

Package ‘ggpmisc’

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Type Package

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Maintainer Pedro J. Aphalo <pedro.aphalo@helsinki.fi>

Description Extensions to 'ggplot2' respecting the grammar of graphics paradigm. Statistics: locate and tag peaks and valleys; label plot with the equation of a fitted polynomial or other types of models; labels with P-value, R² or adjusted R² 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' and 'broom.mixed' 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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ByteCompile TRUE

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URL <https://docs.r4photobiology.info/ggpmisc/>,
<https://github.com/aphalo/ggpmisc>

BugReports <https://github.com/aphalo/ggpmisc/issues>

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Author Pedro J. Aphalo [aut, cre] (<<https://orcid.org/0000-0003-3385-972X>>),
 Kamil Slowikowski [ctb] (<<https://orcid.org/0000-0002-2843-6370>>),
 Samer Mouksassi [ctb] (<<https://orcid.org/0000-0002-7152-6654>>)

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R topics documented:

ggpmisc-package	3
coef.lmodel2	5
confint.lmodel2	6
keep_tidy	7
Moved	8
outcome2factor	8
predict.lmodel2	9
quadrant_example.df	11
scale_colour_logFC	11
scale_colour_outcome	15
scale_shape_outcome	17
scale_x_logFC	19
scale_y_Pvalue	21
stat_correlation	24
stat_fit_augment	29
stat_fit_deviations	33
stat_fit_glance	37
stat_fit_residuals	41
stat_fit_tb	45
stat_fit_tidy	51
stat_ma_eq	56
stat_ma_line	61
stat_peaks	65
stat_poly_eq	69
stat_poly_line	78
stat_quant_band	81
stat_quant_eq	84
stat_quant_line	92
swap_xy	97
symmetric_limits	97
use_label	98
volcano_example.df	100
xy_outcomes2factor	101

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

Extensions to 'ggplot2' respecting the grammar of graphics paradigm. Statistics: locate and tag peaks and valleys; label plot with the equation of a fitted polynomial or other types of models; labels with P-value, R² or adjusted R² 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' and 'broom.mixed' are supported. Scales and stats to build volcano and quadrant plots based on outcomes, fold changes, p-values and false discovery rates.

Details

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

Extensions provided:

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

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

Warning!

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

Acknowledgements

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

Note

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

Author(s)

Maintainer: Pedro J. Aphalo <pedro.aphalo@helsinki.fi> ([ORCID](#))

Other contributors:

- Kamil Slowikowski ([ORCID](#)) [contributor]
- Samer Mouksassi <samerkouksassi@gmail.com> ([ORCID](#)) [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://github.com/aphalo/ggpmisc>
- Report bugs at <https://github.com/aphalo/ggpmisc/issues>

Examples

```
library(tibble)

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

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

```

        formula = formula,
        parse = TRUE) +
  labs(x = expression("Speed, " * x ~ ("mph")),
       y = expression("Stopping distance, " * y ~ ("ft")))

formula <- y ~ x
ggplot(PlantGrowth, aes(group, weight)) +
  stat_summary(fun.data = "mean_se") +
  stat_fit_tb(method = "lm",
             method.args = list(formula = formula),
             tb.type = "fit.anova",
             tb.vars = c(Term = "term", "df", "M.S." = "meansq",
                       "italic(F)" = "statistic",
                       "italic(p)" = "p.value"),
             tb.params = c("Group" = 1, "Error" = 2),
             table.theme = ttheme_gtbw(parse = TRUE)) +
  labs(x = "Group", y = "Dry weight of plants") +
  theme_classic()

```

coef.lmodel2

Extract Model Coefficients

Description

coef is a generic function which extracts model coefficients from objects returned by modeling functions. coefficients is an alias for it.

Usage

```
## S3 method for class 'lmodel2'
coef(object, method = "MA", ...)
```

Arguments

object	a fitted model object.
method	character One of the methods available in object.
...	ignored by this method.

Details

Function lmodel2() from package 'lmodel2' returns a fitted model object of class "lmodel2" which differs from that returned by lm(). Here we implement a coef() method for objects of this class. It differs from the generic method and that for lm objects in having an additional formal parameter method that must be used to select estimates based on which of the methods supported by lmodel2() are to be extracted. The returned object is identical in its structure to that returned by coef.lm().

Value

A named numeric vector of length two.

See Also

[lmodel2](#)

confint.lmodel2 *Confidence Intervals for Model Parameters*

Description

Computes confidence intervals for one or more parameters in a fitted model. This a method for objects inheriting from class "lmodel2".

Usage

```
## S3 method for class 'lmodel2'  
confint(object, parm, level = 0.95, method = "MA", ...)
```

Arguments

object	a fitted model object.
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	the confidence level required. Currently only 0.95 accepted.
method	character One of the methods available in object.
...	ignored by this method.

Details

Function `lmodel2()` from package 'lmodel2' returns a fitted model object of class "lmodel2" which differs from that returned by `lm()`. Here we implement a `confint()` method for objects of this class. It differs from the generic method and that for `lm` objects in having an additional formal parameter `method` that must be used to select estimates based on which of the methods supported by `lmodel2()` are to be extracted. The returned object is identical in its structure to that returned by `confint.lm()`.

Value

A data frame with two rows and three columns.

See Also

[lmodel2](#)

`keep_tidy`*Tidy, glance or augment an object keeping a trace of its origin*

Description

Methods implemented in package 'broom' to tidy, glance and augment the output from model fits return a consistently organized tibble with generic column names. Although this simplifies later steps in the data analysis and reporting, it drops key information needed for interpretation. `keep_tidy()` makes it possible to retain fields from the model fit object passed as argument to parameter `x` in the attribute "fm". The class of `x` is always stored, and by default also fields "call", "terms", "formula", "fixed" and "random" if available.

Usage

```
keep_tidy(x, ..., to.keep = c("call", "terms", "formula", "fixed", "random"))

keep_glance(x, ..., to.keep = c("call", "terms", "formula", "fixed", "random"))

keep_augment(
  x,
  ...,
  to.keep = c("call", "terms", "formula", "fixed", "random")
)
```

Arguments

<code>x</code>	An object for which <code>tidy()</code> , <code>glance</code> and/or <code>augment</code> method is available.
<code>...</code>	Other named arguments passed along to <code>tidy()</code> , <code>glance</code> or <code>augment</code> .
<code>to.keep</code>	character vector of field names in <code>x</code> to copy to attribute "fm" of the tibble returned by <code>tidy()</code> , <code>glance</code> or <code>augment</code> .

Details

Functions `keep_tidy()`, `keep_glance` or `keep_augment` are simple wrappers of the generic methods which make it possible to add to the returned values an attribute named "fm" preserving user selected fields and class of the model fit object. Fields names in `to.keep` missing in `x` are silently ignored.

Examples

```
# these examples can only be run if package 'broom' is available

if (requireNamespace("broom", quietly = TRUE)) {
  library(broom)
```

```

mod <- lm(mpg ~ wt + qsec, data = mtcars)

attr(keep_tidy(mod), "fm")[[ "class" ]]
attr(keep_glance(mod), "fm")[[ "class" ]]
attr(keep_augment(mod), "fm")[[ "class" ]]

attr(keep_tidy(summary(mod)), "fm")[[ "class" ]]

library(MASS)
rmod <- rlm(mpg ~ wt + qsec, data = mtcars)
attr(keep_tidy(rmod), "fm")[[ "class" ]]

}

```

Moved

Moved to package 'gginnards'

Description

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

Details

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

See Also

[gginnards-package](#), [geom_null](#), [stat_debug_group](#), [stat_debug_panel](#), [geom_debug](#) and [delete_layers](#).

outcome2factor

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\(\)](#), [scale_colour_outcome\(\)](#), [scale_shape_outcome\(\)](#), [scale_y_Pvalue\(\)](#), [xy_outcomes2factor\(\)](#)

Other scales for omics data: [scale_colour_logFC\(\)](#), [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))
```

predict.lmodel2

Model Predictions

Description

predict is a generic function for predictions from the results of various model fitting functions. predict.lmodel2 is the method for model fit objects of class "lmodel2".

Usage

```
## S3 method for class 'lmodel2'
predict(
  object,
  method = "MA",
  newdata = NULL,
  interval = c("none", "confidence"),
  level = 0.95,
  ...
)
```

Arguments

object	a fitted model object.
method	character One of the methods available in object.
newdata	An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
interval	Type of interval calculation.
level	the confidence level required. Currently only 0.95 accepted.
...	ignored by this method.

Details

Function `lmodel2()` from package 'lmodel2' returns a fitted model object of class "lmodel2" which differs from that returned by `lm()`. Here we implement a `predict()` method for objects of this class. It differs from the generic method and that for `lm` objects in having an additional formal parameter `method` that must be used to select which of the methods supported by `lmodel2()` are to be used in the prediction. The returned object is similar in its structure to that returned by `predict.lm()` but lacking names or rownames.

Value

If `interval = "none"` a numeric vector is returned, while if `interval = "confidence"` a data frame with columns `fit`, `lwr` and `upr` is returned.

See Also

[lmodel2](#)

quadrant_example.df *Example gene expression data*

Description

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

Usage

```
quadrant_example.df
```

Format

A data.frame object with 6088 rows and 6 variables

See Also

Other Transcriptomics data examples: [volcano_example.df](#)

Examples

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

scale_colour_logFC *Colour and fill scales for log fold change data*

Description

Continuous scales for colour and fill 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 legend title passed as argument to the name formal parameter.

Usage

```
scale_colour_logFC(
  name = "Abundance of y%unit",
  breaks = NULL,
  labels = NULL,
  limits = symmetric_limits,
  oob = scales::squish,
  expand = expansion(mult = 0.05, add = 0),
  log.base.labels = FALSE,
```

```
log.base.data = 2L,  
midpoint = NULL,  
low.colour = "dodgerblue2",  
mid.colour = "grey50",  
high.colour = "red",  
na.colour = "black",  
aesthetics = "colour",  
...  
)  
  
scale_color_logFC(  
  name = "Abundance of y%unit",  
  breaks = NULL,  
  labels = NULL,  
  limits = symmetric_limits,  
  oob = scales::squish,  
  expand = expansion(mult = 0.05, add = 0),  
  log.base.labels = FALSE,  
  log.base.data = 2L,  
  midpoint = NULL,  
  low.colour = "dodgerblue2",  
  mid.colour = "grey50",  
  high.colour = "red",  
  na.colour = "black",  
  aesthetics = "colour",  
  ...  
)  
  
scale_fill_logFC(  
  name = "Abundance of y%unit",  
  breaks = NULL,  
  labels = NULL,  
  limits = symmetric_limits,  
  oob = scales::squish,  
  expand = expansion(mult = 0.05, add = 0),  
  log.base.labels = FALSE,  
  log.base.data = 2L,  
  midpoint = 1,  
  low.colour = "dodgerblue2",  
  mid.colour = "grey50",  
  high.colour = "red",  
  na.colour = "black",  
  aesthetics = "fill",  
  ...  
)
```

Arguments

name	The name of the scale without units, used for the legend title.
------	---

breaks	The positions of ticks or a function to generate them. Default varies depending on argument passed to <code>log.base.labels</code> . if supplied as a numeric vector they should be given using the data as passed to parameter 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 <code>log.base.data</code> and <code>log.base.labels</code> to generate suitable labels.
limits	limits One of: NULL to use the default scale range from <code>ggplot2</code> . 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 <code>symmetric_limits()</code> which keep 1 at the middle of the axis..
oob	Function that handles limits outside of the scale limits (out of bounds). The default squishes out-of-bounds values to the boundary.
expand	Vector of range expansion constants used to add some padding around the data, to ensure that they are placed some distance away from the axes. The default is to expand the scale by 15% on each end for log-fold-data, so as to leave space for counts annotations.
<code>log.base.labels</code> , <code>log.base.data</code>	integer or logical Base of logarithms used to express fold-change values in tick labels and in data. Use FALSE for no logarithm transformation.
midpoint	numeric Value at the middle of the colour gradient, defaults to FC = 1, assuming data is expressed as logarithm.
<code>low.colour</code> , <code>mid.colour</code> , <code>high.colour</code> , <code>na.colour</code>	character Colour definitions to use for the gradient extremes and middle.
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 <code>aesthetics = c("colour", "fill")</code> .
...	other named arguments passed to <code>scale_y_continuous</code> .

Details

These scales only alter default arguments of `scale_colour_gradient2()` and `scale_fill_gradient2()`. 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 in the legend 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). The default for handling out of bounds values is to "squish" them to the extreme of the scale, which is different from the default used in 'ggplot2'.

See Also

Other scales for omics data: [outcome2factor\(\)](#), [scale_shape_outcome\(\)](#), [scale_x_logFC\(\)](#), [xy_outcomes2factor\(\)](#)

Examples

```

set.seed(12346)
my.df <- data.frame(x = rnorm(50, sd = 4), y = rnorm(50, sd = 4))
# we assume that both x and y values are expressed as log2 fold change

ggplot(my.df, aes(x, y, colour = y)) +
  geom_point(shape = "circle", size = 2.5) +
  scale_x_logFC() +
  scale_y_logFC() +
  scale_colour_logFC()

ggplot(my.df, aes(x, y, fill = y)) +
  geom_point(shape = "circle filled", colour = "black", size = 2.5) +
  scale_x_logFC() +
  scale_y_logFC() +
  scale_fill_logFC()

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

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

ggplot(my.df, aes(x, y, colour = y)) +
  geom_point() +
  scale_x_logFC(log.base.labels = 10) +
  scale_y_logFC(log.base.labels = 10) +
  scale_colour_logFC(log.base.labels = 10)

ggplot(my.df, aes(x, y, colour = y)) +
  geom_point() +
  scale_x_logFC(log.base.labels = 10) +
  scale_y_logFC(log.base.labels = 10) +
  scale_colour_logFC(log.base.labels = 10,
                     labels = FC_format(log.base.labels = 10,
                                         log.base.data = 2L,
                                         fmt = "%.*g"))

# override default arguments.
ggplot(my.df, aes(x, y, colour = y)) +
  geom_point() +
  scale_x_logFC() +
  scale_y_logFC() +

```

```
scale_colour_logFC(name = "Change",  
  labels = function(x) {paste(2^x, "fold")})
```

scale_colour_outcome *Colour and fill scales for ternary outcomes*

Description

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

Usage

```
scale_colour_outcome(  
  ...,  
  name = "Outcome",  
  ns.colour = "grey80",  
  up.colour = "red",  
  down.colour = "dodgerblue2",  
  de.colour = "goldenrod",  
  na.colour = "black",  
  values = "outcome:updown",  
  drop = TRUE,  
  aesthetics = "colour"  
)
```

```
scale_color_outcome(  
  ...,  
  name = "Outcome",  
  ns.colour = "grey80",  
  up.colour = "red",  
  down.colour = "dodgerblue2",  
  de.colour = "goldenrod",  
  na.colour = "black",  
  values = "outcome:updown",  
  drop = TRUE,  
  aesthetics = "colour"  
)
```

```
scale_fill_outcome(  
  ...,  
  name = "Outcome",  
  ns.colour = "grey80",  
  up.colour = "red",  
  down.colour = "dodgerblue2",  
  de.colour = "goldenrod",
```

```

na.colour = "black",
values = "outcome:both",
drop = TRUE,
aesthetics = "fill"
)

```

Arguments

...	other named arguments passed to <code>scale_colour_manual</code> .
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.
values	a set of aesthetic values to map data values to. The values will be matched in order (usually alphabetical) with the limits of the scale, or with breaks if provided. If this is a named vector, then the values will be matched based on the names instead. Data values that don't match will be given <code>na.value</code> . In addition the special values "outcome:updown", "outcome:de" and "outcome:both" set predefined values, with "outcome:both" as default.
drop	logical Should unused factor levels be omitted from the scale? The default, TRUE, uses the levels that appear in the data; FALSE uses all the levels in the factor.
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 <code>aesthetics = c("colour", "fill")</code> .

