression labels automatically, for these functions the mapping of aesthetic label needs to be explicitly supplied in the call, and labels built on the fly.

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

Handling of grouping

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

Computed variables

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

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

Note

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

See Also

broom

Other ggplot2 statistics based on 'broom': stat_fit_glance(), stat_fit_tb(), stat_fit_tidy()
Examples

library(gginnards)

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

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

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

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

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

# Weighted regression example
ggplot(mtcars, aes(x = disp, y = mpg, weight = cyl)) +
  geom_point(aes(colour = factor(cyl))) +
  stat_fit_augment(method = "lm",
      method.args = list(formula = y ~ x,
      weights = quote(weight)))

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

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 instead of the original variable names, while data is automatically passed the data frame. This helps ensure that the model is fitted to the same data as plotted in other layers.

Computed variables

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

- `x` x coordinates of observations
- `y.fitted` x coordinates of fitted values
- `y` y coordinates of observations
- `y.fitted` y coordinates of fitted values

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

Note

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

See Also

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

Examples

```r
library(gginnards) # needed for geom_debug()
# generate artificial data
ggplot(my.data, aes(x, y)) +
   geom_smooth(method = "lm", formula = y ~ poly(x, 3, raw = TRUE)) +
   stat_fit_deviations(formula = y ~ poly(x, 3, raw = TRUE), colour = "red")
```
`stat_fit_glance` fits a model and returns a summary "glance" of the model’s statistics, using package 'broom'.

**Usage**

```r
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`.
stat_fit_glance

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 which can generate text or expression labels automatically, for these functions the mapping of aesthetic label needs to be explicitly supplied in the call, and labels built on the fly.

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

Handling of grouping

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

Model formula required

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

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

See Also

*broom*

Other ggplot2 statistics based on 'broom': `stat_fit_augment()`, `stat_fit_tb()`, `stat_fit_tidy()`

Examples

```r
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
# 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("\textit{r}^2"="%.3f\text{--}italic(P)="%.2g",
                                        r.squared, p.value)),
                  parse = TRUE)

# Regression by group example
# Regression by group example
# Regression by group example
# 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("\textit{r}^2"="%.3f\text{--}italic(P)="%.2g",
                                           r.squared, p.value)),
                  parse = TRUE)

# Weighted regression example
# Weighted regression example
# Weighted regression example
# 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")
```
**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

```r
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.
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 instead of the original variable names, while data is automatically passed the data frame. This helps ensure that the model is fitted to the same data as plotted in other layers.

**Computed variables**

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

- **x** x coordinates of observations
- **y.resid** residuals from fitted values
- **y.resid.abs** absolute residuals from the fit

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

**See Also**

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

**Examples**

```r
# 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",
```
**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**

```r
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,
  tb.params = 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, tb.params**  
character or numeric vectors, optionally named, used to select and/or rename the columns or the parameters in 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` theme definition, or a constructor for a theme or NULL for default.

**table.rownames, table.colnames**  
logical flag to enable or disabling printing of row names and column names.

**table.hjust**  
numeric Horizontal justification for the core and column headings of the table.

**parse**  
If TRUE, the labels will be parsed into expressions and displayed as described in `?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 aesthetic mappings in the fitted model. This is suitable, for example for analysis of variance used to test for differences among groups.

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

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

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 fit summary, by default
ggplot(my.df, aes(covariate, x)) +
  geom_point() +
  stat_fit_tb() +
  expand_limits(y = 70)

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

# Linear regression ANOVA table
ggplot(my.df, aes(covariate, x)) +
  geom_point() +
  stat_fit_tb(tb.type = "fit.anova") +
  expand_limits(y = 70)

# Linear regression fit coefficients
ggplot(my.df, aes(covariate, x)) +
  geom_point() +
  stat_fit_tb(tb.type = "fit.coefs") +
  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)
# Polynomial regression with renamed parameters

```r
ggplot(my.df, aes(covariate, x)) +
  geom_point() +
  stat_fit_tb(method.args = list(formula = y ~ poly(x, 2)),
              tb.params = c("x^0" = 1, "x^1" = 2, "x^2" = 3),
              parse = TRUE) +
  expand_limits(y = 70)
```

# Polynomial regression with renamed parameters and columns

# using numeric indexes

