

Package ‘ggstats’

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Type Package

Title Extension to 'ggplot2' for Plotting Stats

Version 0.5.1

Description Provides new statistics, new geometries and new positions for 'ggplot2' and a suite of functions to facilitate the creation of statistical plots.

License GPL (>= 3)

URL <https://larmarange.github.io/ggstats/>,
<https://github.com/larmarange/ggstats>

BugReports <https://github.com/larmarange/ggstats/issues>

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R topics documented:

augment_chisq_add_phi	2
geom_stripped_rows	3
ggcoef_model	5
gglikert	15
ggsurvey	20
label_number_abs	21
position_likert	22
signif_stars	24
stat_cross	25
stat_prop	28
stat_weighted_mean	31
weighted.median	33
Index	35

augment_chisq_add_phi *Augment a chi-squared test and compute phi coefficients*

Description

Augment a chi-squared test and compute phi coefficients

Usage

```
augment_chisq_add_phi(x)
```

Arguments

x a chi-squared test as returned by `stats::chisq.test()`

Details

Phi coefficients are a measurement of the degree of association between two binary variables.

- A value between -1.0 to -0.7 indicates a strong negative association.
- A value between -0.7 to -0.3 indicates a weak negative association.
- A value between -0.3 to +0.3 indicates a little or no association.
- A value between +0.3 to +0.7 indicates a weak positive association.
- A value between +0.7 to +1.0 indicates a strong positive association.

Value

A tibble.

See Also

`stat_cross()`, `GDAtools::phi.table()` or `psych::phi()`

Examples

```
tab <- xtabs(Freq ~ Sex + Class, data = as.data.frame(Titanic))
augment_chisq_add_phi(chisq.test(tab))
```

geom_stripped_rows *Alternating Background Color*

Description

Add alternating background color along the y-axis. The geom takes default aesthetics odd and even that receive color codes.

Usage

```
geom_stripped_rows(  
  mapping = NULL,  
  data = NULL,  
  stat = "identity",  
  position = "identity",  
  ...,  
  show.legend = NA,  
  inherit.aes = TRUE,  
  xfrom = -Inf,  
  xto = Inf,  
  width = 1,  
  nudge_y = 0  
)
```

```
geom_stripped_cols(  
  mapping = NULL,  
  data = NULL,  
  stat = "identity",  
  position = "identity",  
  ...,  
  show.legend = NA,  
  inherit.aes = TRUE,  
  yfrom = -Inf,  
  yto = Inf,  
  width = 1,  
  nudge_x = 0  
)
```

Arguments

mapping Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data	<p>The data to be displayed in this layer. There are three options:</p> <p>If NULL, the default, the data is inherited from the plot data as specified in the call to <code>ggplot()</code>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <code>fortify()</code> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).</p>
stat	The statistical transformation to use on the data for this layer, either as a <code>ggproto</code> <code>Geom</code> subclass or as a string naming the stat stripped of the <code>stat_</code> prefix (e.g. "count" rather than "stat_count")
position	Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use <code>position_jitter</code>), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
...	Other arguments passed on to <code>layer()</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>colour = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired <code>geom/stat</code> .
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders()</code> .
xfrom, xto	limitation of the strips along the x-axis
width	width of the strips
yfrom, yto	limitation of the strips along the y-axis
nudge_x, nudge_y	horizontal or vertical adjustment to nudge strips by

Value

A `ggplot2` plot with the added geometry.

Examples

```
data(tips, package = "reshape")

library(ggplot2)
p <- ggplot(tips) +
  aes(x = time, y = day) +
  geom_count() +
  theme_light()

p
p + geom_stripped_rows()
```

```

p + geom_stripped_cols()
p + geom_stripped_rows() + geom_stripped_cols()

p <- ggplot(tips) +
  aes(x = total_bill, y = day) +
  geom_count() +
  theme_light()
p
p + geom_stripped_rows()
p + geom_stripped_rows() + scale_y_discrete(expand = expansion(0, 0.5))
p + geom_stripped_rows(xfrom = 10, xto = 35)
p + geom_stripped_rows(odd = "blue", even = "yellow")
p + geom_stripped_rows(odd = "blue", even = "yellow", alpha = .1)
p + geom_stripped_rows(odd = "#00FF0022", even = "#FF000022")

p + geom_stripped_cols()
p + geom_stripped_cols(width = 10)
p + geom_stripped_cols(width = 10, nudge_x = 5)

```

ggcoef_model

Plot model coefficients

Description

ggcoef_model(), ggcoef_table(), ggcoef_multinom(), ggcoef_multicomponents() and ggcoef_compare() use [broom.helpers::tidy_plus_plus\(\)](#) to obtain a tibble of the model coefficients, apply additional data transformation and then pass the produced tibble to ggcoef_plot() to generate the plot.

Usage

```

ggcoef_model(
  model,
  tidy_fun = broom.helpers::tidy_with_broom_or_parameters,
  tidy_args = NULL,
  conf.int = TRUE,
  conf.level = 0.95,
  exponentiate = FALSE,
  variable_labels = NULL,
  term_labels = NULL,
  interaction_sep = " * ",
  categorical_terms_pattern = "{level}",
  add_reference_rows = TRUE,
  no_reference_row = NULL,
  intercept = FALSE,
  include = dplyr::everything(),

```

```

    add_pairwise_contrasts = FALSE,
    pairwise_variables = broom.helpers::all_categorical(),
    keep_model_terms = FALSE,
    pairwise_reverse = TRUE,
    emmeans_args = list(),
    significance = 1 - conf.level,
    significance_labels = NULL,
    show_p_values = TRUE,
    signif_stars = TRUE,
    return_data = FALSE,
    ...
  )

ggcoef_table(
  model,
  tidy_fun = broom.helpers::tidy_with_broom_or_parameters,
  tidy_args = NULL,
  conf.int = TRUE,
  conf.level = 0.95,
  exponentiate = FALSE,
  variable_labels = NULL,
  term_labels = NULL,
  interaction_sep = " * ",
  categorical_terms_pattern = "{level}",
  add_reference_rows = TRUE,
  no_reference_row = NULL,
  intercept = FALSE,
  include = dplyr::everything(),
  add_pairwise_contrasts = FALSE,
  pairwise_variables = broom.helpers::all_categorical(),
  keep_model_terms = FALSE,
  pairwise_reverse = TRUE,
  emmeans_args = list(),
  significance = 1 - conf.level,
  significance_labels = NULL,
  show_p_values = FALSE,
  signif_stars = FALSE,
  table_stat = c("estimate", "ci", "p.value"),
  table_header = NULL,
  table_text_size = 3,
  table_stat_label = NULL,
  ci_pattern = "{conf.low}, {conf.high}",
  table_widths = c(3, 2),
  plot_title = NULL,
  ...
)

ggcoef_compare(