Details

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

Note

In 'ggplot2' (3.3.4, 3.3.5, 3.3.6) `scale_colour_manual()` and `scale_fill_manual()` do not obey `drop`, most likely due to a bug as this worked in version 3.3.3 and earlier. This results in spurious levels in the plot legend when using versions 3.3.4, 3.3.5, 3.3.6 of 'ggplot2'.

See Also

Other Functions for quadrant and volcano plots: [FC_format\(\)](#), [outcome2factor\(\)](#), [scale_shape_outcome\(\)](#), [scale_y_Pvalue\(\)](#), [xy_outcomes2factor\(\)](#)

Examples

```

set.seed(12346)
outcome <- sample(c(-1, 0, +1), 50, replace = TRUE)

```



```
my.df <- data.frame(x = rnorm(50),
                   y = rnorm(50),
                   outcome2 = outcome2factor(outcome, n.levels = 2),
                   outcome3 = outcome2factor(outcome))

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

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

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

scale_shape_outcome *Shape scale for ternary outcomes*

Description

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

Usage

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

Arguments

...	other named arguments passed to scale_manual.
name	The name of the scale, used for the axis-label.
ns.shape, down.shape, up.shape, de.shape	The shapes to use for each of the three possible outcomes.
na.shape	Shape used for NA.

Details

These scales only alter the values, and na.value default arguments of `scale_shape_manual()`. Please, see documentation for [scale_manual](#) for details.

See Also

Other Functions for quadrant and volcano plots: [FC_format\(\)](#), [outcome2factor\(\)](#), [scale_colour_outcome\(\)](#), [scale_y_Pvalue\(\)](#), [xy_outcomes2factor\(\)](#)

Other scales for omics data: [outcome2factor\(\)](#), [scale_colour_logFC\(\)](#), [scale_x_logFC\(\)](#), [xy_outcomes2factor\(\)](#)

Examples

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

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

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

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

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

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

 scale_x_logFC

Position scales for log fold change data

Description

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

Usage

```
scale_x_logFC(
  name = "Abundance of x%unit",
  breaks = NULL,
  labels = NULL,
  limits = symmetric_limits,
  oob = scales::squish,
  expand = expansion(mult = 0.05, add = 0),
  log.base.labels = FALSE,
  log.base.data = 2L,
  ...
)

scale_y_logFC(
  name = "Abundance of y%unit",
  breaks = NULL,
  labels = NULL,
  limits = symmetric_limits,
  oob = scales::squish,
  expand = expansion(mult = 0.05, add = 0),
  log.base.labels = FALSE,
  log.base.data = 2L,
  ...
)
```

Arguments

name	The name of the scale without units, used for the axis-label.
breaks	The positions of ticks or a function to generate them. Default varies depending on argument passed to <code>log.base.labels</code> . If supplied as a numeric vector they should be given using the data as passed to parameter <code>data</code> .
labels	The tick labels or a function to generate them from the tick positions. The default is function that uses the arguments passed to <code>log.base.data</code> and <code>log.base.labels</code> to generate suitable labels.


```

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

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

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

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

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

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

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

```

Description

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

Usage

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

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

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

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

)

Arguments

...	other named arguments passed to <code>scale_y_continuous</code> .
<code>name</code>	The name of the scale without units, used for the axis-label.
<code>trans</code>	Either the name of a transformation object, or the object itself. Use <code>NULL</code> for the default.
<code>breaks</code>	The positions of ticks or a function to generate them. Default varies depending on argument passed to <code>log.base.labels</code> .
<code>labels</code>	The tick labels or a function to generate them from the tick positions. The default is function that uses the arguments passed to <code>log.base.data</code> and <code>log.base.labels</code> to generate suitable labels.
<code>limits</code>	Use one of: <code>NULL</code> to use the default scale range, a numeric vector of length two providing limits of the scale; <code>NA</code> to refer to the existing minimum or maximum; a function that accepts the existing (automatic) limits and returns new limits.
<code>oob</code>	Function that handles limits outside of the scale limits (out of bounds). The default squishes out-of-bounds values to the boundary.
<code>expand</code>	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\(\)](#), [outcome2factor\(\)](#), [scale_colour_outcome\(\)](#), [scale_shape_outcome\(\)](#), [xy_outcomes2factor\(\)](#)

Examples

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

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

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

```
scale_y_FDR(limits = c(NA, 1e-20))
```

stat_correlation *Annotate plot with correlation test*

Description

stat_correlation() applies `stats::cor.test()` respecting grouping with `method = "pearson"` default but alternatively using "kendall" or "spearman" methods. It generates labels for correlation coefficients and p-value, coefficient of determination (R^2) for method "pearson" and number of observations.

Usage

```
stat_correlation(  
  mapping = NULL,  
  data = NULL,  
  geom = "text_npc",  
  position = "identity",  
  ...,  
  method = "pearson",  
  alternative = "two.sided",  
  exact = NULL,  
  r.conf.level = 0.95,  
  continuity = FALSE,  
  small.r = FALSE,  
  small.p = FALSE,  
  coef.keep.zeros = TRUE,  
  r.digits = 2,  
  t.digits = 3,  
  p.digits = 3,  
  CI.brackets = c("[", "]"),  
  label.x = "left",  
  label.y = "top",  
  hstep = 0,  
  vstep = NULL,  
  output.type = NULL,  
  boot.R = ifelse(method == "pearson", 0, 999),  
  na.rm = FALSE,  
  parse = NULL,  
  show.legend = FALSE,  
  inherit.aes = TRUE  
)
```


Arguments

mapping	The aesthetic mapping, usually constructed with <code>aes</code> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset, only needed if you want to override the plot defaults.
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 <code>layer</code> . This can include aesthetics whose values you want to set, not map. See <code>layer</code> for more details.
method	character One of "pearson", "kendall" or "spearman".
alternative	character One of "two.sided", "less" or "greater".
exact	logical Whether an exact p-value should be computed. Used for Kendall's tau and Spearman's rho.
r.conf.level	numeric Confidence level for the returned confidence interval.
continuity	logical If TRUE, a continuity correction is used for Kendall's tau and Spearman's rho when not computed exactly.
small.r, small.p	logical Flags to switch use of lower case r and p for coefficient of correlation (only for method = "pearson") and p-value.
coef.keep.zeros	logical Keep or drop trailing zeros when formatting the correlation coefficients and t-value, z-value or S-value (see note below).
r.digits, t.digits, p.digits	integer Number of digits after the decimal point to use for R, r.squared, tau or rho and P-value in labels.
CI.brackets	character vector of length 2. The opening and closing brackets used for the CI label.
label.x, label.y	numeric with range 0..1 "normalized parent coordinates" (npc units) or character if using <code>geom_text_npc()</code> or <code>geom_label_npc()</code> . If using <code>geom_text()</code> or <code>geom_label()</code> numeric in native data units. If too short they will be recycled.
hstep, vstep	numeric in npc units, the horizontal and vertical step used between labels for different groups.
output.type	character One of "expression", "LaTeX", "text", "markdown" or "numeric".
boot.R	integer The number of bootstrap resamples. Set to zero for no bootstrap estimates for the CI.
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
parse	logical Passed to the geom. If TRUE, the labels will be parsed into expressions and displayed as described in <code>?plotmath</code> . Default is TRUE if <code>output.type = "expression"</code> and FALSE otherwise.
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. <code>borders</code> .

Details

This statistic can be used to annotate a plot with the correlation coefficient and the outcome of its test of significance. It supports Pearson, Kendall and Spearman methods to compute correlation. This statistic generates labels as R expressions by default but LaTeX (use TikZ device), markdown (use package 'ggtext') and plain text are also supported, as well as numeric values for user-generated text labels. The character labels include the symbol describing the quantity together with the numeric value. For the confidence interval (CI) the default is to follow the APA recommendation of using square brackets.

The value of `parse` is set automatically based on `output-type`, but if you assemble labels that need parsing from numeric output, the default needs to be overridden. By default the value of `output.type` is guessed from the name of the geometry.

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. `cor.test()` is always applied to the variables mapped to the `x` and `y` aesthetics, so the scales used for `x` and `y` should both be continuous scales rather than discrete.

Aesthetics

`stat_correlation()` requires `x` and `y`. In addition, the aesthetics understood by the geom ("text" is the default) are understood and grouping respected.

Computed variables

If `output.type` is "numeric" the returned tibble contains the columns listed below with variations depending on the method. If the model fit function used does not return a value, the variable is set to `NA_real_`.

x, npcx x position

y, npey y position

r, and cor, tau or rho numeric values for correlation coefficient estimates

t.value and its df, z.value or S.value numeric values for statistic estimates

p.value, n numeric values.

r.conf.level numeric value, as fraction of one.

r.confint.low Confidence interval limit for `r`.

r.confint.high Confidence interval limit for `r`.

grp.label Set according to mapping in `aes`.

method.label Set according method used.

method, test character values

If `output.type` different from "numeric" the returned tibble contains in addition to the columns listed above those listed below. If the numeric value is missing the label is set to `character(0L)`.

r.label, and cor.label, tau.label or rho.label Correlation coefficient as a character string.

t.value.label, z.value.label or S.value.label t-value and degrees of freedom, z-value or S-value as a character string.

p.value.label P-value for test against zero, as a character string.

r.confint.label, and cor.confint.label, tau.confint.label or rho.confint.label Confidence interval for r (only with method = "pearson").

n.label Number of observations used in the fit, as a character string.

grp.label Set according to mapping in aes, as a character string.

To explore the computed values returned for a given input we suggest the use of [geom_debug](#) as shown in the last examples below.

Note

Currently `coef.keep.zeros` is ignored, with trailing zeros always retained in the labels but not protected from being dropped by R when character strings are parsed into expressions.

See Also

[cor.test](#) for details on the computations.

Examples

```
# generate artificial data
set.seed(4321)
x <- (1:100) / 10
y <- x + rnorm(length(x))
my.data <- data.frame(x = x,
                      y = y,
                      y.desc = - y,
                      group = c("A", "B"))

# by default only R is displayed
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation()

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(small.r = TRUE)

ggplot(my.data, aes(x, y.desc)) +
  geom_point() +
  stat_correlation(label.x = "right")

# non-default methods
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(method = "kendall")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(method = "spearman")
```

```

# use_label() can map a user selected label
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(use_label("R2"))

# use_label() can assemble and map a combined label
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(use_label(c("R", "P", "n", "method")))

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(use_label(c("R", "R.CI")))

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(use_label(c("R", "R.CI")), boot.R = 999)

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(use_label(c("R", "R.CI")), method = "kendall")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(use_label(c("R", "R.CI")), method = "spearman")

# manually assemble and map a specific label using paste() and aes()
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(aes(label = paste(after_stat(r.label),
                                   after_stat(p.value.label),
                                   after_stat(n.label),
                                   sep = "*\ ", "\*"))))

# manually format and map a specific label using sprintf() and aes()
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_correlation(aes(label = sprintf("%s\ " with \*%s*\ " for \*%s",
                                   after_stat(r.label),
                                   after_stat(p.value.label),
                                   after_stat(t.value.label))))

# Inspecting the returned data using geom_debug()
# This provides a quick way of finding out the names of the variables that
# are available for mapping to aesthetics with after_stat().

gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

# the whole of computed data
if (gginnards.installed)

```

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

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_correlation(geom = "debug", method = "pearson")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_correlation(geom = "debug", method = "kendall")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_correlation(geom = "debug", method = "spearman")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_correlation(geom = "debug", output.type = "numeric")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_correlation(geom = "debug", output.type = "markdown")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_correlation(geom = "debug", output.type = "LaTeX")
```

stat_fit_augment

Augment data with fitted values and statistics

Description

stat_fit_augment fits a model and returns a "tidy" version of the model's data with prediction added, using 'augment()' methods from packages 'broom', 'broom.mixed', or other sources. The prediction can be added to the plot as a curve.

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 . 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 or function.
method.args, augment.args	list of arguments to pass to method and to 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.

Warning!

Not all `'glance()'` methods are defined in package `'broom'`. `'glance()'` specializations for mixed models fits of classes `'lme'`, `'nlme'`, `'lme4'`, and many others are defined in package `'broom.mixed'`.

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 `generics::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.

Although arguments passed to parameter `augment.args` will be passed to `[generics::augment()]` whether they are silently ignored or obeyed depends on each specialization of `[augment()]`, so do carefully read the documentation for the version of `[augment()]` corresponding to the `'method'` used to fit the model.

See Also

[broom](#) and `broom.mixed` for details on how the tidying of the result of model fits is done.

Other `ggplot` statistics for model fits: [stat_fit_deviations\(\)](#), [stat_fit_glance\(\)](#), [stat_fit_residuals\(\)](#), [stat_fit_tb\(\)](#), [stat_fit_tidy\(\)](#)

Examples

```
# Package 'broom' needs to be installed to run these examples.
# We check availability before running them to avoid errors.

if (requireNamespace("broom", quietly = TRUE)) {
  broom.installed <- TRUE
  library(broom)
  library(quantreg)

# Inspecting the returned data using geom_debug()
if (requireNamespace("gginnards", quietly = TRUE)) {
  library(gginnards)
```

```

# Regression by panel, inspecting data
  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
if (broom.installed)
  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
if (broom.installed)
  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
if (broom.installed)
  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
if (broom.installed)
  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
if (broom.installed)
  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
if (broom.installed)
  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")

# Quantile regression
if (broom.installed)
  ggplot(mtcars, aes(x = disp, y = mpg)) +
    geom_point() +
    stat_fit_augment(method = "rq",
                    label.y = "bottom")

```

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",
  method.args = list(),
  formula = NULL,
  position = "identity",
  na.rm = FALSE,
  orientation = NA,
  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

method	function or character If character, "lm", "rlm", "lqs", "rq" and the name of a function to be matched, possibly followed by the fit function's method argument separated by a colon (e.g. "rq:br"). Functions implementing methods must accept arguments to parameters formula, data, weights and method. A fitted() method must exist for the returned model fit object class.
method.args	named list with additional arguments.
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.
orientation	character Either "x" or "y" controlling the default for formula.
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. 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. 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

In the case of `method = "rq"` quantiles are fixed at $\tau = 0.5$ unless `method.args` has `length > 0`. Parameter orientation is redundant as it only affects the default for `formula` but is included for consistency with `ggplot2`.

