Package ‘gtsummary’

January 29, 2022

Title Presentation-Ready Data Summary and Analytic Result Tables

Version 1.5.2

Description Creates presentation-ready tables summarizing data sets, regression models, and more. The code to create the tables is concise and highly customizable. Data frames can be summarized with any function, e.g. mean(), median(), even user-written functions. Regression models are summarized and include the reference rows for categorical variables. Common regression models, such as logistic regression and Cox proportional hazards regression, are automatically identified and the tables are pre-filled with appropriate column headers.

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URL `https://github.com/ddsjoberg/gtsummary`,
`https://www.danieldsjoberg.com/gtsummary/`

BugReports `https://github.com/ddsjoberg/gtsummary/issues`

Depends R (>= 3.4)

Imports broom (>= 0.7.11),
broom.helpers (>= 1.6.0),
cli (>= 3.1.1),
dplyr (>= 1.0.7),
forcats (>= 0.5.1),
glue (>= 1.6.0),
gt (>= 0.3.1),
knitr (>= 1.37),
lifecycle (>= 1.0.1),
purrr (>= 0.3.4),
rlang (>= 0.4.12),
stringr (>= 1.4.0),
tibble (>= 3.1.6),
tidyr (>= 1.1.4)

Suggests broom.mixed (>= 0.2.7),
car (>= 3.0-11),
covr,
effectsize (>= 0.6.0),
emmeans (>= 1.7.2),
flextable (>= 0.6.10),

geepack,
GGally (>= 2.1.0),
Hmisc,
huxtable (>= 5.4.0),
insight (>= 0.15.0),
kableExtra (>= 1.3.4),
lme4,
mgcv,
mice (>= 3.10.0),
nnet,
officer,
parameters (>= 0.16.0),
parsnip (>= 0.1.7),
rmarkdown,
sandwich (>= 3.0.1),
scales,
smd (>= 0.6.6),
spelling (>= 2.2),
survey,
survival (>= 3.2-11),
testthat (>= 3.0.4),
workflows (>= 0.2.4)

VignetteBuilder knitr

RdMacros lifecycle

Encoding UTF-8

Language en-US

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

Config/testthat/edition 3

Config/testthat/parallel true

R topics documented:

`add_ci` *Add CI Column*

Description

Add a new column with the confidence intervals for proportions, means, etc.

Usage

```
add_ci(x, ...)

## S3 method for class 'tbl_summary'
add_ci(
  x,
  method = NULL,
  include = everything(),
  statistic = NULL,
  conf.level = 0.95,
  style_fun = NULL,
  pattern = NULL,
  ...
)
```

Arguments

`x`	A `tbl_summary` object
`...`	Not used
`method`	Confidence interval method. Default is `list(all_categorical() ~ "wilson", all_continuous() ~ "t.test")`. Must be one of `c("wilson", "wilson.no.correct", "exact", "asymptotic")` for categorical variables, and `c("t.test", "wilcox.test")` for continuous variables. See details below.
`include`	variables to include in the summary table. Default is `everything()`
`statistic`	Formula indicating how the confidence interval will be displayed. Default is `list(all_categorical() ~ "{conf.low}%, {conf.high}%", all_continuous() ~ "{conf.low}, {conf.high}")`
`conf.level`	Confidence level. Default is `0.95`
`style_fun`	Function to style upper and lower bound of confidence interval. Default is `list(all_categorical() ~ purrr::partial(style_sigfig, scale = 100), all_continuous() ~ style_sigfig)`.
`pattern`	string indicating the pattern to use to merge the CI with the statistics cell. The default is NULL, where no columns are merged. The two columns that will be merged are the statistics column, represented by `"{stat}"` and the CI column represented by `"{ci}"`, e.g. `pattern = "{stat} ({ci})"` will merge the two columns with the CI in parentheses.

Value

gtsummary table

method argument

Methods `c("wilson","wilson.no.correct")` are calculated with `prop.test(correct = c(TRUE,FALSE))`. The default method, `"wilson"`, includes the Yates continuity correction. Methods `c("exact","asymptotic")` are calculated with `Hmisc::binconf(method=)`. Confidence intervals for means are calculated using `t.test()` and `wilcox.test()` for pseudo-medians.