```

```
models,
type = c("dodged", "faceted"),
tidy_fun = broom.helpers::tidy_with_broom_or_parameters,
tidy_args = NULL,
conf.int = TRUE,
conf.level = 0.95,
exponentiate = FALSE,
variable_labels = NULL,
term_labels = NULL,
interaction_sep = " * ",
categorical_terms_pattern = "{level}",
add_reference_rows = TRUE,
no_reference_row = NULL,
intercept = FALSE,
include = dplyr::everything(),
add_pairwise_contrasts = FALSE,
pairwise_variables = broom.helpers::all_categorical(),
keep_model_terms = FALSE,
pairwise_reverse = TRUE,
emmeans_args = list(),
significance = 1 - conf.level,
significance_labels = NULL,
return_data = FALSE,
...
)

ggcoef_multinom(
  model,
  type = c("dodged", "faceted", "table"),
  y.level_label = NULL,
  tidy_fun = broom.helpers::tidy_with_broom_or_parameters,
  tidy_args = NULL,
  conf.int = TRUE,
  conf.level = 0.95,
  exponentiate = FALSE,
  variable_labels = NULL,
  term_labels = NULL,
  interaction_sep = " * ",
  categorical_terms_pattern = "{level}",
  add_reference_rows = TRUE,
  no_reference_row = NULL,
  intercept = FALSE,
  include = dplyr::everything(),
  significance = 1 - conf.level,
  significance_labels = NULL,
  return_data = FALSE,
  table_stat = c("estimate", "ci", "p.value"),
  table_header = NULL,
```

```
    table_text_size = 3,
    table_stat_label = NULL,
    ci_pattern = "{conf.low}, {conf.high}",
    table_widths = c(3, 2),
    ...
  )

ggcoef_multicomponents(
  model,
  type = c("dodged", "faceted", "table"),
  component_col = "component",
  component_label = NULL,
  tidy_fun = broom.helpers::tidy_with_broom_or_parameters,
  tidy_args = NULL,
  conf.int = TRUE,
  conf.level = 0.95,
  exponentiate = FALSE,
  variable_labels = NULL,
  term_labels = NULL,
  interaction_sep = " * ",
  categorical_terms_pattern = "{level}",
  add_reference_rows = TRUE,
  no_reference_row = NULL,
  intercept = FALSE,
  include = dplyr::everything(),
  significance = 1 - conf.level,
  significance_labels = NULL,
  return_data = FALSE,
  table_stat = c("estimate", "ci", "p.value"),
  table_header = NULL,
  table_text_size = 3,
  table_stat_label = NULL,
  ci_pattern = "{conf.low}, {conf.high}",
  table_widths = c(3, 2),
  ...
)

ggcoef_plot(
  data,
  x = "estimate",
  y = "label",
  exponentiate = FALSE,
  point_size = 2,
  point_stroke = 2,
  point_fill = "white",
  colour = NULL,
  colour_guide = TRUE,
  colour_lab = "",
```

```

colour_labels = ggplot2::waiver(),
shape = "significance",
shape_values = c(16, 21),
shape_guide = TRUE,
shape_lab = "",
errorbar = TRUE,
errorbar_height = 0.1,
errorbar_coloured = FALSE,
stripped_rows = TRUE,
strips_odd = "#11111111",
strips_even = "#00000000",
vline = TRUE,
vline_colour = "grey50",
dodged = FALSE,
dodged_width = 0.8,
facet_row = "var_label",
facet_col = NULL,
facet_labeller = "label_value"
)

```

Arguments

<code>model</code>	a regression model object
<code>tidy_fun</code>	option to specify a custom tidier function
<code>tidy_args</code>	Additional arguments passed to <code>broom.helpers::tidy_plus_plus()</code> and to <code>tidy_fun</code>
<code>conf.int</code>	should confidence intervals be computed? (see <code>broom::tidy()</code>)
<code>conf.level</code>	the confidence level to use for the confidence interval if <code>conf.int = TRUE</code> ; must be strictly greater than 0 and less than 1; defaults to 0.95, which corresponds to a 95 percent confidence interval
<code>exponentiate</code>	if TRUE a logarithmic scale will be used for x-axis
<code>variable_labels</code>	a named list or a named vector of custom variable labels
<code>term_labels</code>	a named list or a named vector of custom term labels
<code>interaction_sep</code>	separator for interaction terms
<code>categorical_terms_pattern</code>	a glue pattern for labels of categorical terms with treatment or sum contrasts (see model_list_terms_levels())
<code>add_reference_rows</code>	should reference rows be added?
<code>no_reference_row</code>	variables (accepts tidyselect notation) for those no reference row should be added, when <code>add_reference_rows = TRUE</code>
<code>intercept</code>	should the intercept(s) be included?