See Also

Other `ggplot` statistics for model fits: [stat_fit_augment\(\)](#), [stat_fit_glance\(\)](#), [stat_fit_residuals\(\)](#), [stat_fit_tb\(\)](#), [stat_fit_tidy\(\)](#)

Examples

```
# generate artificial data
library(MASS)

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)

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

# plot residuals from linear model with y as explanatory variable
ggplot(my.data, aes(x, y)) +
  geom_smooth(method = "lm", formula = y ~ x, orientation = "y") +
  stat_fit_deviations(method = "lm", formula = x ~ y, colour = "red") +
  geom_point()

# as above using orientation
ggplot(my.data, aes(x, y)) +
  geom_smooth(method = "lm", orientation = "y") +
  stat_fit_deviations(orientation = "y", colour = "red") +
  geom_point()

# both regressions and their deviations
ggplot(my.data, aes(x, y)) +
  geom_smooth(method = "lm") +
  stat_fit_deviations(colour = "blue") +
  geom_smooth(method = "lm", orientation = "y", colour = "red") +
  stat_fit_deviations(orientation = "y", colour = "red") +
  geom_point()

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

# plot linear regression
ggplot(my.data, aes(x, y)) +
  geom_smooth(method = "lm", formula = my.formula) +
```

```

stat_fit_deviations(formula = my.formula, colour = "red") +
geom_point()

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

# plot robust regression
ggplot(my.data, aes(x, y)) +
  stat_smooth(method = "rlm", formula = my.formula) +
  stat_fit_deviations(formula = my.formula, method = "rlm", colour = "red") +
  geom_point()

# plot robust regression with weights indicated by colour
my.data.outlier <- my.data
my.data.outlier[6, "y"] <- my.data.outlier[6, "y"] * 10
ggplot(my.data.outlier, aes(x, y)) +
  stat_smooth(method = MASS::rlm, formula = my.formula) +
  stat_fit_deviations(formula = my.formula, method = "rlm",
                      mapping = aes(colour = after_stat(weights)),
                      show.legend = TRUE) +
  scale_color_gradient(low = "red", high = "blue", limits = c(0, 1),
                      guide = "colourbar") +
  geom_point()

# plot quantile regression (= median regression)
ggplot(my.data, aes(x, y)) +
  stat_quantile(formula = my.formula, quantiles = 0.5) +
  stat_fit_deviations(formula = my.formula, method = "rq", colour = "red") +
  geom_point()

# plot quantile regression (= "quartile" regression)
ggplot(my.data, aes(x, y)) +
  stat_quantile(formula = my.formula, quantiles = 0.75) +
  stat_fit_deviations(formula = my.formula, colour = "red",
                      method = "rq", method.args = list(tau = 0.75)) +
  geom_point()

# inspecting the returned data with geom_debug()
gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

# plot, using geom_debug() to explore the after_stat data
if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_smooth(method = "lm", formula = my.formula) +
    stat_fit_deviations(formula = my.formula, geom = "debug") +
    geom_point()

if (gginnards.installed)

```

```
ggplot(my.data.outlier, aes(x, y)) +
  stat_smooth(method = MASS::rlm, formula = my.formula) +
  stat_fit_deviations(formula = my.formula, method = "rlm", geom = "debug") +
  geom_point()
```

stat_fit_glance

One row summary data frame for a fitted model

Description

stat_fit_glance fits a model and returns a "tidy" version of the model's fit, using 'glance()' methods from packages 'broom', 'broom.mixed', or other sources.

Usage

```
stat_fit_glance(
  mapping = NULL,
  data = NULL,
  geom = "text_npc",
  method = "lm",
  method.args = list(formula = y ~ x),
  glance.args = list(),
  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 <code>aes</code> . 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 or function.
method.args, glance.args	list of arguments to pass to method and to <code>[generics::glance()]</code> , respectively.
label.x, label.y	numeric with range 0..1 "normalized parent coordinates" (npc units) or character if using <code>geom_text_npc()</code> or <code>geom_label_npc()</code> . If using <code>geom_text()</code> or <code>geom_label()</code> numeric in native data units. If too short they will be recycled.

<code>hstep, vstep</code>	numeric in npc units, the horizontal and vertical step used between labels for different groups.
<code>position</code>	The position adjustment to use for overlapping points on this layer
<code>na.rm</code>	a logical indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders .
<code>...</code>	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.

Value

The output of the `glance()` methods is returned almost as is in the data object, as a data frame. 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 including the name of variables/columns, which vary depending on the model fitting function and model formula we suggest the use of [geom_debug](#). An example is shown below.

Warning!

Not all 'glance()' methods are defined in package 'broom'. 'glance()' specializations for mixed models fits of classes 'lme', 'nlme', 'lme4', and many others are defined in package 'broom.mixed'.

Handling of grouping

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


```

        mapping = aes(label = sprintf('italic(r)^2=="%.3f~~italic(P)=="%.2g',
                                     after_stat(r.squared), after_stat(p.value))),
        parse = TRUE)

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

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

# correlation test
if (broom.installed)
  ggplot(mtcars, aes(x = disp, y = mpg)) +
    geom_point() +
    stat_fit_glance(method = "cor.test",
                   label.y = "bottom",
                   method.args = list(formula = ~ x + y),
                   mapping = aes(label = sprintf('r[Pearson]=="%.3f~~italic(P)=="%.2g',
                                               after_stat(estimate), after_stat(p.value))),
                   parse = TRUE)

if (broom.installed)
  ggplot(mtcars, aes(x = disp, y = mpg)) +
    geom_point() +
    stat_fit_glance(method = "cor.test",
                   label.y = "bottom",
                   method.args = list(formula = ~ x + y, method = "spearman", exact = FALSE),
                   mapping = aes(label = sprintf('r[Spearman]=="%.3f~~italic(P)=="%.2g',
                                               after_stat(estimate), after_stat(p.value))),
                   parse = TRUE)

# Quantile regression by group example
if (broom.installed)
  ggplot(mtcars, aes(x = disp, y = mpg)) +
    stat_smooth(method = "lm") +

```



```

geom_point() +
stat_fit_glance(method = "rq",
                label.y = "bottom",
                method.args = list(formula = y ~ x),
                mapping = aes(label = sprintf('AIC = %.3g, BIC = %.3g',
                                             after_stat(AIC), after_stat(BIC))))

```

stat_fit_residuals *Residuals from a model fit*

Description

stat_fit_residuals fits a linear model and returns residuals ready to be plotted as points.

Usage

```

stat_fit_residuals(
  mapping = NULL,
  data = NULL,
  geom = "point",
  method = "lm",
  method.args = list(),
  formula = NULL,
  resid.type = NULL,
  weighted = FALSE,
  position = "identity",
  na.rm = FALSE,
  orientation = NA,
  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
method	function or character If character, "lm", "rlm", "rq" and the name of a function to be matched, possibly followed by the fit function's method argument separated by a colon (e.g. "rq:br"). Functions implementing methods must accept arguments to parameters formula, data, weights and method. A residuals() method must exist for the returned model fit object class.
method.args	named list with additional arguments.

formula	a "formula" object. Using aesthetic names instead of original variable names.
resid.type	character passed to residuals() as argument for type (defaults to "working" except if weighted = TRUE when it is forced to "deviance").
weighted	logical If true weighted residuals will be returned.
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.
orientation	character Either "x" or "y" controlling the default for formula.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and should not inherit behaviour from the default plot specification, e.g. borders.
...	other arguments passed on to layer. This can include aesthetics whose values you want to set, not map. See layer for more details.

Details

This stat can be used to automatically plot residuals as points in a plot. At the moment it supports only linear models fitted with function `lm()` or `rlm()`. It applies to the fitted model object methods `residuals` or `weighted.residuals` depending on the argument passed to parameter `weighted`.

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 value of `nrow` as `data` as subset for each group containing five numeric variables.

x x coordinates of observations or x residuals from fitted values,

y y coordinates of observations or y residuals from fitted values,

x.resid residuals from fitted values,

y.resid residuals from fitted values,

weights the weights passed as input to `lm` or those computed by `rlm`

.

For `orientation = "x"`, the default, `stat(y.resid)` is copied to variable `y`, while for `orientation = "y"` `stat(x.resid)` is copied to variable `x`.

Note

How weights are applied to residuals depends on the method used to fit the model. For ordinary least squares (OLS), weights are applied to the squares of the residuals, so the weighted residuals are obtained by multiplying the "deviance" residuals by the square root of the weights. When residuals are penalized differently to fit a model, the weighted residuals need to be computed accordingly. Say if we use the absolute value of the residuals instead of the squared values, weighted residuals are obtained by multiplying the residuals by the weights.

See Also

Other ggplot statistics for model fits: [stat_fit_augment\(\)](#), [stat_fit_deviations\(\)](#), [stat_fit_glance\(\)](#), [stat_fit_tb\(\)](#), [stat_fit_tidy\(\)](#)

Examples

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

# plot residuals from linear model
ggplot(my.data, aes(x, y)) +
  geom_hline(yintercept = 0, linetype = "dashed") +
  stat_fit_residuals(formula = y ~ x)

ggplot(my.data, aes(x, y)) +
  geom_hline(yintercept = 0, linetype = "dashed") +
  stat_fit_residuals(formula = y ~ x, weighted = TRUE)

# plot residuals from linear model with y as explanatory variable
ggplot(my.data, aes(x, y)) +
  geom_vline(xintercept = 0, linetype = "dashed") +
  stat_fit_residuals(formula = x ~ y) +
  coord_flip()

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

# plot residuals from linear model
ggplot(my.data, aes(x, y)) +
  geom_hline(yintercept = 0, linetype = "dashed") +
  stat_fit_residuals(formula = my.formula) +
  coord_flip()

ggplot(my.data, aes(x, y)) +
  geom_hline(yintercept = 0, linetype = "dashed") +
  stat_fit_residuals(formula = my.formula, resid.type = "response")

# plot residuals from robust regression
ggplot(my.data, aes(x, y)) +
```

```

geom_hline(yintercept = 0, linetype = "dashed") +
stat_fit_residuals(formula = my.formula, method = "rlm")

# plot residuals with weights indicated by colour
my.data.outlier <- my.data
my.data.outlier[6, "y"] <- my.data.outlier[6, "y"] * 10
ggplot(my.data.outlier, aes(x, y)) +
  stat_fit_residuals(formula = my.formula, method = "rlm",
                    mapping = aes(colour = after_stat(weights)),
                    show.legend = TRUE) +
  scale_color_gradient(low = "red", high = "blue", limits = c(0, 1),
                      guide = "colourbar")

# plot weighted residuals with weights indicated by colour
ggplot(my.data.outlier) +
  stat_fit_residuals(formula = my.formula, method = "rlm",
                    mapping = aes(x = x,
                                   y = stage(start = y, after_stat = y * weights),
                                   colour = after_stat(weights)),
                    show.legend = TRUE) +
  scale_color_gradient(low = "red", high = "blue", limits = c(0, 1),
                      guide = "colourbar")

# plot residuals from quantile regression (median)
ggplot(my.data, aes(x, y)) +
  geom_hline(yintercept = 0, linetype = "dashed") +
  stat_fit_residuals(formula = my.formula, method = "rq")

# plot residuals from quantile regression (upper quartile)
ggplot(my.data, aes(x, y)) +
  geom_hline(yintercept = 0, linetype = "dashed") +
  stat_fit_residuals(formula = my.formula, method = "rq",
                    method.args = list(tau = 0.75))

# inspecting the returned data
gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    stat_fit_residuals(formula = my.formula, resid.type = "working",
                      geom = "debug")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    stat_fit_residuals(formula = my.formula, method = "rlm",
                      geom = "debug")

```

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

Description

stat_fit_tb fits a model and returns a "tidy" version of the model's summary or ANOVA table, using tidy() methods from packages 'broom', 'broom.mixed', or other 'broom' extensions. The annotation is added to the plots in tabular form.

Usage

```
stat_fit_tb(  
  mapping = NULL,  
  data = NULL,  
  geom = "table_npc",  
  method = "lm",  
  method.args = list(formula = y ~ x),  
  tidy.args = list(),  
  tb.type = "fit.summary",  
  tb.vars = NULL,  
  tb.params = NULL,  
  digits = 3,  
  p.digits = digits,  
  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. 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, tidy.args	lists of arguments to pass to method and to tidy().
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 for all numeric values in the table.
p.digits	integer indicating the number of decimal places to round p-values to, with those rounded to zero displayed as the next larger possible value preceded by "<". If p.digits is outside the range 1..22 no rounding takes place.
label.x, label.y	numeric Coordinates (in data units) to be used for absolute positioning of the output. If too short they will be recycled.
label.x.npc, label.y.npc	numeric with range 0..1 or character. Coordinates to be used for positioning the output, expressed in "normalized parent coordinates" or character string. If too short they will be recycled.
position	The position adjustment to use for overlapping points on this layer
table.theme	NULL, list or function A 'gridExtra' ttheme definition, or a constructor for a ttheme or NULL for default.
table.rownames, table.colnames	logical flag to enable or disabling printing of row names and column names.
table.hjust	numeric Horizontal justification for the core and column headings of the table.
parse	If TRUE, the labels will be parsed into expressions and displayed as described in ?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. The plot's default data is used by default, which helps ensure that the model is fitted to the same data as plotted in other layers.

Value

A tibble with columns named `fm.tb` (a tibble returned by `tidy()` with possibly renamed and subset columns and rows, within a list), `fm.tb.type` (copy of argument passed to `tb.type`), `fm.class` (the class of the fitted model object), `fm.method` (the fit function's name), `fm.call` (the call if available), `x` and `y`.

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](#).

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 tibble, containing the result from a single model fit to all data in a panel. If grouping is present, it is ignored in the sense of returning a single table, but the grouping aesthetic can be a term in the fitted model.