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_summary tools: `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit(`
`modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Examples

```
# Example 1 ----------------------------------
add_ci_ex1 <-
  trial %>%
  select(marker, response, trt) %>%
  tbl_summary(missing = "no",
              statistic = all_continuous() ~ "{mean} ({sd})") %>%
  add_ci()

# Example 2 ----------------------------------
add_ci_ex2 <-
  trial %>%
    select(response, grade) %>%
    tbl_summary(statistic = all_categorical() ~ "{p}%",
                missing = "no") %>%
    add_ci(pattern = "{stat} ({ci})") %>%
    modify_footnote(everything() ~ NA)
```

`add_difference` *Add difference between groups*

Description

Add the difference between two groups (typically mean difference), along with the difference confidence interval and p-value.

Usage

```
add_difference(
  x,
  test = NULL,
  group = NULL,
  adj.vars = NULL,
  test.args = NULL,
  conf.level = 0.95,
  include = everything(),
  pvalue_fun = NULL,
  estimate_fun = NULL
)
```

Arguments

`x`	`"tbl_summary"` or `"tbl_svysummary"` object
`test`	List of formulas specifying statistical tests to perform for each variable, e.g. `list(all_continuous() ~ "t.test")`. Common tests include `"t.test"` or `"ancova"` for continuous data, and `"prop.test"` for dichotomous variables. See tests for details and more tests.
`group`	Column name (unquoted or quoted) of an ID or grouping variable. The column can be used to calculate p-values with correlated data. Default is `NULL`. See tests for methods that utilize the group= argument.
`adj.vars`	Variables to include in mean difference adjustment (e.g. in ANCOVA models)
`test.args`	List of formulas containing additional arguments to pass to tests that accept arguments. For example, add an argument for all t-tests, use `test.args = all_tests("t.test") ~ list(var.equal = TRUE)`
`conf.level`	Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval.
`include`	Variables to include in output. Input may be a vector of quoted variable names, unquoted variable names, or tidyselect select helper functions. Default is `everything()`.
`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x, digits = 2)` or equivalently, `purrr::partial(style_pvalue, digits = 2)`).
`estimate_fun`	List of formulas specifying the formatting functions to round and format differences. Default is `list(all_continuous() ~ style_sigfig, all_categorical() ~ function(x) paste0(style_sigfig(x * 100), "%"))` Function to round and format difference. Default is `style_sigfig()`

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Examples

```
# Example 1 ----------------------------------
add_difference_ex1 <-
  trial %>%
  select(trt, age, marker, response, death) %>%
  tbl_summary(
    by = trt,
    statistic =
      list(
        all_continuous() ~ "{mean} ({sd})",
        all_dichotomous() ~ "{p}%"
      ),
    missing = "no"
  ) %>%
  add_n() %>%
  add_difference()

# Example 2 ----------------------------------
# ANCOVA adjusted for grade and stage
add_difference_ex2 <-
  trial %>%
  select(trt, age, marker, grade, stage) %>%
  tbl_summary(
    by = trt,
    statistic = list(all_continuous() ~ "{mean} ({sd})"),
    missing = "no",
    include = c(age, marker, trt)
  ) %>%
  add_n() %>%
  add_difference(adj.vars = c(grade, stage))
```

`add_glance` *Add Model Statistics*

Description

Add model statistics returned from `broom::glance()`. Statistics can either be appended to the table (`add_glance_table()`), or added as a table source note (`add_glance_source_note()`).

Usage

```
add_glance_table(
  x,
  include = everything(),
  label = NULL,
  fmt_fun = NULL,
  glance_fun = broom::glance
)

add_glance_source_note(
  x,
  include = everything(),
```

```
  label = NULL,
  fmt_fun = NULL,
  glance_fun = broom::glance,
  text_interpret = c("md", "html"),
  sep1 = " = ",
  sep2 = "; "
)
```