include	variables to include. Accepts <code>tidyselect</code> syntax. Use <code>-</code> to remove a variable. Default is <code>everything()</code> . See also <code>all_continuous()</code> , <code>all_categorical()</code> , <code>all_dichotomous()</code> and <code>all_interaction()</code>
add_pairwise_contrasts	apply <code>tidy_add_pairwise_contrasts()</code> ? [Experimental]
pairwise_variables	variables to add pairwise contrasts (accepts <code>tidyselect</code> notation)
keep_model_terms	keep original model terms for variables where pairwise contrasts are added? (default is FALSE)
pairwise_reverse	determines whether to use "pairwise" (if TRUE) or "revpairwise" (if FALSE), see <code>emmeans::contrast()</code>
emmeans_args	list of additional parameter to pass to <code>emmeans::emmeans()</code> when computing pairwise contrasts
significance	level (between 0 and 1) below which a coefficient is consider to be significantly different from 0 (or 1 if <code>exponentiate = TRUE</code>), NULL for not highlighting such coefficients
significance_labels	optional vector with custom labels for significance variable
show_p_values	if TRUE, add p-value to labels
signif_stars	if TRUE, add significant stars to labels
return_data	if TRUE, will return the data.frame used for plotting instead of the plot
...	parameters passed to <code>ggcoef_plot()</code>
table_stat	statistics to display in the table, use any column name returned by the tidier or "ci" for confidence intervals formatted according to <code>ci_pattern</code>
table_header	optional custom headers for the table
table_text_size	text size for the table
table_stat_label	optional named list of labeller functions for the displayed statistic (see examples)
ci_pattern	glue pattern for confidence intervals in the table
table_widths	relative widths of the forest plot and the coefficients table
plot_title	an optional plot title
models	named list of models
type	a dodged plot, a faceted plot or multiple table plots?
y.level_label	an optional named vector for labeling y.level (see examples)
component_col	name of the component column
component_label	an optional named vector for labeling components
data	a data frame containing data to be plotted, typically the output of <code>ggcoef_model()</code> , <code>ggcoef_compare()</code> or <code>ggcoef_multinom()</code> with the option <code>return_data = TRUE</code>

<code>x, y</code>	variables mapped to x and y axis
<code>point_size</code>	size of the points
<code>point_stroke</code>	thickness of the points
<code>point_fill</code>	fill colour for the points
<code>colour</code>	optional variable name to be mapped to colour aesthetic
<code>colour_guide</code>	should colour guide be displayed in the legend?
<code>colour_lab</code>	label of the colour aesthetic in the legend
<code>colour_labels</code>	labels argument passed to <code>ggplot2::scale_colour_discrete()</code> and <code>ggplot2::discrete_scale()</code>
<code>shape</code>	optional variable name to be mapped to the shape aesthetic
<code>shape_values</code>	values of the different shapes to use in <code>ggplot2::scale_shape_manual()</code>
<code>shape_guide</code>	should shape guide be displayed in the legend?
<code>shape_lab</code>	label of the shape aesthetic in the legend
<code>errorbar</code>	should error bars be plotted?
<code>errorbar_height</code>	height of error bars
<code>errorbar_coloured</code>	should error bars be colored as the points?
<code>stripped_rows</code>	should stripped rows be displayed in the background?
<code>strips_odd</code>	color of the odd rows
<code>strips_even</code>	color of the even rows
<code>vline</code>	should a vertical line be drawn at 0 (or 1 if <code>exponentiate = TRUE</code>)?
<code>vline_colour</code>	colour of vertical line
<code>dodged</code>	should points be dodged (according to the colour aesthetic)?
<code>dodged_width</code>	width value for <code>ggplot2::position_dodge()</code>
<code>facet_row</code>	variable name to be used for row facets
<code>facet_col</code>	optional variable name to be used for column facets
<code>facet_labeller</code>	labeller function to be used for labeling facets; if labels are too long, you can use <code>ggplot2::label_wrap_gen()</code> (see examples), more information in the documentation of <code>ggplot2::facet_grid()</code>

Details

For more control, you can use the argument `return_data = TRUE` to get the produced tibble, apply any transformation of your own and then pass your customized tibble to `ggcoef_plot()`.

Value

A `ggplot2` plot or a tibble if `return_data = TRUE`.

Functions

- `ggcoef_table()`: a variation of `ggcoef_model()` adding a table with estimates, confidence intervals and p-values
- `ggcoef_compare()`: designed for displaying several models on the same plot.
- `ggcoef_multinom()`: a variation of `ggcoef_model()` adapted to multinomial logistic regressions performed with `nnet::multinom()`.
- `ggcoef_multicomponents()`: a variation of `ggcoef_model()` adapted to multi-component models such as zero-inflated models or beta regressions. `ggcoef_multicomponents()` has been tested with `pscl::zeroinfl()`, `pscl::hurdle()` and `betareg::betareg()`
- `ggcoef_plot()`: plot a tidy tibble of coefficients

See Also

`vignette("ggcoef_model")`

Examples

```
mod <- lm(Sepal.Length ~ Sepal.Width + Species, data = iris)
ggcoef_model(mod)

ggcoef_table(mod)

ggcoef_table(mod, table_stat = c("estimate", "ci"))

ggcoef_table(
  mod,
  table_stat_label = list(
    estimate = scales::label_number(.001)
  )
)

ggcoef_table(mod, table_text_size = 5, table_widths = c(1, 1))

# a logistic regression example
d_titanic <- as.data.frame(Titanic)
d_titanic$Survived <- factor(d_titanic$Survived, c("No", "Yes"))
mod_titanic <- glm(
  Survived ~ Sex * Age + Class,
  weights = Freq,
  data = d_titanic,
  family = binomial
)

# use 'exponentiate = TRUE' to get the Odds Ratio
ggcoef_model(mod_titanic, exponentiate = TRUE)

ggcoef_table(mod_titanic, exponentiate = TRUE)
```

```

# display intercepts
ggcoef_model(mod_titanic, exponentiate = TRUE, intercept = TRUE)

# customize terms labels
ggcoef_model(
  mod_titanic,
  exponentiate = TRUE,
  show_p_values = FALSE,
  signif_stars = FALSE,
  add_reference_rows = FALSE,
  categorical_terms_pattern = "{level} (ref: {reference_level})",
  interaction_sep = " x "
) +
  ggplot2::scale_y_discrete(labels = scales::label_wrap(15))

# display only a subset of terms
ggcoef_model(mod_titanic, exponentiate = TRUE, include = c("Age", "Class"))

# do not change points' shape based on significance
ggcoef_model(mod_titanic, exponentiate = TRUE, significance = NULL)

# a black and white version
ggcoef_model(
  mod_titanic,
  exponentiate = TRUE,
  colour = NULL, stripped_rows = FALSE
)

# show dichotomous terms on one row
ggcoef_model(
  mod_titanic,
  exponentiate = TRUE,
  no_reference_row = broom.helpers::all_dichotomous(),
  categorical_terms_pattern =
    "{ifelse(dichotomous, paste0(level, ' / ', reference_level), level)}",
  show_p_values = FALSE
)

data(tips, package = "reshape")
mod_simple <- lm(tip ~ day + time + total_bill, data = tips)
ggcoef_model(mod_simple)

# custom variable labels
# you can use the labelled package to define variable labels
# before computing model
if (requireNamespace("labelled")) {
  tips_labelled <- tips %>%
    labelled::set_variable_labels(
      day = "Day of the week",
      time = "Lunch or Dinner",