See Also

[broom](#), [broom.mixed](#), and [tidy](#) 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 ggplot statistics for model fits: [stat_fit_augment\(\)](#), [stat_fit_deviations\(\)](#), [stat_fit_glance\(\)](#), [stat_fit_residuals\(\)](#), [stat_fit_tidy\(\)](#)

Examples

```
# Package 'broom' needs to be installed to run these examples.
# We check availability before running them to avoid errors.
broom.installed <- requireNamespace("broom", quietly = TRUE)

if (broom.installed)
  library(broom)

# 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)

gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

## covariate is a numeric or continuous variable
```

```

# Linear regression fit summary, all defaults
if (broom.installed)
  ggplot(my.df, aes(covariate, x)) +
    geom_point() +
    stat_fit_tb() +
    expand_limits(y = 70)

# we can use geom_debug() and str() to inspect the returned value
# and discover the variables that can be mapped to aesthetics with
# after_stat()
if (broom.installed && gginnards.installed)
  ggplot(my.df, aes(covariate, x)) +
    geom_point() +
    stat_fit_tb(geom = "debug", summary.fun = str) +
    expand_limits(y = 70)

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

# Linear regression fit summary, with manual table formatting
if (broom.installed)
  ggplot(my.df, aes(covariate, x)) +
    geom_point() +
    stat_fit_tb(digits = 2,
                p.digits = 4,
                tb.params = c("intercept" = 1, "covariate" = 2),
                tb.vars = c(Term = 1, Estimate = 2,
                            "italic(s)" = 3, "italic(t)" = 4,
                            "italic(P)" = 5),
                parse = TRUE) +
    expand_limits(y = 70)

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

# Linear regression ANOVA table, with manual table formatting
if (broom.installed)
  ggplot(my.df, aes(covariate, x)) +
    geom_point() +
    stat_fit_tb(tb.type = "fit.anova",
                tb.params = c("Covariate" = 1, 2),
                tb.vars = c(Effect = 1, d.f. = 2,
                            "M.S." = 4, "italic(F)" = 5,
                            "italic(P)" = 6),
                parse = TRUE) +

```



```

    expand_limits(y = 67)

# Linear regression fit coefficients, with default formatting
if (broom.installed)
  ggplot(my.df, aes(covariate, x)) +
    geom_point() +
    stat_fit_tb(tb.type = "fit.coefs") +
    expand_limits(y = 67)

# Linear regression fit coefficients, with manual table formatting
if (broom.installed)
  ggplot(my.df, aes(covariate, x)) +
    geom_point() +
    stat_fit_tb(tb.type = "fit.coefs",
               tb.params = c(a = 1, b = 2),
               tb.vars = c(Term = 1, Estimate = 2)) +
    expand_limits(y = 67)

## x is also a numeric or continuous variable
# Polynomial regression, with default formatting
if (broom.installed)
  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 manual table formatting
if (broom.installed)
  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(t)" = 4, "italic(P)" = 5),
               parse = TRUE) +
    expand_limits(y = 70)

## group is a factor or discrete variable
# ANOVA summary, with default formatting
if (broom.installed)
  ggplot(my.df, aes(group, x)) +
    geom_point() +
    stat_fit_tb() +
    expand_limits(y = 70)

# ANOVA table, with default formatting
if (broom.installed)
  ggplot(my.df, aes(group, x)) +
    geom_point() +
    stat_fit_tb(tb.type = "fit.anova") +
    expand_limits(y = 70)

# ANOVA table, with manual table formatting

```

```

if (broom.installed)
  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"),
               tb.params = c(Group = 1, Error = 2),
               parse = TRUE)

# ANOVA table, with manual table formatting
# using column names with partial matching
if (broom.installed)
  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"),
               tb.params = c(Group = "x", Error = "Resid"),
               parse = TRUE)

# ANOVA summary, with default formatting
if (broom.installed)
  ggplot(my.df, aes(group, x)) +
    geom_point() +
    stat_fit_tb() +
    expand_limits(y = 70)

## covariate is a numeric variable and group is a factor
# ANCOVA (covariate not plotted) ANOVA table, with default formatting
if (broom.installed)
  ggplot(my.df, aes(group, x, z = covariate)) +
    geom_point() +
    stat_fit_tb(tb.type = "fit.anova",
               method.args = list(formula = y ~ x + z))

# ANCOVA (covariate not plotted) ANOVA table, with manual table formatting
if (broom.installed)
  ggplot(my.df, aes(group, x, z = covariate)) +
    geom_point() +
    stat_fit_tb(tb.type = "fit.anova",
               method.args = list(formula = y ~ x + z),
               tb.vars = c(Effect = 1, d.f. = 2,
                           "M.S." = 4, "italic(F)" = 5,
                           "italic(P)" = 6),
               tb.params = c(Group = 1,
                              Covariate = 2,
                              Error = 3),
               parse = TRUE)

## group is a factor or discrete variable
# t-test, minimal output, with manual table formatting
if (broom.installed)
  ggplot(my.df, aes(group, x)) +

```

```

    geom_point() +
    stat_fit_tb(method = "t.test",
               tb.vars = c("italic(t)" = "statistic", "italic(P)" = "p.value"),
               parse = TRUE)

# t-test, more detailed output, with manual table formatting
if (broom.installed)
  ggplot(my.df, aes(group, x)) +
    geom_point() +
    stat_fit_tb(method = "t.test",
               tb.vars = c("\Delta \"*italic(x)\" = \"estimate\",
                           \"CI low\" = \"conf.low\", \"CI high\" = \"conf.high\",
                           \"italic(t)\" = \"statistic\", \"italic(P)\" = \"p.value\"),
               parse = TRUE) +
    expand_limits(y = 67)

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

## covariate is a numeric or continuous variable
# Linear regression using a table theme and non-default position
if (broom.installed)
  ggplot(my.df, aes(covariate, x)) +
    geom_point() +
    stat_fit_tb(table.theme = ttheme_gtlight,
               npcx = "left", npcy = "bottom") +
    expand_limits(y = 35)

```

stat_fit_tidy

One row data frame with fitted parameter estimates

Description

stat_fit_tidy fits a model and returns a "tidy" version of the model's summary, using `tidy()` methods from packages `'broom'`, `'broom.mixed'`, or other sources. To add the summary in tabular form use `stat_fit_tb` instead of this statistic. When using `stat_fit_tidy()` you will most likely want to change the default mapping for label.

Usage

```

stat_fit_tidy(
  mapping = NULL,
  data = NULL,

```

```

geom = "text_npc",
method = "lm",
method.args = list(formula = y ~ x),
tidy.args = list(),
label.x = "left",
label.y = "top",
hstep = 0,
vstep = NULL,
sanitize.names = FALSE,
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
method	character or function.
method.args, tidy.args	list of arguments to pass to method, and to [generics::tidy], respectively.
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.
sanitize.names	logical If true sanitize column names in the returned data with R's <code>make.names()</code> function.
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.

Value

The output of `tidy()` is returned after reshaping it into a single row. Grouping is respected, and the model fitted 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`. Otherwise, the names of the columns in the returned data are based on those returned by the `tidy()` method for the model fit class returned by the fit function. These 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 including the name of variables/columns, which vary depending on the model fitting function and model formula, we suggest the use of `geom_debug`. An example is shown below. Names of columns as returned by default are not always syntactically valid R names making it necessary to use back ticks to access them. Syntactically valid names are guaranteed if `sanitize.names = TRUE` is added to the call.

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.

Warning!

Not all 'glance()' methods are defined in package 'broom'. 'glance()' specializations for mixed models fits of classes 'lme', 'nlme', 'lme4', and many others are defined in package 'broom.mixed'.

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.

Note

The statistic `stat_fit_tidy` 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.

Although arguments passed to parameter `tidy.args` will be passed to `[generics::tidy()]` whether they are silently ignored or obeyed depends on each specialization of `[tidy()]`, so do carefully read

the documentation for the version of [tidy()] corresponding to the ‘method’ used to fit the model. You will also need to manually install the package, such as ‘broom’, where the tidier you intend to use are defined.

See Also

[broom](#) and `broom.mixed` for details on how the tidying of the result of model fits is done.

Other ggplot statistics for model fits: [stat_fit_augment\(\)](#), [stat_fit_deviations\(\)](#), [stat_fit_glance\(\)](#), [stat_fit_residuals\(\)](#), [stat_fit_tb\(\)](#)

Examples

```
# Package 'broom' needs to be installed to run these examples.
# We check availability before running them to avoid errors.

if (requireNamespace("broom", quietly = TRUE)) {
  broom.installed <- TRUE
  library(broom)
  library(quantreg)

# Inspecting the returned data using geom_debug()
  if (requireNamespace("gginnards", quietly = TRUE)) {
    library(gginnards)

# This provides a quick way of finding out the names of the variables that
# are available for mapping to aesthetics. This is specially important for
# this stat as these names depend on the specific tidy() method used, which
# depends on the method used, such as lm(), used to fit the model.

# Regression by panel, default column names
  ggplot(mtcars, aes(x = disp, y = mpg)) +
    stat_smooth(method = "lm", formula = y ~ x + I(x^2)) +
    geom_point(aes(colour = factor(cyl))) +
    stat_fit_tidy(method = "lm",
                 method.args = list(formula = y ~ x + I(x^2)),
                 geom = "debug")

# Regression by panel, sanitized column names
  ggplot(mtcars, aes(x = disp, y = mpg)) +
    stat_smooth(method = "lm", formula = y ~ x + I(x^2)) +
    geom_point(aes(colour = factor(cyl))) +
    stat_fit_tidy(method = "lm",
                 method.args = list(formula = y ~ x + I(x^2)),
                 geom = "debug", sanitize.names = TRUE)
  }
}

# Regression by panel example
if (broom.installed)
  ggplot(mtcars, aes(x = disp, y = mpg)) +
    stat_smooth(method = "lm") +
    geom_point(aes(colour = factor(cyl))) +
```

```

stat_fit_tidy(method = "lm",
              label.x = "right",
              method.args = list(formula = y ~ x),
              mapping = aes(label = sprintf("Slope = %.3g\np-value = %.3g",
                                             after_stat(x_estimate),
                                             after_stat(x_p.value))))

# Regression by group example
if (broom.installed)
  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",
                                                 after_stat(x_estimate),
                                                 after_stat(x_p.value))))

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

# Correlation test
if (broom.installed)
  ggplot(mtcars, aes(x = disp, y = mpg)) +
    stat_smooth(method = "lm") +
    geom_point() +
    stat_fit_tidy(method = "cor.test",
                  label.y = "bottom",
                  method.args = list(formula = ~ x + y),
                  mapping = aes(label = sprintf("R = %.3g\np-value = %.3g",
                                                 after_stat(`_estimate`),
                                                 after_stat(`_p.value`))))

# Quantile regression
if (broom.installed)
  ggplot(mtcars, aes(x = disp, y = mpg)) +
    stat_smooth(method = "lm") +
    geom_point() +
    stat_fit_tidy(method = "rq",
                  label.y = "bottom",
                  method.args = list(formula = y ~ x),
                  tidy.args = list(se.type = "nid"),
                  mapping = aes(label = sprintf("Slope = %.3g\np-value = %.3g",

```

```
after_stat(x_estimate),
after_stat(x_p.value)))
```

stat_ma_eq

Equation, p-value, R² of major axis regression

Description

stat_ma_eq fits model II regressions. From the fitted model it generates several labels including the equation, p-value, coefficient of determination (R^2), and number of observations.

Usage

```
stat_ma_eq(
  mapping = NULL,
  data = NULL,
  geom = "text_npc",
  position = "identity",
  ...,
  method = "lmodel2:MA",
  method.args = list(),
  formula = NULL,
  range.y = NULL,
  range.x = NULL,
  nperm = 99,
  eq.with.lhs = TRUE,
  eq.x.rhs = NULL,
  small.r = FALSE,
  small.p = FALSE,
  coef.digits = 3,
  coef.keep.zeros = TRUE,
  rr.digits = 2,
  theta.digits = 2,
  p.digits = max(1, ceiling(log10(nperm))),
  label.x = "left",
  label.y = "top",
  hstep = 0,
  vstep = NULL,
  output.type = NULL,
  na.rm = FALSE,
  orientation = NA,
  parse = NULL,
  show.legend = FALSE,
  inherit.aes = TRUE
)
```


Arguments

mapping	The aesthetic mapping, usually constructed with <code>aes</code> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset, only needed if you want to override the plot defaults.
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 <code>layer</code> . This can include aesthetics whose values you want to set, not map. See <code>layer</code> for more details.
method	function or character If character, "MA", "SMA", "RMA" or "OLS", alternatively "lmodel2" or the name of a model fit function are accepted, possibly followed by the fit function's method argument separated by a colon (e.g. "lmodel2:MA"). If a function different to <code>lmodel2()</code> , it must accept arguments named <code>formula</code> , <code>data</code> , <code>range.y</code> , <code>range.x</code> and <code>nperm</code> and return a model fit object of class <code>lmodel2</code> .
method.args	named list with additional arguments.
formula	a formula object. Using aesthetic names <code>x</code> and <code>y</code> instead of original variable names.
range.y, range.x	character Pass "relative" or "interval" if method "RMA" is to be computed.
nperm	integer Number of permutation used to estimate significance.
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.
small.r, small.p	logical Flags to switch use of lower case r and p for coefficient of determination and p-value.
coef.digits	integer Number of significant digits to use for the fitted coefficients.
coef.keep.zeros	logical Keep or drop trailing zeros when formatting the fitted coefficients and F-value.
rr.digits, p.digits, theta.digits	integer Number of digits after the decimal point to use for R^2 , theta and P-value in labels.
label.x, label.y	numeric with range 0..1 "normalized parent coordinates" (npc units) or character if using <code>geom_text_npc()</code> or <code>geom_label_npc()</code> . If using <code>geom_text()</code> or <code>geom_label()</code> numeric in native data units. If too short they will be recycled.
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.

orientation	character Either "x" or "y" controlling the default for formula.
parse	logical Passed to the geom. If TRUE, the labels will be parsed into expressions and displayed as described in ?plotmath. Default is TRUE if output.type = "expression" and FALSE otherwise.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders .

Details

This stat can be used to automatically annotate a plot with R^2 , P -value, n and/or the fitted model equation. It supports linear major axis (MA), standard major axis (SMA) and ranged major axis (RMA) regression by means of function `lmodel2`. Please see the documentation, including the vignette of package 'lmodel2' for details. The parameters in `stat_ma_eq()` follow the same naming as in function `lmodel2()`.

It is important to keep in mind that although the fitted line does not depend on whether the x or y appears on the rhs of the model formula, the numeric estimates for the parameters do depend on this.

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_ma_eq()` mimics how `stat_smooth()` works, except that only linear regression can be fitted. Similarly to these statistics the model fits respect grouping, so the scales used for x and y should both be continuous scales rather than discrete.

Aesthetics

`stat_ma_eq` understands x and y , to be referenced in the formula while the weight aesthetic is ignored. Both x and y must be mapped to numeric variables. In addition, the aesthetics understood by the geom ("text" is the default) are understood and grouping respected.

Computed variables

If `output.type` different from "numeric" the returned tibble contains columns listed below. If the fitted model does not contain a given value, the label is set to `character(0L)`.

x,npcx x position

y,npcy y position

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

p.value.label P -value if available, depends on method.

theta.label Angle in degrees between the two OLS lines for lines estimated from $y \sim x$ and $x \sim y$ linear model (`lm`) fits.

n.label Number of observations used in the fit.

grp.label Set according to mapping in `aes`.

method.label Set according method used.

r.squared, theta, p.value, n numeric values, from the model fit object

If `output.type` is "numeric" the returned tibble contains columns listed below. If the model fit function used does not return a value, the variable is set to `NA_real_`.

x, npcx x position

y, npcy y position

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

r.squared, theta, p.value, n numeric values, from the model fit object

grp.label Set according to mapping in `aes`.

b_0.constant TRUE is polynomial is forced through the origin

b_i One or two columns with the coefficient estimates

To explore the computed values returned for a given input we suggest the use of `geom_debug` as shown in the last examples below.

Note

For backward compatibility a logical is accepted as argument for `eq.with.lhs`. If TRUE, the default is used, either "x" or "y", depending on the argument passed to `formula`. However, "x" or "y" can be substituted by providing a suitable replacement character string through `eq.x.rhs`. Parameter orientation is redundant as it only affects the default for `formula` but is included for consistency with `ggplot2::stat_smooth()`.

Methods in `lmodel2` are all computed always except for RMA that requires a numeric argument to at least one of `range.y` or `range.x`. The results for specific methods are extracted a posteriori from the model fit object. When a function is passed as argument to `method`, the method can be passed in a list to `method.args` as member `method`. More easily, the name of the function can be passed as a character string together with the `lmodel2`-supported method.

R option `OutDec` is obeyed based on its value at the time the plot is rendered, i.e., displayed or printed. Set `options(OutDec = ",")` for languages like Spanish or French.

See Also

The major axis regression model is fitted with function `lmodel2`, please consult its documentation. Statistic `stat_ma_eq()` can return different ready formatted labels depending on the argument passed to `output.type`. If ordinary least squares polynomial regression is desired, then `stat_poly_eq`. If quantile-fitted polynomial regression is desired, `stat_quant_eq` should be used. For other types of models such as non-linear models, statistics `stat_fit_glance` and `stat_fit_tidy` should be used and the code for construction of character strings from numeric values and their mapping to aesthetic `label` explicitly supplied in the call.

Other ggplot statistics for major axis regression: `stat_ma_line()`

Examples