Arguments

`x`	'tbl_regression' object
`include`	list of statistics to include in output. Must be column names of the tibble returned by `broom::glance()`. The include argument can also be used to specify the order the statistics appear in the table.
`label`	List of formulas specifying statistic labels, e.g. `list(r.squared ~ "R2",p.value ~ "P")`
`fmt_fun`	List of formulas where the LHS is a statistic and the RHS is a function to format/round the statistics. The default is to round the number of observations and degrees of freedom to the nearest integer, p-values are styled with `style_pvalue()` and the remaining statistics are styled with `style_sigfig(x,digits = 3)`
`glance_fun`	function that returns model statistics. Default is `broom::glance()`. Custom functions must return a single row tibble.
`text_interpret`	String indicates whether source note text will be interpreted with `gt::md()` or `gt::html()`. Must be `"md"` (default) or `"html"`.
`sep1`	Separator between statistic name and statistic. Default is `" = "`, e.g. `"R2 = 0.456"`
`sep2`	Separator between statistics. Default is `"; "`

Value

gtsummary table

Default Labels

The following statistics have set default labels when printed. When there is no default, the column name from `broom::glance()` is printed.

Statistic Name	Default Label
r.squared	R^2
adj.r.squared	Adjusted R^2
p.value	p-value
logLik	Log-likelihood
statistic	Statistic
df.residual	Residual df
null.deviance	Null deviance
df.null	Null df
nevent	N events
concordance	c-index
std.error.concordance	c-index SE
nobs	No. Obs.

deviance	Deviance
sigma	Sigma

Tips

When combining `add_glance_table()` with `tbl_merge()`, the ordering of the model terms and the glance statistics may become jumbled. To re-order the rows with glance statistics on bottom, use the script below:

```
tbl_merge(list(tbl1, tbl2)) %>%
  modify_table_body(~.x %>% arrange(row_type == "glance_statistic"))
```

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Examples

```
mod <- lm(age ~ marker + grade, trial) %>% tbl_regression()

# Example 1 ----------------------------------
add_glance_ex1 <-
  mod %>%
  add_glance_table(
    label = list(sigma ~ "\U03C3"),
    include = c(r.squared, AIC, sigma)
  )

# Example 2 ----------------------------------
add_glance_ex2 <-
  mod %>%
  add_glance_source_note(
    label = list(sigma ~ "\U03C3"),
    include = c(r.squared, AIC, sigma)
  )
```

`add_global_p` *Add the global p-values*

Description

This function uses `car::Anova(type = "III")` to calculate global p-values variables. Output from `tbl_regression` and `tbl_uvregression` objects supported.

Usage

```
add_global_p(x, ...)

## S3 method for class 'tbl_regression'
add_global_p(
  x,
  include = everything(),
  type = NULL,
  keep = FALSE,
  quiet = NULL,
  ...,
  terms = NULL
)

## S3 method for class 'tbl_uvregression'
add_global_p(
  x,
  type = NULL,
  include = everything(),
  keep = FALSE,
  quiet = NULL,
  ...
)
```

Arguments

`x`	Object with class `tbl_regression` from the tbl_regression function
`...`	Additional arguments to be passed to `car::Anova`
`include`	Variables to calculate global p-value for. Input may be a vector of quoted or unquoted variable names. Default is `everything()`
`type`	Type argument passed to `car::Anova`. Default is `"III"`
`keep`	Logical argument indicating whether to also retain the individual p-values in the table output for each level of the categorical variable. Default is `FALSE`
`quiet`	Logical indicating whether to print messages in console. Default is `FALSE`
`terms`	DEPRECATED. Use include= argument instead.

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_uvregression tools: `add_q()`, `bold_italicize_labels_levels`, `inline_text.tbl_uvregression()`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_uvregression()`

Other tbl_regression tools: `add_q()`, `bold_italicize_labels_levels`, `combine_terms()`, `inline_text.tbl_regres`
`modify`, `tbl_merge()`, `tbl_regression()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Examples

```
# Example 1 ----------------------------------
tbl_lm_global_ex1 <-
  lm(marker ~ age + grade, trial) %>%
  tbl_regression() %>%
  add_global_p()

# Example 2 ----------------------------------
tbl_uv_global_ex2 <-
  trial[c("response", "trt", "age", "grade")] %>%
  tbl_uvregression(
    method = glm,
    y = response,
    method.args = list(family = binomial),
    exponentiate = TRUE
  ) %>%
  add_global_p()
```

`add_n.tbl_summary` *Add column with N*

Description

For each variable in a `tbl_summary` table, the `add_n` function adds a column with the total number of non-missing (or missing) observations