```

```

    total_bill = "Bill's total"
  )
  mod_labelled <- lm(tip ~ day + time + total_bill, data = tips_labelled)
  ggcoef_model(mod_labelled)
}

# you can provide custom variable labels with 'variable_labels'
ggcoef_model(
  mod_simple,
  variable_labels = c(
    day = "Week day",
    time = "Time (lunch or dinner ?)",
    total_bill = "Total of the bill"
  )
)
# if labels are too long, you can use 'facet_labeller' to wrap them
ggcoef_model(
  mod_simple,
  variable_labels = c(
    day = "Week day",
    time = "Time (lunch or dinner ?)",
    total_bill = "Total of the bill"
  ),
  facet_labeller = ggplot2::label_wrap_gen(10)
)

# do not display variable facets but add colour guide
ggcoef_model(mod_simple, facet_row = NULL, colour_guide = TRUE)

# works also with with polynomial terms
mod_poly <- lm(
  tip ~ poly(total_bill, 3) + day,
  data = tips,
)
ggcoef_model(mod_poly)

# or with different type of contrasts
# for sum contrasts, the value of the reference term is computed
if (requireNamespace("emmeans")) {
  mod2 <- lm(
    tip ~ day + time + sex,
    data = tips,
    contrasts = list(time = contr.sum, day = contr.treatment(4, base = 3))
  )
  ggcoef_model(mod2)
}

# Use ggcoef_compare() for comparing several models on the same plot
mod1 <- lm(Fertility ~ ., data = swiss)
mod2 <- step(mod1, trace = 0)
mod3 <- lm(Fertility ~ Agriculture + Education * Catholic, data = swiss)

```

```

models <- list(
  "Full model" = mod1,
  "Simplified model" = mod2,
  "With interaction" = mod3
)

ggcoef_compare(models)
ggcoef_compare(models, type = "faceted")

# you can reverse the vertical position of the point by using a negative
# value for dodged_width (but it will produce some warnings)
ggcoef_compare(models, dodged_width = -.9)

# specific function for nnet::multinom models
mod <- nnet::multinom(Species ~ ., data = iris)
ggcoef_multinom(mod, exponentiate = TRUE)
ggcoef_multinom(mod, type = "faceted")
ggcoef_multinom(
  mod,
  type = "faceted",
  y.level_label = c("versicolor" = "versicolor\n(ref: setosa)")
)

library(pscl)
data("bioChemists", package = "pscl")
mod <- zeroinfl(art ~ fem * mar | fem + mar, data = bioChemists)
ggcoef_multicomponents(mod)

ggcoef_multicomponents(mod, type = "f")

ggcoef_multicomponents(mod, type = "t")

ggcoef_multicomponents(
  mod,
  type = "t",
  component_label = c(conditional = "Count", zero_inflated = "Zero-inflated")
)

mod2 <- zeroinfl(art ~ fem + mar | 1, data = bioChemists)
ggcoef_multicomponents(mod2, type = "t")

```

Description**[Experimental]****Usage**

```
gglikert(  
  data,  
  include = dplyr::everything(),  
  weights = NULL,  
  y = ".question",  
  variable_labels = NULL,  
  sort = c("none", "ascending", "descending"),  
  sort_method = c("prop", "mean", "median"),  
  sort_prop_include_center = totals_include_center,  
  exclude_fill_values = NULL,  
  add_labels = TRUE,  
  labels_size = 3.5,  
  labels_color = "black",  
  labels_accuracy = 1,  
  labels_hide_below = 0.05,  
  add_totals = TRUE,  
  totals_size = labels_size,  
  totals_color = "black",  
  totals_accuracy = labels_accuracy,  
  totals_fontface = "bold",  
  totals_include_center = FALSE,  
  totals_hjust = 0.1,  
  y_reverse = TRUE,  
  y_label_wrap = 50,  
  reverse_likert = FALSE,  
  width = 0.9,  
  facet_rows = NULL,  
  facet_cols = NULL,  
  facet_label_wrap = 50  
)  
  
gglikert_data(  
  data,  
  include = dplyr::everything(),  
  weights = NULL,  
  variable_labels = NULL,  
  sort = c("none", "ascending", "descending"),  
  sort_method = c("prop", "mean", "median"),  
  sort_prop_include_center = TRUE,  
  exclude_fill_values = NULL  
)  
  
gglikert_stacked(  
  data,  
  include = dplyr::everything(),  
  weights = NULL,  
  variable_labels = NULL,  
  sort = c("none", "ascending", "descending"),  
  sort_method = c("prop", "mean", "median"),  
  sort_prop_include_center = TRUE,  
  exclude_fill_values = NULL  
)
```

```

data,
include = dplyr::everything(),
weights = NULL,
y = ".question",
variable_labels = NULL,
sort = c("none", "ascending", "descending"),
sort_method = c("prop", "mean", "median"),
sort_prop_include_center = FALSE,
add_labels = TRUE,
labels_size = 3.5,
labels_color = "black",
labels_accuracy = 1,
labels_hide_below = 0.05,
add_median_line = FALSE,
y_reverse = TRUE,
y_label_wrap = 50,
reverse_fill = TRUE,
width = 0.9
)

```

Arguments

<code>data</code>	a data frame
<code>include</code>	variables to include, accept tidy-select syntax
<code>weights</code>	optional variable name of a weighting variable, accept tidy-select syntax
<code>y</code>	name of the variable to be plotted on y axis (relevant when <code>.question</code> is mapped to "facets, see examples), accept tidy-select syntax
<code>variable_labels</code>	a named list or a named vector of custom variable labels
<code>sort</code>	should variables be sorted?
<code>sort_method</code>	method used to sort the variables: "prop" sort according to the proportion of answers higher than the centered level, "mean" considers answer as a score and sort according to the mean score, "median" used the median and the majority judgment rule for tie-breaking.
<code>sort_prop_include_center</code>	when sorting with "prop" and if the number of levels is uneven, should half of the central level be taken into account to compute the proportion?
<code>exclude_fill_values</code>	Vector of values that should not be displayed (but still taken into account for computing proportions), see position_likert()
<code>add_labels</code>	should percentage labels be added to the plot?
<code>labels_size</code>	size of the percentage labels
<code>labels_color</code>	color of the percentage labels
<code>labels_accuracy</code>	accuracy of the percentages, see scales::label_percent()