```

# generate artificial data
set.seed(98723)
my.data <- data.frame(x = rnorm(100) + (0:99) / 10 - 5,
                     y = rnorm(100) + (0:99) / 10 - 5,
                     group = c("A", "B"))

# using defaults (major axis regression)
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line() +
  stat_ma_eq()

# use_label() can assemble and map a combined label
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(method = "MA") +
  stat_ma_eq(use_label(c("eq", "R2", "P")))

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(method = "MA") +
  stat_ma_eq(use_label(c("R2", "P", "theta", "method")))

# using ranged major axis regression
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(method = "RMA",
              range.y = "interval",
              range.x = "interval") +
  stat_ma_eq(use_label(c("eq", "R2", "P")),
            method = "RMA",
            range.y = "interval",
            range.x = "interval")

# No permutation-based test
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(method = "MA") +
  stat_ma_eq(use_label(c("eq", "R2")),
            method = "MA",
            nperm = 0)

# explicit formula "x explained by y"
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(formula = x ~ y) +
  stat_ma_eq(formula = x ~ y,
            use_label(c("eq", "R2", "P")))

# grouping
ggplot(my.data, aes(x, y, color = group)) +

```

```

    geom_point() +
    stat_ma_line() +
    stat_ma_eq()

# labelling equations
ggplot(my.data,
       aes(x, y, shape = group, linetype = group, grp.label = group)) +
  geom_point() +
  stat_ma_line(color = "black") +
  stat_ma_eq(use_label(c("grp", "eq", "R2"))) +
  theme_classic()

# Inspecting the returned data using geom_debug()
# This provides a quick way of finding out the names of the variables that
# are available for mapping to aesthetics with after_stat().

gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

# default is output.type = "expression"
if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_ma_eq(geom = "debug")

## Not run:
if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_ma_eq(aes(label = after_stat(eq.label)),
              geom = "debug",
              output.type = "markdown")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_ma_eq(geom = "debug", output.type = "text")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_ma_eq(geom = "debug", output.type = "numeric")

## End(Not run)

```

Description

Predicted values and a confidence band are computed and, by default, plotted. `stat_ma_line()` behaves similarly to `stat_smooth` except for fitting the model with `lmodel2::lmodel2()` with "MA" as default for method.

Usage

```
stat_ma_line(
  mapping = NULL,
  data = NULL,
  geom = "smooth",
  position = "identity",
  ...,
  method = "lmodel2:MA",
  method.args = list(),
  formula = NULL,
  range.y = NULL,
  range.x = NULL,
  se = TRUE,
  fm.values = FALSE,
  n = 80,
  nperm = 99,
  fullrange = FALSE,
  level = 0.95,
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

mapping	The aesthetic mapping, usually constructed with <code>aes</code> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset, only needed if you want to override the plot defaults.
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 <code>layer</code> . This can include aesthetics whose values you want to set, not map. See <code>layer</code> for more details.
method	function or character If character, "MA", "SMA" , "RMA" or "OLS", alternatively "lmodel2" or the name of a model fit function are accepted, possibly followed by the fit function's method argument separated by a colon (e.g. "lmodel2:MA"). If a function different to <code>lmodel2()</code> , it must accept arguments named <code>formula</code> , <code>data</code> , <code>range.y</code> , <code>range.x</code> and <code>nperm</code> and return a model fit object of class <code>lmodel2</code> .
method.args	named list with additional arguments.

formula	a formula object. Using aesthetic names x and y instead of original variable names.
range.y, range.x	character Pass "relative" or "interval" if method "RMA" is to be computed.
se	logical Return confidence interval around smooth? ('TRUE' by default, see 'level' to control.)
fm.values	logical Add R2, p-value and n as columns to returned data? ('FALSE' by default.)
n	Number of points at which to evaluate smoother.
nperm	integer Number of permutation used to estimate significance.
fullrange	Should the fit span the full range of the plot, or just the data?
level	Level of confidence interval to use (only 0.95 currently).
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
orientation	character Either "x" or "y" controlling the default for formula.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders .

Details

This statistic fits major axis ("MA") and other model II regressions with function [lmodel2](#). Model II regression is called for when both x and y are subject to random variation and the intention is not to predict y from x by means of the model but rather to study the relationship between two independent variables. A frequent case in biology are allometric relationships among body parts.

As the fitted line is the same whether x or y is on the rhs of the model equation, `orientation` even is accepted does not have an effect on the fit. In contrast, [geom_smooth](#) treats each axis differently and can thus have two orientations. The orientation is easy to deduce from the argument passed to `formula`. Thus, `stat_ma_line()` will by default guess which orientation the layer should have. If no argument is passed to `formula`, the orientation can be specified directly passing an argument to the `orientation` parameter, which can be either "x" or "y". The value gives the axis that is on the rhs of the model equation, "x" being the default orientation. Package 'ggpmisc' does not define new geometries matching the new statistics as they are not needed and conceptually transformations of data are expressed as statistics.

Value

The value returned by the statistic is a data frame, that will have n rows of predicted values and their confidence limits. Optionally it will also include additional values related to the model fit.

Computed variables

'stat_ma_line()' provides the following variables, some of which depend on the orientation:

y *or* **x** predicted value
ymin *or* **xmin** lower pointwise confidence interval around the mean
ymax *or* **xmax** upper pointwise confidence interval around the mean
se standard error

If `fm.values = TRUE` is passed then columns based on the summary of the model fit are added, with the same value in each row within a group. This is wasteful and disabled by default, but provides a simple and robust approach to achieve effects like colouring or hiding of the model fit line based on P-values, r-squared or the number of observations.

Aesthetics

`stat_ma_line` understands `x` and `y`, to be referenced in the formula. Both must be mapped to numeric variables. In addition, the aesthetics understood by the geom ("`geom_smooth`" is the default) are understood and grouping respected.

See Also

Other ggplot statistics for major axis regression: [stat_ma_eq\(\)](#)

Examples

```
# generate artificial data
set.seed(98723)
my.data <- data.frame(x = rnorm(100) + (0:99) / 10 - 5,
                      y = rnorm(100) + (0:99) / 10 - 5,
                      group = c("A", "B"))

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

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(method = "MA")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(method = "SMA")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(method = "RMA",
              range.y = "interval", range.x = "interval")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(method = "OLS")

# plot line to the ends of range of data (the default)
ggplot(my.data, aes(x, y)) +
```



```

    geom_point() +
    stat_ma_line(fullrange = FALSE) +
    expand_limits(x = c(-10, 10), y = c(-10, 10))

# plot line to the limits of the scales
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(fullrange = TRUE) +
  expand_limits(x = c(-10, 10), y = c(-10, 10))

# plot line to the limits of the scales
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(orientation = "y", fullrange = TRUE) +
  expand_limits(x = c(-10, 10), y = c(-10, 10))

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line(formula = x ~ y)

# Smooths are automatically fit to each group (defined by categorical
# aesthetics or the group aesthetic) and for each facet.

ggplot(my.data, aes(x, y, colour = group)) +
  geom_point() +
  stat_ma_line()

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_ma_line() +
  facet_wrap(~group)

# Inspecting the returned data using geom_debug()
gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    stat_ma_line(geom = "debug")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    stat_ma_line(geom = "debug", fm.values = TRUE)

```

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 a subset of data with rows matching for peaks or valleys with formatted character labels added. The formatting is determined by a format string compatible with sprintf() or strftime().

Usage

```
stat_peaks(  
  mapping = NULL,  
  data = NULL,  
  geom = "point",  
  span = 5,  
  ignore_threshold = 0,  
  strict = FALSE,  
  label.fmt = NULL,  
  x.label.fmt = NULL,  
  y.label.fmt = NULL,  
  orientation = "x",  
  position = "identity",  
  na.rm = FALSE,  
  show.legend = FALSE,  
  inherit.aes = TRUE,  
  ...  
)  
  
stat_valleys(  
  mapping = NULL,  
  data = NULL,  
  geom = "point",  
  span = 5,  
  ignore_threshold = 0,  
  strict = FALSE,  
  label.fmt = NULL,  
  x.label.fmt = NULL,  
  y.label.fmt = NULL,  
  orientation = "x",  
  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.
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 <code>sprintf</code> or <code>strptime</code> , its use is deprecated.
x.label.fmt	character string giving a format definition for converting <code>\$x\$</code> -values into character strings by means of function <code>sprintf</code> or <code>strftime</code> . The default argument varies depending on the scale in use.
y.label.fmt	character string giving a format definition for converting <code>\$y\$</code> -values into character strings by means of function <code>sprintf</code> .
orientation	character Either "x" or "y".
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. <code>borders</code> .
...	other arguments passed on to <code>layer</code> . This can include aesthetics whose values you want to set, not map. See <code>layer</code> for more details.

Details

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.

The default for parameter `strict` is TRUE in functions `splus2R::peaks()` and `find_peaks()`, while the default is FALSE in `stat_peaks()` and in `stat_valleys()`.

Returned and 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

Warning!

The current version of these statistics do not support passing `nudge_x` or `nudge_y` named parameters to the geometry. Use `'position'` and one of the position functions such as `position_nudge_keep` instead.

Note

These statistics 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 `Date` or `POSIXct` objects, respectively. In which case the `x.label.fmt` must follow the syntax supported by `strftime()` rather than by `sprintf()`. Overlap of labels with points can be avoided by use of one of the nudge positions, possibly together with geometry `geom_text_s` from package `ggpp`, or with `geom_text_repel` or `geom_label_repel` from package `ggrepel`. To discard overlapping labels use `check_overlap = TRUE` as argument to `geom_text` or `geom_text_s`. By default the labels are character values suitable to be plotted as is, but with a suitable format passed as argument to `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.

Examples

```
# lynx is a time.series object
lynx_num.df <-
  try_tibble(lynx,
             col.names = c("year", "lynx"),
             as.numeric = TRUE) # years -> as numeric

ggplot(lynx_num.df, aes(year, lynx)) +
  geom_line() +
  stat_peaks(colour = "red") +
  stat_valleys(colour = "blue")

ggplot(lynx_num.df, aes(lynx, year)) +
  geom_line(orientation = "y") +
  stat_peaks(colour = "red", orientation = "y") +
  stat_valleys(colour = "blue", orientation = "y")

ggplot(lynx_num.df, aes(year, lynx)) +
  geom_line() +
  stat_peaks(colour = "red") +
  stat_peaks(colour = "red", geom = "rug")

ggplot(lynx_num.df, aes(year, lynx)) +
  geom_line() +
  stat_peaks(colour = "red") +
  stat_peaks(colour = "red", geom = "text", hjust = -0.1, angle = 33)

ggplot(lynx_num.df, aes(lynx, year)) +
  geom_line(orientation = "y") +
  stat_peaks(colour = "red", orientation = "y") +
  stat_peaks(colour = "red", orientation = "y",
            geom = "text", hjust = -0.1)
```

```

lynx_datetime.df <-
  try_tibble(lynx,
             col.names = c("year", "lynx")) # years -> POSIXct

ggplot(lynx_datetime.df, aes(year, lynx)) +
  geom_line() +
  stat_peaks(colour = "red") +
  stat_valleys(colour = "blue")

ggplot(lynx_datetime.df, aes(year, lynx)) +
  geom_line() +
  stat_peaks(colour = "red") +
  stat_peaks(colour = "red",
             geom = "text",
             hjust = -0.1,
             x.label.fmt = "%Y",
             angle = 33)

ggplot(lynx_datetime.df, aes(year, lynx)) +
  geom_line() +
  stat_peaks(colour = "red") +
  stat_peaks(colour = "red",
             geom = "text_s",
             position = position_nudge_keep(x = 0, y = 200),
             hjust = -0.1,
             x.label.fmt = "%Y",
             angle = 90) +
  expand_limits(y = 8000)

ggplot(lynx_datetime.df, aes(year, lynx)) +
  geom_line() +
  stat_peaks(colour = "red",
             geom = "text_s",
             position = position_nudge_to(y = 7600),
             arrow = arrow(length = grid::unit(1.5, "mm")),
             point.padding = 0.7,
             x.label.fmt = "%Y",
             angle = 90) +
  expand_limits(y = 9000)

```

stat_poly_eq

Equation, p-value, R², AIC and BIC of fitted polynomial

Description

stat_poly_eq fits a polynomial by default with `stats::lm()` but alternatively using robust regression. From the fitted model it generates several labels including the equation, p-value, F-value, coefficient of determination (R^2), 'AIC', 'BIC', and number of observations.

Usage

```

stat_poly_eq(
  mapping = NULL,
  data = NULL,
  geom = "text_npc",
  position = "identity",
  ...,
  method = "lm",
  method.args = list(),
  formula = NULL,
  eq.with.lhs = TRUE,
  eq.x.rhs = NULL,
  small.r = FALSE,
  small.p = FALSE,
  CI.brackets = c("[", "]"),
  rsquared.conf.level = 0.95,
  coef.digits = 3,
  coef.keep.zeros = TRUE,
  rr.digits = 2,
  f.digits = 3,
  p.digits = 3,
  label.x = "left",
  label.y = "top",
  label.x.npc = NULL,
  label.y.npc = NULL,
  hstep = 0,
  vstep = NULL,
  output.type = NULL,
  na.rm = FALSE,
  orientation = NA,
  parse = NULL,
  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
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.
method	function or character If character, "lm", "rlm" or the name of a model fit function are accepted, possibly followed by the fit function's method argument separated by a colon (e.g. "rlm:M"). If a function different to <code>lm()</code> , it must accept as a

	minimum a model formula through its first parameter, and have formal parameters named data, weights, and method, and return a model fit object of class <code>lm</code> .
<code>method.args</code>	named list with additional arguments.
<code>formula</code>	a formula object. Using aesthetic names <code>x</code> and <code>y</code> instead of original variable names.
<code>eq.with.lhs</code>	If character the string is pasted to the front of the equation label before parsing or a logical (see note).
<code>eq.x.rhs</code>	character this string will be used as replacement for "x" in the model equation when generating the label before parsing it.
<code>small.r</code> , <code>small.p</code>	logical Flags to switch use of lower case r and p for coefficient of determination and p-value.
<code>CI.brackets</code>	character vector of length 2. The opening and closing brackets used for the CI label.
<code>rsquared.conf.level</code>	numeric Confidence level for the returned confidence interval.
<code>coef.digits</code> , <code>f.digits</code>	integer Number of significant digits to use for the fitted coefficients and F-value.
<code>coef.keep.zeros</code>	logical Keep or drop trailing zeros when formatting the fitted coefficients and F-value.
<code>rr.digits</code> , <code>p.digits</code>	integer Number of digits after the decimal point to use for R^2 and P-value in labels.
<code>label.x</code> , <code>label.y</code>	numeric with range 0..1 "normalized parent coordinates" (npc units) or character if using <code>geom_text_npc()</code> or <code>geom_label_npc()</code> . If using <code>geom_text()</code> or <code>geom_label()</code> numeric in native data units. If too short they will be recycled.
<code>label.x.npc</code> , <code>label.y.npc</code>	numeric with range 0..1 (npc units) DEPRECATED, use <code>label.x</code> and <code>label.y</code> instead; together with a geom using <code>npcx</code> and <code>npcy</code> aesthetics.
<code>hstep</code> , <code>vstep</code>	numeric in npc units, the horizontal and vertical step used between labels for different groups.
<code>output.type</code>	character One of "expression", "LaTeX", "text", "markdown" or "numeric".
<code>na.rm</code>	a logical indicating whether NA values should be stripped before the computation proceeds.
<code>orientation</code>	character Either "x" or "y" controlling the default for formula.
<code>parse</code>	logical Passed to the geom. If TRUE, the labels will be parsed into expressions and displayed as described in <code>?plotmath</code> . Default is TRUE if <code>output.type</code> = "expression" and FALSE otherwise.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders</code> .