Usage

```
## S3 method for class 'tbl_summary'
add_n(
  x,
  statistic = "{n}",
  col_label = "**N**",
  footnote = FALSE,
  last = FALSE,
  missing = NULL,
  ...
)

## S3 method for class 'tbl_svysummary'
add_n(
  x,
  statistic = "{n}",
  col_label = "**N**",
  footnote = FALSE,
  last = FALSE,
  missing = NULL,
  ...
)
```

Arguments

`x`	Object with class `tbl_summary` from the tbl_summary function or with class `tbl_svysummary` from the tbl_svysummary function
`statistic`	String indicating the statistic to report. Default is the number of non-missing observation for each variable, `statistic = "{n}"`. Other statistics available to report include: • `"{N}"` total number of observations, • `"{n}"` number of non-missing observations, • `"{n_miss}"` number of missing observations, • `"{p}"` percent non-missing data, • `"{p_miss}"` percent missing data The argument uses glue::glue syntax and multiple statistics may be reported, e.g. `statistic = "{n} / {N} ({p}%)"`
`col_label`	String indicating the column label. Default is `"**N**"`
`footnote`	Logical argument indicating whether to print a footnote clarifying the statistics presented. Default is `FALSE`
`last`	Logical indicator to include N column last in table. Default is `FALSE`, which will display N column first.
`missing`	DEPRECATED. Logical argument indicating whether to print N (`missing = FALSE`), or N missing (`missing = TRUE`). Default is `FALSE`
`...`	Not used

Value

A `tbl_summary` or `tbl_svysummary` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_summary tools: `add_ci()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Other tbl_svysummary tools: `add_overall()`, `add_p.tbl_svysummary()`, `add_q()`, `add_stat_label()`, `modify`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_svysummary()`

Examples

```
# Example 1 ----------------------------------
tbl_n_ex <-
  trial[c("trt", "age", "grade", "response")] %>%
  tbl_summary(by = trt) %>%
  add_n()
```

`add_n.tbl_survfit` *Add column with number of observations*

Description

[Maturing] For each `survfit()` object summarized with `tbl_survfit()` this function will add the total number of observations in a new column.

Usage

```
## S3 method for class 'tbl_survfit'
add_n(x, ...)
```

Arguments

`x`	object of class `"tbl_survfit"`
`...`	Not used

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_survfit tools: `add_nevent.tbl_survfit()`, `add_p.tbl_survfit()`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_survfit()`

Examples

```
library(survival)
fit1 <- survfit(Surv(ttdeath, death) ~ 1, trial)
fit2 <- survfit(Surv(ttdeath, death) ~ trt, trial)

# Example 1 ----------------------------------
add_n.tbl_survfit_ex1 <-
  list(fit1, fit2) %>%
  tbl_survfit(times = c(12, 24)) %>%
  add_n()
```

`add_nevent.tbl_survfit` *Add column with number of observed events*

Description

[Maturing] For each `survfit()` object summarized with `tbl_survfit()` this function will add the total number of events observed in a new column.

Usage

```
## S3 method for class 'tbl_survfit'
add_nevent(x, ...)
```

Arguments

`x`	object of class 'tbl_survfit'
`...`	Not used

Example Output

See Also

Other tbl_survfit tools: `add_n.tbl_survfit()`, `add_p.tbl_survfit()`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_survfit()`

Examples

```
library(survival)
fit1 <- survfit(Surv(ttdeath, death) ~ 1, trial)
fit2 <- survfit(Surv(ttdeath, death) ~ trt, trial)

# Example 1 ----------------------------------
add_nevent.tbl_survfit_ex1 <-
  list(fit1, fit2) %>%
  tbl_survfit(times = c(12, 24)) %>%
  add_n() %>%
  add_nevent()
```

`add_nevent_regression` *Add event N to regression table*

Description

Add event N to regression table

Usage

```
## S3 method for class 'tbl_regression'
add_nevent(x, location = NULL, ...)

## S3 method for class 'tbl_uvregression'
add_nevent(x, location = NULL, ...)
```

Arguments

`x`	a `tbl_regression` or `tbl_uvregression` table
`location`	location to place Ns. When `"label"` total Ns are placed on each variable's label row. When `"level"` level counts are placed on the variable level for categorical variables, and total N on the variable's label row for continuous.
`...`	Not used