<code>labels_hide_below</code>	if provided, values below will be masked, see label_percent_abs()
<code>add_totals</code>	should the total proportions of negative and positive answers be added to plot? This option is not compatible with facets!
<code>totals_size</code>	size of the total proportions
<code>totals_color</code>	color of the total proportions
<code>totals_accuracy</code>	accuracy of the total proportions, see scales::label_percent()
<code>totals_fontface</code>	font face of the total proportions
<code>totals_include_center</code>	if the number of levels is uneven, should half of the center level be added to the total proportions?
<code>totals_hjust</code>	horizontal adjustment of totals labels on the x axis
<code>y_reverse</code>	should the y axis be reversed?
<code>y_label_wrap</code>	number of characters per line for y axis labels, see scales::label_wrap()
<code>reverse_likert</code>	if TRUE, will reverse the default stacking order, see position_likert()
<code>width</code>	bar width, see ggplot2::geom_bar()
<code>facet_rows, facet_cols</code>	A set of variables or expressions quoted by ggplot2::vars() and defining faceting groups on the rows or columns dimension (see examples)
<code>facet_label_wrap</code>	number of characters per line for facet labels, see ggplot2::label_wrap_gen()
<code>add_median_line</code>	add a vertical line at 50%?
<code>reverse_fill</code>	if TRUE, will reverse the default stacking order, see ggplot2::position_fill()

Details

Combines several factor variables using the same list of ordered levels (e.g. Likert-type scales) into a unique data frame and generates a centered bar plot.

You could use `gglikert_data()` to just produce the dataset to be plotted.

If variable labels have been defined (see [labelled::var_label\(\)](#)), they will be considered. You can also pass custom variables labels with the `variable_labels` argument.

Value

A `ggplot2` plot or a tibble.

See Also

`vignette("gglikert")`, [position_likert\(\)](#), [stat_prop\(\)](#)

Examples

```
library(ggplot2)
library(dplyr)

likert_levels <- c(
  "Strongly disagree",
  "Disagree",
  "Neither agree nor disagree",
  "Agree",
  "Strongly agree"
)
set.seed(42)
df <-
  tibble(
    q1 = sample(likert_levels, 150, replace = TRUE),
    q2 = sample(likert_levels, 150, replace = TRUE, prob = 5:1),
    q3 = sample(likert_levels, 150, replace = TRUE, prob = 1:5),
    q4 = sample(likert_levels, 150, replace = TRUE, prob = 1:5),
    q5 = sample(c(likert_levels, NA), 150, replace = TRUE),
    q6 = sample(likert_levels, 150, replace = TRUE, prob = c(1, 0, 1, 1, 0))
  ) %>%
  mutate(across(everything(), ~ factor(.x, levels = likert_levels)))

gglikert(df)

gglikert(df, include = q1:3)

gglikert(df, sort = "ascending")

gglikert(df, sort = "ascending", sort_prop_include_center = TRUE)

gglikert(df, sort = "ascending", sort_method = "mean")

gglikert(df, reverse_likert = TRUE)

gglikert(df, add_totals = FALSE, add_labels = FALSE)

gglikert(
  df,
  totals_include_center = TRUE,
  totals_hjust = .25,
  totals_size = 4.5,
  totals_fontface = "italic",
  totals_accuracy = .01,
  labels_accuracy = 1,
  labels_size = 2.5,
  labels_hide_below = .25
)

gglikert(df, exclude_fill_values = "Neither agree nor disagree")
```

```

if (require("labelled")) {
  df %>%
    set_variable_labels(
      q1 = "First question",
      q2 = "Second question"
    ) %>%
    gglikert(
      variable_labels = c(
        q4 = "a custom label",
        q6 = "a very very very very very very very very very long label"
      ),
      y_label_wrap = 25
    )
}

# Facets
df_group <- df
df_group$group <- sample(c("A", "B"), 150, replace = TRUE)

gglikert(df_group, q1:q6, facet_rows = vars(group))

gglikert(df_group, q1:q6, facet_cols = vars(group))

gglikert(df_group, q1:q6, y = "group", facet_rows = vars(.question))

gglikert_stacked(df, q1:q6)

gglikert_stacked(df, q1:q6, add_median_line = TRUE, sort = "asc")

gglikert_stacked(df_group, q1:q6, y = "group", add_median_line = TRUE) +
  facet_grid(rows = vars(.question))

```

ggsurvey

Easy ggplot2 with survey objects

Description

A function to facilitate ggplot2 graphs using a survey object. It will initiate a ggplot and map survey weights to the corresponding aesthetic.

Usage

```
ggsurvey(design = NULL, mapping = NULL, ...)
```

Arguments

design	A survey design object, usually created with <code>survey::svydesign()</code>
mapping	Default list of aesthetic mappings to use for plot, to be created with <code>ggplot2::aes()</code> .
...	Other arguments passed on to methods. Not currently used.

Details

Graphs will be correct as long as only weights are required to compute the graph. However, statistic or geometry requiring correct variance computation (like `ggplot2::geom_smooth()`) will be statistically incorrect.

Value

A `ggplot2` plot.

Examples

```
data(api, package = "survey")
dstrat <- survey::svydesign(
  id = ~1, strata = ~stype,
  weights = ~pw, data = apistrat,
  fpc = ~fpc
)
ggsurvey(dstrat) +
  ggplot2::aes(x = cnum, y = dnum) +
  ggplot2::geom_count()

d <- as.data.frame(Titanic)
dw <- survey::svydesign(ids = ~1, weights = ~Freq, data = d)
ggsurvey(dw) +
  ggplot2::aes(x = Class, fill = Survived) +
  ggplot2::geom_bar(position = "fill")
```

label_number_abs	<i>Label absolute values</i>
------------------	------------------------------

Description

Label absolute values

Usage

```
label_number_abs(..., hide_below = NULL)

label_percent_abs(..., hide_below = NULL)
```

Arguments

...	arguments passed to <code>scales::label_number()</code> or <code>scales::label_percent()</code>
hide_below	if provided, values below <code>hide_below</code> will be masked (i.e. an empty string "" will be returned)

Value

A "labelling" function, , i.e. a function that takes a vector and returns a character vector of same length giving a label for each input value.