Details

This statistic can be used to automatically annotate a plot with R^2 , adjusted R^2 or the fitted model equation. It supports linear regression, robust linear regression and median regression fitted with functions `lm`, `rlm` or `rq`. The R^2 and adjusted R^2 annotations can be used with any linear model formula. The confidence interval for R^2 is computed with package `ci_rsquared`. 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" or "+ 0" 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 statistic generates labels as R expressions by default but LaTeX (use TikZ device), markdown (use package 'ggtext') and plain text are also supported, as well as numeric values for user-generated text labels. The value of `parse` is set automatically based on `output.type`, but if you assemble labels that need parsing from numeric output, the default needs to be overridden. This stat only generates annotation labels, the predicted values/line need to be added to the plot as a separate layer using `stat_poly_line` or `stat_smooth`, 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. Similarly to these statistics the model fits respect grouping, so the scales used for x and y should both be continuous scales rather than discrete.

IMPORTANT

`stat_regline_equation()` in package 'ggpubr' is a renamed but almost unchanged copy of `stat_poly_eq()` taken from an earlier version of this package (without acknowledgement of source and authorship). `stat_regline_equation()` lacks important functionality and contains bugs that have been fixed in `stat_poly_eq()`.

Aesthetics

`stat_poly_eq()` understands x and y, to be referenced in the formula and weight passed as argument to parameter weights. All three must be mapped to numeric variables. In addition, the aesthetics understood by the geom ("text" is the default) are understood and grouping respected.

Computed variables

If `output.type` different from "numeric" the returned tibble contains columns listed below. If the model fit function used does not return a value, the label is set to `character(0L)`.

x, npcx x position

y, npcy y position

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

rr.confint.label Confidence interval for 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.

n.label Number of observations used in the fit.

grp.label Set according to mapping in aes.

method.label Set according method used.

r.squared, adj.r.squared, p.value, n numeric values, from the model fit object

If `output.type` is "numeric" the returned tibble contains columns listed below. If the model fit function used does not return a value, the variable is set to `NA_real_`.

x, npcx x position

y, npcy y position

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

r.squared, rr.confint.level, rr.confint.low, rr.confint.high, adj.r.squared, f.value, f.df1, f.df2, p.value, AIC, BIC, n numeric values, from the model fit object

grp.label Set according to mapping in aes.

b_0.constant TRUE is polynomial is forced through the origin

b_i One or columns with the coefficient estimates

To explore the computed values returned for a given input we suggest the use of [geom_debug](#) as shown in the last examples below.

Note

For backward compatibility a logical is accepted as argument for `eq.with.lhs`. If TRUE, the default is used, either "x" or "y", depending on the argument passed to `formula`. However, "x" or "y" can be substituted by providing a suitable replacement character string through `eq.x.rhs`. Parameter orientation is redundant as it only affects the default for `formula` but is included for consistency with `ggplot2::stat_smooth()`.

R option `OutDec` is obeyed based on its value at the time the plot is rendered, i.e., displayed or printed. Set `options(OutDec = ",")` for languages like Spanish or French.

References

Written as an answer to question 7549694 at Stackoverflow.

See Also

This `stat_poly_eq` statistic can return ready formatted labels depending on the argument passed to `output.type`. This is possible because only polynomial models are supported. For quantile regression [stat_quant_eq](#) should be used instead of `stat_poly_eq` while for model II or major axis regression [stat_ma_eq](#) should be used. For other types of models such as non-linear models, statistics [stat_fit_glance](#) and [stat_fit_tidy](#) should be used and the code for construction of character strings from numeric values and their mapping to aesthetic label needs to be explicitly supplied by the user.

Other ggplot statistics for linear and polynomial regression: [stat_poly_line\(\)](#)

Examples

```

# generate artificial data
set.seed(4321)
x <- 1:100
y <- (x + x^2 + x^3) + rnorm(length(x), mean = 0, sd = mean(x^3) / 4)
y <- y / max(y)
my.data <- data.frame(x = x, y = y,
                      group = c("A", "B"),
                      y2 = y * c(1, 2) + c(0, 0.1),
                      w = sqrt(x))

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

# using defaults
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line() +
  stat_poly_eq()

# no weights
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(formula = formula)

# other labels
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(use_label("eq"), formula = formula)

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(use_label(c("eq", "R2")), formula = formula)

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(use_label(c("R2", "R2.CI", "P", "method")), formula = formula)

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(use_label(c("R2", "F", "P", "n"), sep = "*\"; \"*"),
              formula = formula)

# grouping
ggplot(my.data, aes(x, y2, color = group)) +
  geom_point() +
  stat_poly_line(formula = formula) +

```

```

stat_poly_eq(formula = formula)

# rotation
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(formula = formula, angle = 90)

# label location
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(formula = formula, label.y = "bottom", label.x = "right")

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(formula = formula, label.y = 0.1, label.x = 0.9)

# using weights
ggplot(my.data, aes(x, y, weight = w)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(formula = formula)

# no weights, 4 digits for R square
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(formula = formula, rr.digits = 4)

# manually assemble and map a specific label using paste() and aes()
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(aes(label = paste(after_stat(rr.label),
                                after_stat(n.label), sep = "*\ ", "\*"),
                                formula = formula)

# manually assemble and map a specific label using sprintf() and aes()
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(aes(label = sprintf("%s*\ " with "\*%s*\ " and "\*%s",
                                after_stat(rr.label),
                                after_stat(f.value.label),
                                after_stat(p.value.label))),
                                formula = formula)

# x on y regression
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula, orientation = "y") +

```

```

stat_poly_eq(use_label(c("eq", "adj.R2")),
             formula = x ~ poly(y, 3, raw = TRUE))

# conditional user specified label
ggplot(my.data, aes(x, y2, color = group)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(aes(label = ifelse(after_stat(adj.r.squared) > 0.96,
                                 paste(after_stat(adj.rr.label),
                                       after_stat(eq.label),
                                       sep = "*\ ", "\*"),
                                 after_stat(adj.rr.label))),
              rr.digits = 3,
              formula = formula)

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

# using numeric values
# Here we use columns b_0 ... b_3 for the coefficient estimates
my.format <-
  "b[0]~`=~%.3g*\ ", \*b[1]~`=~%.3g*\ ", \*b[2]~`=~%.3g*\ ", \*b[3]~`=~%.3g"
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(formula = formula,
              output.type = "numeric",
              parse = TRUE,
              mapping =
                aes(label = sprintf(my.format,
                                    after_stat(b_0), after_stat(b_1),
                                    after_stat(b_2), after_stat(b_3))))

# Inspecting the returned data using geom_debug()
# This provides a quick way of finding out the names of the variables that
# are available for mapping to aesthetics with after_stat().

gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_poly_line(formula = formula) +
    stat_poly_eq(formula = formula, geom = "debug")

if (gginnards.installed)

```

```

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

# names of the variables
if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_poly_line(formula = formula) +
    stat_poly_eq(formula = formula, geom = "debug",
                 summary.fun = colnames)

# only data$eq.label
if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_poly_line(formula = formula) +
    stat_poly_eq(formula = formula, geom = "debug",
                 output.type = "expression",
                 summary.fun = function(x) {x[["eq.label"]]}))

# only data$eq.label
if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_poly_line(formula = formula) +
    stat_poly_eq(aes(label = after_stat(eq.label)),
                 formula = formula, geom = "debug",
                 output.type = "markdown",
                 summary.fun = function(x) {x[["eq.label"]]}))

# only data$eq.label
if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_poly_line(formula = formula) +
    stat_poly_eq(formula = formula, geom = "debug",
                 output.type = "latex",
                 summary.fun = function(x) {x[["eq.label"]]}))

# only data$eq.label
if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_poly_line(formula = formula) +
    stat_poly_eq(formula = formula, geom = "debug",
                 output.type = "text",
                 summary.fun = function(x) {x[["eq.label"]]}))

# show the content of a list column
if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +

```

```
geom_point() +
stat_poly_line(formula = formula) +
stat_poly_eq(formula = formula, geom = "debug", output.type = "numeric",
             summary.fun = function(x) {x[["coef.ls"]][[1]]})
```

stat_poly_line

Predicted line from linear model fit

Description

Predicted values and a confidence band are computed and, by default, plotted.

Usage

```
stat_poly_line(
  mapping = NULL,
  data = NULL,
  geom = "smooth",
  position = "identity",
  ...,
  method = "lm",
  formula = NULL,
  se = TRUE,
  fm.values = FALSE,
  n = 80,
  fullrange = FALSE,
  level = 0.95,
  method.args = list(),
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  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
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.

method	function or character If character, "lm", "rlm" or the name of a model fit function are accepted, possibly followed by the fit function's method argument separated by a colon (e.g. "rlm:M"). If a function different to lm(), it must accept arguments named formula, data, weights, and method and return a model fit object of class lm.
formula	a formula object. Using aesthetic names x and y instead of original variable names.
se	Display confidence interval around smooth? ('TRUE' by default, see 'level' to control.)
fm.values	logical Add R2, adjusted R2, p-value and n as columns to returned data? ('FALSE' by default.)
n	Number of points at which to evaluate smoother.
fullrange	Should the fit span the full range of the plot, or just the data?
level	Level of confidence interval to use (0.95 by default).
method.args	named list with additional arguments.
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
orientation	character Either "x" or "y" controlling the default for formula.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders .

Details

This statistic is similar to [stat_smooth](#) but has different defaults. It interprets the argument passed to formula differently, accepting y as explanatory variable and setting orientation automatically. The default for method is "lm" and spline-based smoothers like loess are not supported. Other defaults are consistent with those in [stat_poly_eq\(\)](#), [stat_quant_line\(\)](#), [stat_quant_eq\(\)](#), [stat_ma_line\(\)](#), [stat_ma_eq\(\)](#).

[geom_poly_line\(\)](#) treats the x and y aesthetics differently and can thus have two orientations. The orientation can be deduced from the argument passed to formula. Thus, [stat_poly_line\(\)](#) will by default guess which orientation the layer should have. If no argument is passed to formula, the formula defaults to $y \sim x$. For consistency with [stat_smooth](#) orientation can be also specified directly passing an argument to the orientation parameter, which can be either "x" or "y". The value of orientation gives the axis that is taken as the explanatory variable or x in the model formula. Package 'ggpmisc' does not define new geometries matching the new statistics as they are not needed and conceptually transformations of data are statistics in the grammar of graphics.

Value

The value returned by the statistic is a data frame, that will have n rows of predicted values and their confidence limits. Optionally it will also include additional values related to the model fit.

Computed variables

'stat_poly_line()' provides the following variables, some of which depend on the orientation:

y *or* x predicted value

ymin *or* xmin lower pointwise confidence interval around the mean

ymax *or* xmax upper pointwise confidence interval around the mean

se standard error

If `fm.values = TRUE` is passed then columns based on the summary of the model fit are added, with the same value in each row within a group. This is wasteful and disabled by default, but provides a simple and robust approach to achieve effects like colouring or hiding of the model fit line based on P-values, r-squared, adjusted r-squared or the number of observations.

Aesthetics

`stat_poly_line` understands `x` and `y`, to be referenced in the formula and weight passed as argument to parameter weights. All three must be mapped to numeric variables. In addition, the aesthetics understood by the geom ("`geom_smooth`" is the default) are understood and grouping respected.

See Also

Other ggplot statistics for linear and polynomial regression: [stat_poly_eq\(\)](#)

Examples

```
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_poly_line()
```

```
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_poly_line(formula = x ~ y)
```

```
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_poly_line(formula = y ~ poly(x, 3))
```

```
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_poly_line(formula = x ~ poly(y, 3))
```

```
# Smooths are automatically fit to each group (defined by categorical
# aesthetics or the group aesthetic) and for each facet.
```

```
ggplot(mpg, aes(displ, hwy, colour = class)) +
  geom_point() +
  stat_poly_line(se = FALSE)
```

```
ggplot(mpg, aes(displ, hwy)) +
```



```

geom_point() +
stat_poly_line() +
facet_wrap(~drv)

# Inspecting the returned data using geom_debug()
gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

if (gginnards.installed)
  ggplot(mpg, aes(displ, hwy)) +
    stat_poly_line(geom = "debug")

if (gginnards.installed)
  ggplot(mpg, aes(displ, hwy)) +
    stat_poly_line(geom = "debug", fm.values = TRUE)

if (gginnards.installed)
  ggplot(mpg, aes(displ, hwy)) +
    stat_poly_line(geom = "debug", method = lm, fm.values = TRUE)

```

stat_quant_band

Predicted band from quantile regression fits

Description

Predicted values are computed and, by default, plotted as a band plus an optional line within. `stat_quant_band()` supports the use of both `x` and `y` as explanatory variable in the model formula.

Usage

```

stat_quant_band(
  mapping = NULL,
  data = NULL,
  geom = "smooth",
  position = "identity",
  ...,
  quantiles = c(0.25, 0.5, 0.75),
  formula = NULL,
  fm.values = FALSE,
  n = 80,
  method = "rq",
  method.args = list(),
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,

```

```
  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.
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.
quantiles	numeric vector Two or three values in 0..1 indicating the quantiles at the edges of the band and optionally a line within the band.
formula	a formula object. Using aesthetic names <i>x</i> and <i>y</i> instead of original variable names.
fm.values	logical Add <i>n</i> as a column to returned data? ('FALSE' by default.)
n	Number of points at which to evaluate smoother.
method	function or character If character, "rq", "rqss" or the name of a model fit function are accepted, possibly followed by the fit function's method argument separated by a colon (e.g. "rq:br"). If a function different to <code>rq()</code> , it must accept arguments named <i>formula</i> , <i>data</i> , <i>weights</i> , <i>tau</i> and <i>method</i> and return a model fit object of class <code>rq</code> , <code>rqs</code> or <code>rqss</code> .
method.args	named list with additional arguments.
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
orientation	character Either "x" or "y" controlling the default for formula.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders .

Details

This statistic is similar to [stat_quant_line](#) but plots the quantiles differently with the band representing a region between two quantiles, while in `stat_quant_line()` the bands plotted when `se = TRUE` represent confidence intervals for the fitted quantile lines.

[geom_smooth](#), which is used by default, treats each axis differently and thus is dependent on orientation. If no argument is passed to *formula*, it defaults to $y \sim x$ but $x \sim y$ is also accepted, and equivalent to $y \sim x$ plus `orientation = "y"`. Package 'ggpmisc' does not define a new geometry matching this statistic as it is enough for the statistic to return suitable 'x' and 'y' values.

Value

The value returned by the statistic is a data frame, that will have n rows of predicted values for three quantiles as y , $ymin$ and $ymax$, plus x .