Example Output

Examples

```
# Example 1 ----------------------------------
add_nevent.tbl_regression_ex1 <-
  trial %>%
  select(response, trt, grade) %>%
  tbl_uvregression(
    y = response,
    method = glm,
    method.args = list(family = binomial),
  ) %>%
  add_nevent()
# Example 2 ----------------------------------
add_nevent.tbl_regression_ex2 <-
  glm(response ~ age + grade, trial, family = binomial) %>%
  tbl_regression(exponentiate = TRUE) %>%
  add_nevent(location = "level")
```

`add_n_regression` *Add N to regression table*

Description

Add N to regression table

Usage

```
## S3 method for class 'tbl_regression'
add_n(x, location = NULL, ...)

## S3 method for class 'tbl_uvregression'
add_n(x, location = NULL, ...)
```

Arguments

`x`	a `tbl_regression` or `tbl_uvregression` table
`location`	location to place Ns. When `"label"` total Ns are placed on each variable's label row. When `"level"` level counts are placed on the variable level for categorical variables, and total N on the variable's label row for continuous.
`...`	Not used

Example Output

Examples

```
# Example 1 ----------------------------------
add_n.tbl_regression_ex1 <-
  trial %>%
  select(response, age, grade) %>%
  tbl_uvregression(
    y = response,
    method = glm,
    method.args = list(family = binomial),
    hide_n = TRUE
  ) %>%
  add_n(location = "label")

# Example 2 ----------------------------------
add_n.tbl_regression_ex2 <-
  glm(response ~ age + grade, trial, family = binomial) %>%
  tbl_regression(exponentiate = TRUE) %>%
  add_n(location = "level")
```

`add_overall` *Add column with overall summary statistics*

Description

Adds a column with overall summary statistics to tables created by `tbl_summary`, `tbl_svysummary`, `tbl_continuous` or `tbl_custom_summary`.

Usage

```
add_overall(x, ...)

## S3 method for class 'tbl_summary'
add_overall(
  x,
  last = FALSE,
  col_label = NULL,
  statistic = NULL,
  digits = NULL,
  ...
)

## S3 method for class 'tbl_svysummary'
add_overall(
  x,
  last = FALSE,
  col_label = NULL,
  statistic = NULL,
  digits = NULL,
  ...
)
```

```
## S3 method for class 'tbl_continuous'
add_overall(
  x,
  last = FALSE,
  col_label = NULL,
  statistic = NULL,
  digits = NULL,
  ...
)

## S3 method for class 'tbl_custom_summary'
add_overall(
  x,
  last = FALSE,
  col_label = NULL,
  statistic = NULL,
  digits = NULL,
  ...
)
```

Arguments

`x`	Object with class `tbl_summary` from the tbl_summary function, object with class `tbl_svysummary` from the tbl_svysummary function, object with class `tbl_continuous` from the tbl_continuous function or object with class `tbl_custom_summary` from the tbl_custom_summary function.
`...`	Not used
`last`	Logical indicator to display overall column last in table. Default is `FALSE`, which will display overall column first.
`col_label`	String indicating the column label. Default is `"**Overall**,N = {N}"`
`statistic`	Override the statistic argument in initial tbl_* function. call. Default is `NULL`.
`digits`	Override the digits argument in initial tbl_* function call. Default is `NULL`.

Value

A tbl_* of same class as `x`

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit(`
`modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Other tbl_svysummary tools: `add_n.tbl_summary()`, `add_p.tbl_svysummary()`, `add_q()`, `add_stat_label()`, `modify`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_svysummary()`

Other tbl_continuous tools: `add_p.tbl_continuous()`, `tbl_continuous()`

Other tbl_custom_summary tools: `continuous_summary()`, `proportion_summary()`, `ratio_summary()`, `tbl_custom_summary()`