See Also

`scales::label_number()`, `scales::label_percent()`

Examples

```
x <- c(-0.2, -.05, 0, .07, .25, .66)

scales::label_number()(x)
label_number_abs()(x)

scales::label_percent()(x)
label_percent_abs()(x)
label_percent_abs(hide_below = .1)(x)
```

position_likert

Stack objects on top of each another and center them around 0

Description

[Experimental]

Usage

```
position_likert(vjust = 1, reverse = FALSE, exclude_fill_values = NULL)

position_likert_count(vjust = 1, reverse = FALSE, exclude_fill_values = NULL)
```

Arguments

vjust	Vertical adjustment for geoms that have a position (like points or lines), not a dimension (like bars or areas). Set to 0 to align with the bottom, 0.5 for the middle, and 1 (the default) for the top.
reverse	If TRUE, will reverse the default stacking order. This is useful if you're rotating both the plot and legend.
exclude_fill_values	Vector of values from the variable associated with the fill aesthetic that should not be displayed (but still taken into account for computing proportions)

Details

position_likert() stacks proportion bars on top of each other and center them around zero (the same number of modalities are displayed on each side). This type of presentation is commonly used to display Likert-type scales. position_likert_count() uses counts instead of proportions.

It is recommended to use position_likert() with stat_prop() and its complete argument (see examples).

See Also

See [ggplot2::position_stack\(\)](#) and [ggplot2::position_fill\(\)](#)

Examples

```
library(ggplot2)

ggplot(diamonds) +
  aes(y = clarity, fill = cut) +
  geom_bar(position = "fill") +
  scale_x_continuous(label = scales::label_percent()) +
  scale_fill_brewer(palette = "PiYG") +
  xlab("proportion")

ggplot(diamonds) +
  aes(y = clarity, fill = cut) +
  geom_bar(position = "likert") +
  scale_x_continuous(label = label_percent_abs()) +
  scale_fill_brewer(palette = "PiYG") +
  xlab("proportion")

ggplot(diamonds) +
  aes(y = clarity, fill = cut) +
  geom_bar(position = "stack") +
  scale_fill_brewer(palette = "PiYG")

ggplot(diamonds) +
  aes(y = clarity, fill = cut) +
  geom_bar(position = "likert_count") +
  scale_x_continuous(label = label_number_abs()) +
  scale_fill_brewer(palette = "PiYG")

# Reverse order -----

ggplot(diamonds) +
  aes(y = clarity, fill = cut) +
  geom_bar(position = position_likert(reverse = TRUE)) +
  scale_x_continuous(label = label_percent_abs()) +
  scale_fill_brewer(palette = "PiYG", direction = -1) +
  xlab("proportion")

# Missing items -----
```

```

# example with a level not being observed for a specific value of y
d <- diamonds
d <- d[!(d$cut == "Premium" & d$clarity == "I1"), ]
d <- d[!(d$cut %in% c("Fair", "Good") & d$clarity == "SI2"), ]

# by default, the two lowest bar are not properly centered
ggplot(d) +
  aes(y = clarity, fill = cut) +
  geom_bar(position = "likert") +
  scale_fill_brewer(palette = "PiYG")

# use stat_prop() with `complete = "fill"` to fix it
ggplot(d) +
  aes(y = clarity, fill = cut) +
  geom_bar(position = "likert", stat = "prop", complete = "fill") +
  scale_fill_brewer(palette = "PiYG")

# Add labels -----
custom_label <- function(x) {
  p <- scales::percent(x, accuracy = 1)
  p[x < .075] <- ""
  p
}

ggplot(diamonds) +
  aes(y = clarity, fill = cut) +
  geom_bar(position = "likert") +
  geom_text(
    aes(by = clarity, label = custom_label(after_stat(prop))),
    stat = "prop",
    position = position_likert(vjust = .5)
  ) +
  scale_x_continuous(label = label_percent_abs()) +
  scale_fill_brewer(palette = "PiYG", direction = -1) +
  xlab("proportion")

# Do not display specific fill values -----
# (but taken into account to compute proportions)

ggplot(diamonds) +
  aes(y = clarity, fill = cut) +
  geom_bar(position = position_likert(exclude_fill_values = "Very Good")) +
  scale_x_continuous(label = label_percent_abs()) +
  scale_fill_brewer(palette = "PiYG") +
  xlab("proportion")

```

Description

Calculate significance stars

Usage

```
signif_stars(x, three = 0.001, two = 0.01, one = 0.05, point = 0.1)
```

Arguments

x	numeric values that will be compared to the point, one, two, and three values
three	threshold below which to display three stars
two	threshold below which to display two stars
one	threshold below which to display one star
point	threshold below which to display one point (NULL to deactivate)

Value

Character vector containing the appropriate number of stars for each x value.

Author(s)

Joseph Larmarange

Examples

```
x <- c(0.5, 0.1, 0.05, 0.01, 0.001)
signif_stars(x)
signif_stars(x, one = .15, point = NULL)
```

stat_cross

Compute cross-tabulation statistics

Description

Computes statistics of a 2-dimensional matrix using [broom::augment.htest](#).

Usage

```
stat_cross(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  ...,
  na.rm = TRUE,
  show.legend = NA,
  inherit.aes = TRUE,
  keep.zero.cells = FALSE
)
```

Arguments

mapping	Set of aesthetic mappings created by <code>aes()</code> . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data	The data to be displayed in this layer. There are three options: If <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <code>ggplot()</code> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <code>fortify()</code> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).
geom	Override the default connection with <code>ggplot2::geom_point()</code> .
position	Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use <code>position_jitter</code>), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
...	Other arguments passed on to <code>layer()</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>colour = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired <code>geom/stat</code> .
na.rm	If <code>TRUE</code> , the default, missing values are removed with a warning. If <code>FALSE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes	If <code>FALSE</code> , 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> .
keep.zero.cells	If <code>TRUE</code> , cells with no observations are kept.