Aesthetics

`stat_quant_eq` expects x and y , aesthetics to be used in the formula rather than the names of the variables mapped to them. If present, the variable mapped to the weight aesthetics is passed as argument to parameter weights of the fitting function. All three must be mapped to numeric variables. In addition, the aesthetics recognized by the geometry ("`geom_smooth`" is the default) are obeyed and grouping respected.

See Also

Other ggplot statistics for quantile regression: [stat_quant_eq\(\)](#), [stat_quant_line\(\)](#)

Examples

```
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_band()

# If you need the fitting to be done along the y-axis set the orientation
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_band(orientation = "y")

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_band(formula = y ~ x)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_band(formula = x ~ y)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_band(formula = y ~ poly(x, 3))

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_band(formula = x ~ poly(y, 3))

# Instead of rq() we can use rqss() to fit an additive model:
library(quantreg)
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_band(method = "rqss",
                  formula = y ~ qss(x))

ggplot(mpg, aes(displ, hwy)) +
```

```

geom_point() +
stat_quant_band(method = "rqss",
                formula = x ~ qss(y, constraint = "D"))

# Regressions are automatically fit to each group (defined by categorical
# aesthetics or the group aesthetic) and for each facet.

ggplot(mpg, aes(displ, hwy, colour = class)) +
  geom_point() +
  stat_quant_band(formula = y ~ x)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_band(formula = y ~ poly(x, 2)) +
  facet_wrap(~drv)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_band(linetype = "dashed", color = "darkred", fill = "red")

ggplot(mpg, aes(displ, hwy)) +
  stat_quant_band(color = NA, alpha = 1) +
  geom_point()

ggplot(mpg, aes(displ, hwy)) +
  stat_quant_band(quantiles = c(0, 0.1, 0.2)) +
  geom_point()

# Inspecting the returned data using geom_debug()
gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

if (gginnards.installed)
  ggplot(mpg, aes(displ, hwy)) +
    stat_quant_band(geom = "debug")

if (gginnards.installed)
  ggplot(mpg, aes(displ, hwy)) +
    stat_quant_band(geom = "debug", fm.values = TRUE)

```

stat_quant_eq

Equation, rho, AIC and BIC from quantile regression

Description

stat_quant_eq fits a polynomial model by quantile regression and generates several labels including the equation, rho, 'AIC' and 'BIC'.

Usage

```

stat_quant_eq(
  mapping = NULL,
  data = NULL,
  geom = "text_npc",
  position = "identity",
  ...,
  formula = NULL,
  quantiles = c(0.25, 0.5, 0.75),
  method = "rq:br",
  method.args = list(),
  eq.with.lhs = TRUE,
  eq.x.rhs = NULL,
  coef.digits = 3,
  coef.keep.zeros = TRUE,
  rho.digits = 2,
  label.x = "left",
  label.y = "top",
  label.x.npc = NULL,
  label.y.npc = NULL,
  hstep = 0,
  vstep = NULL,
  output.type = "expression",
  na.rm = FALSE,
  orientation = NA,
  parse = NULL,
  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
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.
quantiles	numeric vector Values in 0..1 indicating the quantiles.
method	function or character If character, "rq" or the name of a model fit function are accepted, possibly followed by the fit function's method argument separated by a colon (e.g. "rq:br"). If a function different to <code>rq()</code> , it must accept arguments named formula, data, weights, tau and method and return a model fit object of class <code>rq</code> or <code>rqs</code> .

method.args	named list with additional arguments passed to <code>rq()</code> or to a function passed as argument to <code>method</code> .
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, rho.digits	integer Number of significant digits to use for the fitted coefficients and rho in labels.
coef.keep.zeros	logical Keep or drop trailing zeros when formatting the fitted coefficients and F-value.
label.x, label.y	numeric with range 0..1 "normalized parent coordinates" (npc units) or character if using <code>geom_text_npc()</code> or <code>geom_label_npc()</code> . If using <code>geom_text()</code> or <code>geom_label()</code> numeric in native data units. If too short they will be recycled.
label.x.npc, label.y.npc	numeric with range 0..1 (npc units) DEPRECATED, use <code>label.x</code> and <code>label.y</code> instead; together with a geom using <code>npcx</code> and <code>npcy</code> aesthetics.
hstep, vstep	numeric in npc units, the horizontal and vertical step used between labels for different groups.
output.type	character One of "expression", "LaTeX", "text", "markdown" or "numeric". In most cases, instead of using this statistics to obtain numeric values, it is better to use <code>stat_fit_tidy()</code> .
na.rm	a logical indicating whether NA values should be stripped before the computation proceeds.
orientation	character Either "x" or "y" controlling the default for formula.
parse	logical Passed to the geom. If TRUE, the labels will be parsed into expressions and displayed as described in <code>?plotmath</code> . Default is TRUE if <code>output.type = "expression"</code> and FALSE otherwise.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders .

Details

This statistic interprets the argument passed to `formula` differently than [stat_quantile](#) accepting `y` as well as `x` as explanatory variable, matching `stat_quant_line()`.

When two variables are subject to mutual constrains, it is useful to consider both of them as explanatory and interpret the relationship based on them. So, from version 0.4.1 'ggpmisc' makes it possible to easily implement the approach described by Cardoso (2019) under the name of "Double quantile regression".

This stat can be used to automatically annotate a plot with rho or the fitted model equation. The model fitting is done using package 'quantreg', please, consult its documentation for the details. It supports only linear models fitted with function `rq()`, passing `method = "br"` to it, should work well with up to several thousand observations. The rho, AIC, BIC and n 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"` or `"+ 0"` in the formula. The validity of the formula is not checked in the current implementation. The default aesthetics sets rho as label for the annotation. This stat generates labels as R expressions by default but LaTeX (use TikZ device), markdown (use package 'ggtext') and plain text are also supported, as well as numeric values for user-generated text labels. The value of `parse` is set automatically based on `output-type`, but if you assemble labels that need parsing from numeric output, the default needs to be overridden. This stat only generates annotation labels, the predicted values/line need to be added to the plot as a separate layer using `stat_quant_line`, `stat_quant_band` or `stat_quantile`, 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_quant_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_quant_eq()` understands `x` and `y`, to be referenced in the formula and weight passed as argument to parameter `weights` of `rq()`. 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 below in addition to a modified version of the original group:

x, npcx x position

y, npcy y position

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

r.label, and one of cor.label, rho.label, or tau.label *rho* of the fitted model as a character string to be parsed

AIC.label AIC for the fitted model.

n.label Number of observations used in the fit.

method.label Set according method used.

rq.method character, method used.

rho, n numeric values extracted or computed from fit object.

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

quantile Numeric value of the quantile used for the fit

quantile.f Factor with a level for each quantile

If `output.type` is "numeric" the returned tibble contains columns in addition to a modified version of the original group:

x, npcx x position

y, npcy y position

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

rho, AIC, n numeric values extracted or computed from fit object

rq.method character, method used.

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

quantile Indicating the quantile used for the fit

quantile.f Factor with a level for each quantile

b_0.constant TRUE is polynomial is forced through the origin

b_i One or columns with the coefficient estimates

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

Note

For backward compatibility a logical is accepted as argument for `eq.with.lhs`. If TRUE, the default is used, either "x" or "y", depending on the argument passed to `formula`. However, "x" or "y" can be substituted by providing a suitable replacement character string through `eq.x.rhs`. Parameter orientation is redundant as it only affects the default for `formula` but is included for consistency with `ggplot2::stat_smooth()`.

R option `OutDec` is obeyed based on its value at the time the plot is rendered, i.e., displayed or printed. Set `options(OutDec = ",")` for languages like Spanish or French.

Support for the `angle` aesthetic is not automatic and requires that the user passes as argument suitable numeric values to override the defaults for label positions.

References

Written as an answer to question 65695409 by Mark Neal at Stackoverflow.

See Also

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

Other ggplot statistics for quantile regression: `stat_quant_band()`, `stat_quant_line()`

Examples

```

# generate artificial data
set.seed(4321)
x <- 1:100
y <- (x + x^2 + x^3) + rnorm(length(x), mean = 0, sd = mean(x^3) / 4)
y <- y / max(y)
my.data <- data.frame(x = x, y = y,
                      group = c("A", "B"),
                      y2 = y * c(1, 2) + max(y) * c(0, 0.1),
                      w = sqrt(x))

# using defaults
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line() +
  stat_quant_eq()

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line() +
  stat_quant_eq(use_label(c("eq", "method")))

# same formula as default
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line(formula = y ~ x) +
  stat_quant_eq(formula = y ~ x)

# explicit formula "x explained by y"
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line(formula = x ~ y) +
  stat_quant_eq(formula = x ~ y)

# using color
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line(aes(color = after_stat(quantile.f))) +
  stat_quant_eq(aes(color = after_stat(quantile.f))) +
  labs(color = "Quantiles")

# location and colour
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line(aes(color = after_stat(quantile.f))) +
  stat_quant_eq(aes(color = after_stat(quantile.f)),
                label.y = "bottom", label.x = "right") +
  labs(color = "Quantiles")

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

```

```

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line(formula = formula, linewidth = 0.5) +
  stat_quant_eq(formula = formula)

# angle
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line(formula = formula, linewidth = 0.5) +
  stat_quant_eq(formula = formula, angle = 90, hstep = 0.05, vstep = 0,
                label.y = 0.98, hjust = 1)

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line(formula = formula) +
  stat_quant_eq(formula = formula, angle = 90,
                hstep = 0.05, vstep = 0, hjust = 0,
                label.y = 0.25)

# user set quantiles
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line(formula = formula, quantiles = 0.5) +
  stat_quant_eq(formula = formula, quantiles = 0.5)

ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_band(formula = formula,
                 quantiles = c(0.1, 0.5, 0.9)) +
  stat_quant_eq(formula = formula, parse = TRUE,
                 quantiles = c(0.1, 0.5, 0.9))

# grouping
ggplot(my.data, aes(x, y2, color = group)) +
  geom_point() +
  stat_quant_line(formula = formula, linewidth = 0.5) +
  stat_quant_eq(formula = formula)

ggplot(my.data, aes(x, y2, color = group)) +
  geom_point() +
  stat_quant_band(formula = formula, linewidth = 0.75) +
  stat_quant_eq(formula = formula) +
  theme_bw()

# labelling equations
ggplot(my.data, aes(x, y2, shape = group, linetype = group,
                    grp.label = group)) +
  geom_point() +
  stat_quant_band(formula = formula, color = "black", linewidth = 0.75) +
  stat_quant_eq(use_label(c("grp", "eq"), sep = "*\\": \\*"),
                formula = formula) +
  expand_limits(y = 3) +
  theme_classic()

```

```

# using weights
ggplot(my.data, aes(x, y, weight = w)) +
  geom_point() +
  stat_quant_line(formula = formula, linewidth = 0.5) +
  stat_quant_eq(formula = formula)

# no weights, quantile set to upper boundary
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line(formula = formula, quantiles = 0.95) +
  stat_quant_eq(formula = formula, quantiles = 0.95)

# manually assemble and map a specific label using paste() and aes()
ggplot(my.data, aes(x, y2, color = group, grp.label = group)) +
  geom_point() +
  stat_quant_line(method = "rq", formula = formula,
                 quantiles = c(0.05, 0.5, 0.95),
                 linewidth = 0.5) +
  stat_quant_eq(aes(label = paste(after_stat(grp.label), "*\": \"*\",
                                after_stat(eq.label), sep = "")),
               quantiles = c(0.05, 0.5, 0.95),
               formula = formula, size = 3)

# manually assemble and map a specific label using sprintf() and aes()
ggplot(my.data, aes(x, y2, color = group, grp.label = group)) +
  geom_point() +
  stat_quant_band(method = "rq", formula = formula,
                 quantiles = c(0.05, 0.5, 0.95)) +
  stat_quant_eq(aes(label = sprintf("%s*\": \"*%s",
                                after_stat(grp.label),
                                after_stat(eq.label))),
               quantiles = c(0.05, 0.5, 0.95),
               formula = formula, size = 3)

# geom = "text"
ggplot(my.data, aes(x, y)) +
  geom_point() +
  stat_quant_line(formula = formula, quantiles = 0.5) +
  stat_quant_eq(label.x = "left", label.y = "top",
               formula = formula,
               quantiles = 0.5)

# Inspecting the returned data using geom_debug()
# This provides a quick way of finding out the names of the variables that
# are available for mapping to aesthetics using after_stat().

gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

if (gginnards.installed)

```

```

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

## Not run:
if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_quant_eq(aes(label = after_stat(eq.label)),
                  formula = formula, geom = "debug",
                  output.type = "markdown")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_quant_eq(formula = formula, geom = "debug", output.type = "text")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_quant_eq(formula = formula, geom = "debug", output.type = "numeric")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_quant_eq(formula = formula, quantiles = c(0.25, 0.5, 0.75),
                  geom = "debug", output.type = "text")

if (gginnards.installed)
  ggplot(my.data, aes(x, y)) +
    geom_point() +
    stat_quant_eq(formula = formula, quantiles = c(0.25, 0.5, 0.75),
                  geom = "debug", output.type = "numeric")

## End(Not run)

```

stat_quant_line

Predicted line from quantile regression fit

Description

Predicted values are computed and, by default, plotted. Depending on the fit method, a confidence band can be computed and plotted. The confidence band can be interpreted similarly as that produced by `stat_smooth()` and `stat_poly_line()`.

Usage

```

stat_quant_line(
  mapping = NULL,

```

```

data = NULL,
geom = "smooth",
position = "identity",
...,
quantiles = c(0.25, 0.5, 0.75),
formula = NULL,
se = length(quantiles) == 1L,
fm.values = FALSE,
n = 80,
method = "rq",
method.args = list(),
level = 0.95,
type = "direct",
interval = "confidence",
na.rm = FALSE,
orientation = NA,
show.legend = NA,
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
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.
quantiles	numeric vector Values in 0..1 indicating the quantiles.
formula	a formula object. Using aesthetic names x and y instead of original variable names.
se	logical Passed to <code>quantreg::predict.rq()</code> .
fm.values	logical Add n as a column to returned data? ('FALSE' by default.)
n	Number of points at which to evaluate smoother.
method	function or character If character, "rq", "rqss" or the name of a model fit function are accepted, possibly followed by the fit function's method argument separated by a colon (e.g. "rq:br"). If a function different to <code>rq()</code> , it must accept arguments named formula, data, weights, tau and method and return a model fit object of class rq, rqs or rqss.
method.args	named list with additional arguments passed to <code>rq()</code> , <code>rqss()</code> or to a function passed as argument to method.
level	numeric in range [0..1] Passed to <code>quantreg::predict.rq()</code> .
type	character Passed to <code>quantreg::predict.rq()</code> .
interval	character Passed to <code>quantreg::predict.rq()</code> .

<code>na.rm</code>	a logical indicating whether NA values should be stripped before the computation proceeds.
<code>orientation</code>	character Either "x" or "y" controlling the default for formula.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders .

Details

`stat_quant_line()` behaves similarly to `ggplot2::stat_smooth()` and `stat_poly_line()` but supports fitting regressions for multiple quantiles in the same plot layer. This statistic interprets the argument passed to `formula` accepting `y` as well as `x` as explanatory variable, matching `stat_quant_eq()`. While `stat_quant_eq()` supports only method "rq", `stat_quant_line()` and `stat_quant_band()` support both "rq" and "rqss", In the case of "rqss" the model formula makes normally use of `qss()` to formulate the spline and its constraints.