```r
ggplot(my.df, aes(covariate, x)) +
  geom_point() +
  stat_fit_tb(method.args = list(formula = y ~ poly(x, 2)),
              tb.params = c("x^0" = 1, "x^1" = 2, "x^2" = 3),
              tb.vars = c("Term" = 1, "Estimate" = 2, "S.E." = 3,
                          "italic(F)-value" = 4, "italic(P)-value" = 5),
                          parse = TRUE) +
  expand_limits(y = 70)
```

# ANOVA summary

```r
ggplot(my.df, aes(group, x)) +
  geom_point() +
  stat_fit_tb() +
  expand_limits(y = 70)
```

# ANOVA table

```r
ggplot(my.df, aes(group, x)) +
  geom_point() +
  stat_fit_tb(tb.type = "fit.anova") +
  expand_limits(y = 70)
```

# ANOVA table with renamed and selected columns

# using column names

```r
ggplot(my.df, aes(group, x)) +
  geom_point() +
  stat_fit_tb(tb.type = "fit.anova",
              tb.vars = c(Effect = "term", "df", "italic(F)" = "statistic",
                          "italic(P)" = "p.value"),
                          parse = TRUE)
```

# ANOVA table with renamed and selected columns

# using column names with partial matching

```r
ggplot(my.df, aes(group, x)) +
  geom_point() +
  stat_fit_tb(tb.type = "fit.anova",
              tb.vars = c(Effect = "term", "df", "italic(F)" = "stat",
                          "italic(P)" = "p"),
                          parse = TRUE)
```

# ANOVA summary

```r
ggplot(my.df, aes(group, x)) +
  geom_point() +
```
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` which can generate text or expression labels automatically, for these functions the mapping of aesthetic `label` needs to be explicitly supplied in the call, and labels built on the fly.

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

**Handling of grouping**

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

**Computed variables**

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

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

**Note**

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

**See Also**

`broom`

Other ggplot2 statistics based on `broom`: `stat_fit_augment()`, `stat_fit_glance()`, `stat_fit_tb()`

**Examples**

```r
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),
```
# Regression by group example

```r
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

```r
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, p-value = %.3g",
                                         stat(x_estimate),
                                         stat(x_p.value))))
```

---

**stat_fmt_tb**

Select and slice a tibble nested in data

**Description**

`stat_fmt_tb` selects, reorders and/or renames columns and or rows of a tibble nested in data. This stat is intended to be used to pre-process tibble objects mapped to the label aesthetic before adding them to a plot with `geom_table`.

**Usage**

```r
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,
)```
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, tb.rows**: character or numeric vectors, optionally named, used to select and/or rename the columns or rows in the table returned.
- **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 definition, or a constructor for a ttheme or NULL for default.
- **table.rownames, table.colnames**: logical flag to enable or disabling printing of row names and column names.
- **table.hjust**: numeric Horizontal justification for the core and column headings of the table.
- **parse**: If TRUE, the labels will be parsed into expressions and displayed as described in ?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.

Value

The returned value is a copy codedata in which the data frames mapped to `label` have been modified.

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

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

# Hide column names, display row names
ggplot(my.df, aes(x, y, label = tbs)) +
  stat_fmt_tb(table.colnames = FALSE,
              table.rownames = TRUE) +
  expand_limits(x = c(0,3), y = c(-2, 6))

# Use a theme for the table
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))

# selection and renaming by column position
ggplot(my.df, aes(x, y, label = tbs)) +
  stat_fmt_tb(tb.vars = c(value = 1, group = 2),
              tb.rows = 1:3) +
  expand_limits(x = c(0,3), y = c(-2, 6))

# selection, reordering and renaming by column position
ggplot(my.df, aes(x, y, label = tbs)) +
  stat_fmt_tb(tb.vars = c(group = 2, value = 1),
              tb.rows = 1:3) +
  expand_limits(x = c(0,3), y = c(-2, 6))

# selection and renaming, using partial matching to column name
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

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

```r
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,
  ...
)
```

```r
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.xnpc = NULL,
label.ynpc = 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.xnpc, label.ynpc: 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", "text", "markdown" or "numeric".
na.rm: a logical indicating whether NA values should be stripped before the computation proceeds.
show.legend: logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
stat_poly_eq

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 understood by the geom used ("text" by default) are understood and grouping respected.

Computed variables

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

- **x,npcx**  x position
- **y,npcy**  y position
- **coeffls, r.squared, adj.r.squared, AIC, BIC**  as numeric values extracted from fit object
- **eq.label**  equation for the fitted polynomial as a character string to be parsed
- **rr.label**  $R^2$ of the fitted model as a character string to be parsed
- **adj.rr.label**  Adjusted $R^2$ of the fitted model as a character string to be parsed
- **f.value.label**  F value and degrees of freedom for the fitted model as a whole.
- **p.value.label**  P-value for the F-value above.
- **AIC.label**  AIC for the fitted model.
- **BIC.label**  BIC for the fitted model.
- **hjust, vjust**  Set to "inward" to override the default of the "text" geom.