Value

A `ggplot2` plot with the added statistic.

Aesthetics

`stat_cross()` requires the `x` and the `y` aesthetics.

Computed variables

observed number of observations in `x,y`

prop proportion of total

row.prop row proportion

col.prop column proportion

expected expected count under the null hypothesis
resid Pearson's residual
std.resid standardized residual
row.observed total number of observations within row
col.observed total number of observations within column
total.observed total number of observations within the table
phi phi coefficients, see [augment_chisq_add_phi\(\)](#)

See Also

`vignette("stat_cross")`

Examples

```
library(ggplot2)
d <- as.data.frame(Titanic)

# plot number of observations
ggplot(d) +
  aes(x = Class, y = Survived, weight = Freq, size = after_stat(observed)) +
  stat_cross() +
  scale_size_area(max_size = 20)

# custom shape and fill colour based on chi-squared residuals
ggplot(d) +
  aes(
    x = Class, y = Survived, weight = Freq,
    size = after_stat(observed), fill = after_stat(std.resid)
  ) +
  stat_cross(shape = 22) +
  scale_fill_steps2(breaks = c(-3, -2, 2, 3), show.limits = TRUE) +
  scale_size_area(max_size = 20)

# custom shape and fill colour based on phi coefficients
ggplot(d) +
  aes(
    x = Class, y = Survived, weight = Freq,
    size = after_stat(observed), fill = after_stat(phi)
  ) +
  stat_cross(shape = 22) +
  scale_fill_steps2(show.limits = TRUE) +
  scale_size_area(max_size = 20)

# plotting the number of observations as a table
ggplot(d) +
  aes(
    x = Class, y = Survived, weight = Freq, label = after_stat(observed)
  ) +
```

```

geom_text(stat = "cross")

# Row proportions with standardized residuals
ggplot(d) +
  aes(
    x = Class, y = Survived, weight = Freq,
    label = scales::percent(after_stat(row.prop)),
    size = NULL, fill = after_stat(std.resid)
  ) +
  stat_cross(shape = 22, size = 30) +
  geom_text(stat = "cross") +
  scale_fill_steps2(breaks = c(-3, -2, 2, 3), show.limits = TRUE) +
  facet_grid(Sex ~ .) +
  labs(fill = "Standardized residuals") +
  theme_minimal()

```

stat_prop

Compute proportions according to custom denominator

Description

stat_prop() is a variation of `ggplot2::stat_count()` allowing to compute custom proportions according to the **by** aesthetic defining the denominator (i.e. all proportions for a same value of **by** will sum to 1). The **by** aesthetic should be a factor. If **by** is not specified, proportions of the total will be computed.

Usage

```

stat_prop(
  mapping = NULL,
  data = NULL,
  geom = "bar",
  position = "fill",
  ...,
  width = NULL,
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE,
  complete = NULL
)

```

Arguments

mapping Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data	<p>The data to be displayed in this layer. There are three options:</p> <p>If NULL, the default, the data is inherited from the plot data as specified in the call to <code>ggplot()</code>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <code>fortify()</code> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).</p>
geom	Override the default connection with <code>ggplot2::geom_bar()</code> .
position	Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use <code>position_jitter</code>), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
...	Other arguments passed on to <code>layer()</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>colour = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
width	Bar width. By default, set to 90% of the <code>resolution()</code> of the data.
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
orientation	The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting <code>orientation</code> to either "x" or "y". See the <i>Orientation</i> section for more detail.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders()</code> .
complete	Name (character) of an aesthetic for those statistics should be completed for unobserved values (see example)

Value

A `ggplot2` plot with the added statistic.

Aesthetics

`stat_prop()` understands the following aesthetics (required aesthetics are in bold):

- **x or y**
- **by** (this aesthetic should be a **factor**)
- group
- weight

Computed variables

count number of points in bin
prop computed proportion

See Also

vignette("stat_prop"), `ggplot2::stat_count()`. For an alternative approach, see <https://github.com/tidyverse/ggplot2/issues/5505#issuecomment-1791324008>.

Examples

```
library(ggplot2)
d <- as.data.frame(Titanic)

p <- ggplot(d) +
  aes(x = Class, fill = Survived, weight = Freq, by = Class) +
  geom_bar(position = "fill") +
  geom_text(stat = "prop", position = position_fill(.5))
p
p + facet_grid(~Sex)

ggplot(d) +
  aes(x = Class, fill = Survived, weight = Freq) +
  geom_bar(position = "dodge") +
  geom_text(
    aes(by = Survived),
    stat = "prop",
    position = position_dodge(0.9), vjust = "bottom"
  )

if (requireNamespace("scales")) {
  ggplot(d) +
    aes(x = Class, fill = Survived, weight = Freq, by = 1) +
    geom_bar() +
    geom_text(
      aes(label = scales::percent(after_stat(prop), accuracy = 1)),
      stat = "prop",
      position = position_stack(.5)
    )
}

# displaying unobserved levels with complete
d <- diamonds %>%
  dplyr::filter(!(cut == "Ideal" & clarity == "I1")) %>%
  dplyr::filter(!(cut == "Very Good" & clarity == "VS2")) %>%
  dplyr::filter(!(cut == "Premium" & clarity == "IF"))
p <- ggplot(d) +
  aes(x = clarity, fill = cut, by = clarity) +
  geom_bar(position = "fill")
p + geom_text(stat = "prop", position = position_fill(.5))
p + geom_text(stat = "prop", position = position_fill(.5), complete = "fill")
```

 stat_weighted_mean *Compute weighted y mean*

Description

This statistic will compute the mean of **y** aesthetic for each unique value of **x**, taking into account **weight** aesthetic if provided.

Usage

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

Arguments

mapping	Set of aesthetic mappings created by aes() . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data	The data to be displayed in this layer. There are three options: If <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to ggplot() . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).
geom	Override the default connection with ggplot2::geom_point() .
position	Position adjustment, either as a string naming the adjustment (e.g. <code>"jitter"</code> to use <code>position_jitter</code>), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
...	Other arguments passed on to layer() . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>colour = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.

orientation	The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the <i>Orientation</i> section for more detail.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders()</code> .

Value

A ggplot2 plot with the added statistic.