[geom_smooth](#), which is used by default, treats each axis differently and thus is dependent on orientation. If no argument is passed to `formula`, it defaults to `y ~ x`. Formulas with `y` as explanatory variable are treated as if `x` was the explanatory variable and `orientation = "y"`.

Package 'ggpmisc' does not define a new geometry matching this statistic as it is enough for the statistic to return suitable `x`, `y`, `ymin`, `ymax` and `group` values.

There are multiple uses for double regression on `x` and `y`. For example, when two variables are subject to mutual constrains, it is useful to consider both of them as explanatory and interpret the relationship based on them. So, from version 0.4.1 'ggpmisc' makes it possible to easily implement the approach described by Cardoso (2019) under the name of "Double quantile regression".

Value

The value returned by the statistic is a data frame, that will have `n` rows of predicted values and their confidence limits for each quantile, with each quantile in a group. The variables are `x` and `y` with `y` containing predicted values. In addition, `quantile` and `quantile.f` indicate the quantile used and edited group preserves the original grouping adding a new "level" for each quantile. If `se = TRUE`, a confidence band is computed and values for it returned in `ymin` and `ymax`.

The value returned by the statistic is a data frame, that will have `n` rows of predicted values and their confidence limits. Optionally it will also include additional values related to the model fit.

Computed variables

'`stat_quant_line()`' provides the following variables, some of which depend on the orientation:

y *or* x predicted value

ymin *or* xmin lower confidence interval around the mean

ymax *or* xmax upper confidence interval around the mean

If `fm.values = TRUE` is passed then one column with the number of observations `n` used for each fit is also included, with the same value in each row within a group. This is wasteful and disabled by default, but provides a simple and robust approach to achieve effects like colouring or hiding of the model fit line based on the number of observations.

Aesthetics

`stat_quant_line` understands `x` and `y`, to be referenced in the formula and weight passed as argument to parameter `weights`. All three must be mapped to numeric variables. In addition, the aesthetics understood by the geom ("`geom_smooth`" is the default) are understood and grouping respected.

References

Cardoso, G. C. (2019) Double quantile regression accurately assesses distance to boundary trade-off. *Methods in ecology and evolution*, 10(8), 1322-1331.

See Also

[rq](#), [rqss](#) and [qss](#).

Other ggplot statistics for quantile regression: [stat_quant_band\(\)](#), [stat_quant_eq\(\)](#)

Examples

```
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_line()

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_line(se = TRUE)

# If you need the fitting to be done along the y-axis set the orientation
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_line(orientation = "y")

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_line(orientation = "y", se = TRUE)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_line(formula = y ~ x)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_line(formula = x ~ y)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
```

```

stat_quant_line(formula = y ~ poly(x, 3))

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_line(formula = x ~ poly(y, 3))

# Instead of rq() we can use rqss() to fit an additive model:
library(quantreg)
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_line(method = "rqss",
                  formula = y ~ qss(x, constraint = "D"),
                  quantiles = 0.5)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_line(method = "rqss",
                  formula = x ~ qss(y, constraint = "D"),
                  quantiles = 0.5)

ggplot(mpg, aes(displ, hwy)) +
  geom_point()+
  stat_quant_line(method="rqss",
                  interval="confidence",
                  se = TRUE,
                  mapping = aes(fill = factor(after_stat(quantile)),
                                      color = factor(after_stat(quantile))),
                  quantiles=c(0.05,0.5,0.95))

# Smooths are automatically fit to each group (defined by categorical
# aesthetics or the group aesthetic) and for each facet.

ggplot(mpg, aes(displ, hwy, colour = drv, fill = drv)) +
  geom_point() +
  stat_quant_line(method = "rqss",
                  formula = y ~ qss(x, constraint = "V"),
                  quantiles = 0.5)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  stat_quant_line(formula = y ~ poly(x, 2)) +
  facet_wrap(~drv)

# Inspecting the returned data using geom_debug()
gginnards.installed <- requireNamespace("gginnards", quietly = TRUE)

if (gginnards.installed)
  library(gginnards)

if (gginnards.installed)
  ggplot(mpg, aes(displ, hwy)) +
    stat_quant_line(geom = "debug")

```



```
if (gginnards.installed)
  ggplot(mpg, aes(displ, hwy)) +
    stat_quant_line(geom = "debug", fm.values = TRUE)
```

swap_xy	<i>Swap x and y in a formula</i>
---------	----------------------------------

Description

By default a formula of x on y is converted into a formula of y on x, while the reverse swap is done only if `backward = TRUE`.

Usage

```
swap_xy(f, backwards = FALSE)
```

Arguments

f	formula	An R model formula
backwards	logical	

Details

This function is meant to be used only as a helper within 'ggplot2' statistics. Normally together with geometries supporting orientation when we want to automate the change in orientation based on a user-supplied formula. Only x and y are changed, and in other respects the formula is rebuilt copying the environment from f.

Value

A copy of f with x and y swapped by each other in the lhs and rhs.

symmetric_limits	<i>Expand a range to make it symmetric</i>
------------------	--

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

```
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

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

use_label

Assemble label and map it

Description

Assemble model-fit-derived text or expressions and map them to the label aesthetic.

Usage

```
use_label(
  labels = c("eq", "p.value"),
  other.mapping = NULL,
  sep = "*\\", "\\*"
)
```

Arguments

`labels` character A vector with the name of the label components in the order they will be included in the combined label.

`other.mapping` An unevaluated expression constructed with function [aes](#).

`sep` character A string used as separator when pasting the label components together.

Details

Statistics [stat_poly_eq](#), [stat_ma_eq](#), [stat_quant_eq](#) and [stat_correlation](#) return multiple text strings to be used individually or assembled into longer character strings depending on the labels actually desired. Assembling and mapping them requires verbose R code and familiarity with R expression syntax. Function `use_label()` automates these two tasks and accepts abbreviated

familiar names for the parameters in addition to the name of the columns in the data object returned by the statistics. The default separator is that for expressions.

The statistics return variables with names ending in `.label`. This ending can be omitted, as well as `.value` for `f.value.label`, `t.value.label`, `z.value.label`, `S.value.label` and `p.value.label`. `R2` can be used in place of `rr`. Furthermore, case is ignored.

Value

A to the label aesthetic as an unevaluated R expression, built using function [aes](#).

Note

Function `use_label()` can be only used to generate an argument passed to formal parameter mapping of the statistics [stat_poly_eq](#), [stat_ma_eq](#), [stat_quant_eq](#) and [stat_correlation](#).

See Also

[stat_poly_eq](#), [stat_ma_eq](#), [stat_quant_eq](#) and [stat_correlation](#).

Examples

```
# generate artificial data
set.seed(4321)
x <- 1:100
y <- (x + x^2 + x^3) + rnorm(length(x), mean = 0, sd = mean(x^3) / 4)
my.data <- data.frame(x = x,
                      y = y * 1e-5,
                      group = c("A", "B"),
                      y2 = y * 1e-5 + c(2, 0))

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

ggplot(my.data, aes(x, y2, colour = group)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(use_label(c("eq", "F")), formula = formula)

ggplot(my.data, aes(x, y2, colour = group)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(use_label(c("R2", "F"), sep = "*\" with \"*"),
              formula = formula)

ggplot(my.data, aes(x, y2, colour = group)) +
  geom_point() +
  stat_poly_line(formula = formula) +
  stat_poly_eq(use_label(c("eq", "adj.R2", "n")), formula = formula)

ggplot(my.data, aes(x, y2, colour = group)) +
  geom_point() +
  stat_poly_line(formula = formula) +
```

```

stat_poly_eq(use_label(c("F", "P", "AIC", "BIC")), formula = formula)

ggplot(my.data, aes(x, y)) +
  stat_quant_band(formula = formula) +
  stat_quant_eq(use_label(c("eq", "n")), formula = formula) +
  geom_point()

ggplot(my.data, aes(x, y)) +
  stat_ma_line() +
  stat_ma_eq(use_label(c("eq", "n"))) +
  geom_point()

ggplot(my.data, aes(x, y)) +
  stat_correlation(use_label(c("r", "t", "p"))) +
  geom_point()

# pass additional mappings if desired
ggplot(my.data, aes(x, y2)) +
  geom_point(aes(colour = group)) +
  stat_poly_line(aes(colour = group), formula = formula) +
  stat_poly_eq(use_label(c("eq", "F"), aes(grp.label = group)), formula = formula)

```

volcano_example.df *Example gene expression data*

Description

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

Usage

```
volcano_example.df
```

Format

A data.frame object with 1218 rows and 5 variables

See Also

Other Transcriptomics data examples: [quadrant_example.df](#)

Examples

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

xy_outcomes2factor *Convert two numeric ternary outcomes into a factor*

Description

Convert two numeric ternary outcomes into a factor

Usage

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

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

Arguments

x, y numeric vectors of -1, 0, and +1 values, indicating down regulation, uncertain response or up-regulation, or numeric vectors that can be converted into such values using a pair of thresholds.

x_threshold, y_threshold
 numeric vector Ranges enclosing the values to be considered uncertain for each of the two vectors..

Details

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

Note

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

See Also

Other Functions for quadrant and volcano plots: [FC_format\(\)](#), [outcome2factor\(\)](#), [scale_colour_outcome\(\)](#), [scale_shape_outcome\(\)](#), [scale_y_Pvalue\(\)](#)

Other scales for omics data: [outcome2factor\(\)](#), [scale_colour_logFC\(\)](#), [scale_shape_outcome\(\)](#), [scale_x_logFC\(\)](#)

Examples

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

Index

- * **Functions for quadrant and volcano plots**
 - outcome2factor, 8
 - scale_colour_outcome, 15
 - scale_shape_outcome, 17
 - scale_y_Pvalue, 21
 - xy_outcomes2factor, 101
- * **Transcriptomics data examples**
 - quadrant_example.df, 11
 - volcano_example.df, 100
- * **datasets**
 - quadrant_example.df, 11
 - volcano_example.df, 100
- * **ggplot statistics for correlation.**
 - stat_correlation, 24
- * **ggplot statistics for linear and polynomial regression**
 - stat_poly_eq, 69
 - stat_poly_line, 78
- * **ggplot statistics for major axis regression**
 - stat_ma_eq, 56
 - stat_ma_line, 61
- * **ggplot statistics for model fits**
 - stat_fit_augment, 29
 - stat_fit_deviations, 33
 - stat_fit_glance, 37
 - stat_fit_residuals, 41
 - stat_fit_tb, 45
 - stat_fit_tidy, 51
- * **ggplot statistics for quantile regression**
 - stat_quant_band, 81
 - stat_quant_eq, 84
 - stat_quant_line, 92
- * **scales for omics data**
 - outcome2factor, 8
 - scale_colour_logFC, 11
 - scale_shape_outcome, 17
 - scale_x_logFC, 19
 - xy_outcomes2factor, 101
- aes, 25, 30, 33, 37, 41, 45, 52, 57, 62, 66, 70, 78, 82, 85, 93, 98, 99
- append_layers (Moved), 8
- borders, 25, 30, 34, 38, 42, 46, 52, 58, 63, 67, 71, 79, 82, 86, 94
- bottom_layer (Moved), 8
- broom, 31, 39, 47, 54
- ci_rsquared, 72
- coef.lmodel2, 5
- confint.lmodel2, 6
- cor.test, 27
- delete_layers, 8
- delete_layers (Moved), 8
- extract_layers (Moved), 8
- factor, 9, 101
- FC_format, 9, 16, 18, 23, 101
- geom_debug, 8, 27, 31, 34, 38, 47, 53, 59, 73, 88
- geom_debug (Moved), 8
- geom_label_repel, 68
- geom_null, 8
- geom_null (Moved), 8
- geom_smooth, 63, 82, 94
- geom_table, 47
- geom_text_repel, 68
- geom_text_s, 68
- ggpmisc (ggpmisc-package), 3
- ggpmisc-package, 3
- ggpp, 68
- ggrepel, 68
- keep_augment (keep_tidy), 7
- keep_glance (keep_tidy), 7
- keep_tidy, 7
- layer, 25, 30, 34, 38, 42, 46, 52, 57, 62, 67, 70, 78, 82, 85, 93

- lm, 72
- lmodel2, 6, 10, 58, 59, 63

- move_layers (Moved), 8
- Moved, 8

- num_layers (Moved), 8

- outcome2factor, 8, 13, 16, 18, 20, 23, 101

- position_nudge_keep, 68
- predict.lmodel2, 9

- qss, 95
- quadrant_example.df, 11, 100

- residuals, 42
- rlm, 72
- rq, 72, 88, 95
- rqss, 95

- scale_color_logFC (scale_colour_logFC), 11
- scale_color_outcome (scale_colour_outcome), 15
- scale_colour_logFC, 9, 11, 18, 20, 101
- scale_colour_outcome, 9, 15, 18, 23, 101
- scale_continuous, 13, 20, 23
- scale_fill_logFC (scale_colour_logFC), 11
- scale_fill_outcome, 9
- scale_fill_outcome (scale_colour_outcome), 15
- scale_manual, 16, 18
- scale_shape_outcome, 9, 13, 16, 17, 20, 23, 101
- scale_x_FDR (scale_y_Pvalue), 21
- scale_x_logFC, 9, 13, 18, 19, 101
- scale_x_Pvalue (scale_y_Pvalue), 21
- scale_y_FDR (scale_y_Pvalue), 21
- scale_y_logFC (scale_x_logFC), 19
- scale_y_Pvalue, 9, 16, 18, 21, 101
- shift_layers (Moved), 8
- sprintf, 67
- stat_correlation, 24, 98, 99
- stat_debug_group, 8
- stat_debug_group (Moved), 8
- stat_debug_panel, 8
- stat_debug_panel (Moved), 8
- stat_fit_augment, 29, 35, 38, 39, 43, 47, 53, 54
- stat_fit_deviations, 31, 33, 39, 43, 47, 54
- stat_fit_glance, 30, 31, 35, 37, 43, 47, 53, 54, 59, 73, 88
- stat_fit_residuals, 31, 35, 39, 41, 47, 54
- stat_fit_tb, 31, 35, 39, 43, 45, 51, 54
- stat_fit_tidy, 30, 31, 35, 38, 39, 43, 47, 51, 59, 73, 88
- stat_ma_eq, 56, 64, 73, 98, 99
- stat_ma_line, 59, 61
- stat_peaks, 65
- stat_poly_eq, 30, 38, 53, 59, 69, 80, 98, 99
- stat_poly_line, 72, 73, 78
- stat_quant_band, 81, 87, 88, 95
- stat_quant_eq, 59, 73, 83, 84, 95, 98, 99
- stat_quant_line, 82, 83, 87, 88, 92
- stat_quantile, 86, 87
- stat_smooth, 62, 72, 79
- stat_valleys (stat_peaks), 65
- strftime, 67
- strptime, 67
- swap_xy, 97
- symmetric_limits, 97

- threshold2factor (outcome2factor), 8
- tidy, 47
- top_layer (Moved), 8
- ttheme_gtdefault, 47

- use_label, 98

- volcano_example.df, 11, 100

- weighted.residuals, 42
- which_layers (Moved), 8

- xy_outcomes2factor, 9, 13, 16, 18, 20, 23, 101
- xy_thresholds2factor (xy_outcomes2factor), 101