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

- **x,npcx**  x position
\text{y.npcy} \hspace{1em} y \hspace{1em} \text{position}

\text{coef.ls} \hspace{1em} \text{list containing the "coefficients" matrix from the summary of the fit object}

\text{r.squared, adj.r.squared, f.value, f.df1, f.df2, p.value, AIC, BIC} \hspace{1em} \text{numeric values extracted or computed from fit object}

\text{hjust, vjust} \hspace{1em} \text{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 \texttt{geom_debug} as shown in the example below.

**Parsing may be required**

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

**Note**

For backward compatibility a logical is accepted as argument for \texttt{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 \texttt{eq.x.rhs}.

**References**

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

**See Also**

This \texttt{stat_poly_eq} statistic can return ready formatted labels depending on the argument passed to \texttt{output.type}. This is possible because only polynomial models are supported. For other types of models, statistics \texttt{stat_fit_glance}, \texttt{stat_fit_tidy} and \texttt{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: \texttt{stat_fit_deviations()}, \texttt{stat_fit_residuals()}

**Examples**

\begin{verbatim}
# 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
\end{verbatim}
```r
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"

```r
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|)".

```r
my.format <- 
  "b[0]=\%.3g", "b[1]=\%.3g", "b[2]=\%.3g", "b[3]=\%.3g"
```

```r
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.

```r
library(gginnards)
```

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

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

```r
ggplot(my.data, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", formula = formula) +
  stat_poly_eq(formula = formula, geom = "debug", output.type = "text")
```
`stat_quadrant_counts()` counts the number of observations in each quadrant of a plot panel. By default it adds a text label to the far corner of each quadrant. It can also be used to obtain the total number of observations in each of two pairs of quadrants or in the whole panel. Grouping is ignored, so in every case a single count is computed for each quadrant in a plot panel.

**Usage**

```r
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
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 positive quadrant. An argument value of zero, passed to formal parameter quadrants is interpreted as a request for the count of all observations in each plot panel.

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

Computed variables

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

quadrant integer, one of 0:4
x x value of label position in data units
y y value of label position in data units
npcx x value of label position in npc units
npcy y value of label position in npc units
count number of observations
As shown in one example below `geom_debug` can be used to print the computed values returned by any statistic. The output shown includes also values mapped to aesthetics, like `label` in the example.

**See Also**

Other Functions for quadrant and volcano plots: `FC_format()`, `geom_quadrant_lines()`, `outcome2factor()`, `scale_colour_outcome()`, `scale_shape_outcome()`, `scale_y_Pvalue()`, `xy_outcomes2factor()`

**Examples**

```r
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")
```

```r
library(ggplot2)

geom_point() +
stat_quadrant_counts(geom = "text") # use "tex" instead
```

### symmetric_limits

**Expand a range to make it symmetric**

#### Description

Expand scale limits to make them symmetric around zero. Can be passed as argument to parameter `limits` of continuous scales from packages 'ggplot2' or 'scales'. Can be also used to obtain an enclosing symmetric range for numeric vectors.

#### Usage

```r
symmetric_limits(x)
```

#### Arguments

- **x**
  - numeric The automatic limits when used as argument to a scale's `limits` formal parameter. Otherwise a numeric vector, possibly a range, for which to compute a symmetric enclosing range.

#### Value

A numeric vector of length two with the new limits, which are always such that the absolute value of upper and lower limits is the same.

#### Examples

```r
symmetric_limits(c(-1, 1.8))
symmetric_limits(c(-10, 1.8))
symmetric_limits(-5:20)
```

### 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**

```r

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"),
  ...
)
```
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.

Examples

library(dplyr)
l library(tibble) 

tcars %>% 
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
ttheme_set

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()
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` theme definition, or a constructor for a theme or NULL for default.

Value

A named list with the previous value of the option.

Note

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

Examples

```r
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)
```
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

```r
volcano_example.df
```

Format

A `data.frame` object with 1218 rows and 5 variables

See Also

Other Transcriptomics data examples: `quadrant_example.df`

Examples

```r
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

```r
xy_outcomes2factor(x, y)
```

```r
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

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