Computed variables

y weighted y (numerator / denominator)

numerator numerator

denominator denominator

See Also

`vignette("stat_weighted_mean")`

Examples

```
library(ggplot2)

data(tips, package = "reshape")

ggplot(tips) +
  aes(x = day, y = total_bill) +
  geom_point()

ggplot(tips) +
  aes(x = day, y = total_bill) +
  stat_weighted_mean()

ggplot(tips) +
  aes(x = day, y = total_bill, group = 1) +
  stat_weighted_mean(geom = "line")

ggplot(tips) +
  aes(x = day, y = total_bill, colour = sex, group = sex) +
  stat_weighted_mean(geom = "line")
```

```

ggplot(tips) +
  aes(x = day, y = total_bill, fill = sex) +
  stat_weighted_mean(geom = "bar", position = "dodge")

# computing a proportion on the fly
if (requireNamespace("scales")) {
  ggplot(tips) +
    aes(x = day, y = as.integer(smoker == "Yes"), fill = sex) +
    stat_weighted_mean(geom = "bar", position = "dodge") +
    scale_y_continuous(labels = scales::percent)
}

library(ggplot2)

# taking into account some weights
if (requireNamespace("scales")) {
  d <- as.data.frame(Titanic)
  ggplot(d) +
    aes(
      x = Class, y = as.integer(Survived == "Yes"),
      weight = Freq, fill = Sex
    ) +
    geom_bar(stat = "weighted_mean", position = "dodge") +
    scale_y_continuous(labels = scales::percent) +
    labs(y = "Survived")
}

```

 weighted.median

Weighted Median and Quantiles

Description

Compute the median or quantiles a set of numbers which have weights associated with them.

Usage

```
weighted.median(x, w, na.rm = TRUE, type = 2)
```

```
weighted.quantile(x, w, probs = seq(0, 1, 0.25), na.rm = TRUE, type = 4)
```

Arguments

x	a numeric vector of values
w	a numeric vector of weights
na.rm	a logical indicating whether to ignore NA values
type	Integer specifying the rule for calculating the median or quantile, corresponding to the rules available for <code>stats::quantile()</code> . The only valid choices are <code>type=1</code> , <code>2</code> or <code>4</code> . See Details .
probs	probabilities for which the quantiles should be computed, a numeric vector of values between 0 and 1

Details

The i th observation $x[i]$ is treated as having a weight proportional to $w[i]$.

The weighted median is a value m such that the total weight of data less than or equal to m is equal to half the total weight. More generally, the weighted quantile with probability p is a value q such that the total weight of data less than or equal to q is equal to p times the total weight.

If there is no such value, then

- if `type = 1`, the next largest value is returned (this is the right-continuous inverse of the left-continuous cumulative distribution function);
- if `type = 2`, the average of the two surrounding values is returned (the average of the right-continuous and left-continuous inverses);
- if `type = 4`, linear interpolation is performed.

Note that the default rule for `weighted.median()` is `type = 2`, consistent with the traditional definition of the median, while the default for `weighted.quantile()` is `type = 4`.

Value

A numeric vector.

Source

These functions are adapted from their homonyms developed by Adrian Baddeley in the `spatstat` package.

Examples

```
x <- 1:20
w <- runif(20)
weighted.median(x, w)
weighted.quantile(x, w)
```

Index

*** datasets**
 position_likert, 22
 stat_cross, 25
 stat_prop, 28
 stat_weighted_mean, 31

aes(), 3, 26, 28, 31
all_categorical(), 10
all_continuous(), 10
all_dichotomous(), 10
all_interaction(), 10
augment_chisq_add_phi, 2
augment_chisq_add_phi(), 27

borders(), 4, 26, 29, 32
broom.helpers::tidy_plus_plus(), 5, 9
broom::augment.htest, 25
broom::tidy(), 9

emmeans::contrast(), 10
emmeans::emmeans(), 10

fortify(), 4, 26, 29, 31

geom_stripped_cols
 (geom_stripped_rows), 3
geom_stripped_rows, 3
ggcoef_compare (ggcoef_model), 5
ggcoef_model, 5
ggcoef_model(), 12
ggcoef_multicomponents (ggcoef_model), 5
ggcoef_multicomponents(), 12
ggcoef_multinom (ggcoef_model), 5
ggcoef_plot (ggcoef_model), 5
ggcoef_plot(), 10
ggcoef_table (ggcoef_model), 5
gglikert, 15
gglikert_data (gglikert), 15
gglikert_stacked (gglikert), 15
ggplot(), 4, 26, 29, 31
ggplot2::aes(), 20
ggplot2::discrete_scale(), 11
ggplot2::facet_grid(), 11
ggplot2::geom_bar(), 18, 29
ggplot2::geom_point(), 26, 31
ggplot2::geom_smooth(), 21
ggplot2::label_wrap_gen(), 11, 18
ggplot2::position_dodge(), 11
ggplot2::position_fill(), 18, 23
ggplot2::position_stack(), 23
ggplot2::scale_colour_discrete(), 11
ggplot2::scale_shape_manual(), 11
ggplot2::stat_count(), 28, 30
ggplot2::vars(), 18
ggsurvey, 20
glue pattern, 9

label_number_abs, 21
label_percent_abs (label_number_abs), 21
label_percent_abs(), 18
labelled::var_label(), 18
layer(), 4, 26, 29, 31

model_list_terms_levels(), 9

nnet::multinom(), 12

position_likert, 22
position_likert(), 17, 18
position_likert_count
 (position_likert), 22
PositionLikert (position_likert), 22
PositionLikertCount (position_likert),
 22

resolution(), 29

scales::label_number(), 21, 22
scales::label_percent(), 17, 18, 21, 22
scales::label_wrap(), 18
signif_stars, 24
stat_cross, 25

`stat_cross()`, 2
`stat_prop`, 28
`stat_prop()`, 18
`stat_weighted_mean`, 31
`StatCross (stat_cross)`, 25
`StatProp (stat_prop)`, 28
`stats::chisq.test()`, 2
`StatWeightedMean (stat_weighted_mean)`,
31
`survey::svydesign()`, 20

`tidy-select`, 17
`tidy_add_pairwise_contrasts()`, 10
`tidyselect`, 9, 10

`weighted.median`, 33
`weighted.quantile (weighted.median)`, 33