Examples

```
# Example 1 ----------------------------------
tbl_overall_ex1 <-
  trial %>%
  tbl_summary(include = c(age, grade), by = trt) %>%
  add_overall()

# Example 2 ----------------------------------
tbl_overall_ex2 <-
  trial %>%
  tbl_summary(
    include = grade,
    by = trt,
    percent = "row",
    statistic = ~ "{p}%",
    digits = ~ 1
  ) %>%
  add_overall(
    last = TRUE,
    statistic = ~ "{p}% (n={n})",
    digits = ~ c(1, 0)
  )

# Example 3 ----------------------------------
tbl_overall_ex3 <-
  trial %>%
  tbl_continuous(
    variable = age,
    by = trt,
    include = grade
  ) %>%
  add_overall(last = TRUE)
```

`add_p.tbl_continuous` *P-values for* `tbl_continuous`

Description

P-values for `tbl_continuous`

Usage

```
## S3 method for class 'tbl_continuous'
add_p(
```

```
    x,
    test = NULL,
    pvalue_fun = NULL,
    include = everything(),
    test.args = NULL,
    group = NULL,
    ...
  )
```

Arguments

`x`	Object with class `tbl_summary` from the tbl_summary function
`test`	List of formulas specifying statistical tests to perform for each variable. Default is two-way ANOVA when by= is not `NULL`, and has the same defaults as `add_p.tbl_continuous()` when `by = NULL`. See tests for details, more tests, and instruction for implementing a custom test.
`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x, digits = 2)` or equivalently, `purrr::partial(style_pvalue, digits = 2)`).
`include`	Variables to include in output. Input may be a vector of quoted variable names, unquoted variable names, or tidyselect select helper functions. Default is `everything()`.
`test.args`	List of formulas containing additional arguments to pass to tests that accept arguments. For example, add an argument for all t-tests, use `test.args = all_tests("t.test") ~ list(var.equal = TRUE)`
`group`	Column name (unquoted or quoted) of an ID or grouping variable. The column can be used to calculate p-values with correlated data. Default is `NULL`. See tests for methods that utilize the group= argument.
`...`	Not used

See Also

Other tbl_continuous tools: `add_overall()`, `tbl_continuous()`

Examples

```
add_p_continuous_ex1 <-
  tbl_continuous(
    data = trial,
    variable = age,
    by = trt,
    include = grade
  ) %>%
  add_p()
```

`add_p.tbl_cross` *Adds p-value to crosstab table*

Description

Calculate and add a p-value comparing the two variables in the cross table. Missing values are included in p-value calculations.

Usage

```
## S3 method for class 'tbl_cross'
add_p(
  x,
  test = NULL,
  pvalue_fun = NULL,
  source_note = NULL,
  test.args = NULL,
  ...
)
```

Arguments

`x`	Object with class `tbl_cross` from the tbl_cross function
`test`	A string specifying statistical test to perform. Default is "`chisq.test`" when expected cell counts >=5 and "`fisher.test`" when expected cell counts <5.
`pvalue_fun`	Function to round and format p-value. Default is style_pvalue, except when `source_note = TRUE` when the default is `style_pvalue(x,prepend_p = TRUE)`
`source_note`	Logical value indicating whether to show p-value in the {gt} table source notes rather than a column.
`test.args`	Named list containing additional arguments to pass to the test (if it accepts additional arguments). For example, add an argument for a chi-squared test with `test.args = list(correct = TRUE)`
`...`	Not used

Example Output

Author(s)

Karissa Whiting

See Also

Other tbl_cross tools: `inline_text.tbl_cross()`, `tbl_cross()`

Examples

```
# Example 1 ----------------------------------
add_p_cross_ex1 <-
  trial %>%
  tbl_cross(row = stage, col = trt) %>%
  add_p()

# Example 2 ----------------------------------
add_p_cross_ex2 <-
  trial %>%
  tbl_cross(row = stage, col = trt) %>%
  add_p(source_note = TRUE)
```

`add_p.tbl_summary` *Adds p-values to summary tables*

Description

Adds p-values to tables created by `tbl_summary` by comparing values across groups.

Usage

```
## S3 method for class 'tbl_summary'
add_p(
  x,
  test = NULL,
  pvalue_fun = NULL,
  group = NULL,
  include = everything(),
  test.args = NULL,
  exclude = NULL,
  ...
)
```

Arguments

`x`	Object with class `tbl_summary` from the tbl_summary function
`test`	List of formulas specifying statistical tests to perform for each variable, e.g. `list(all_continuous() ~ "t.test",all_categorical() ~ "fisher.test")`. Common tests include `"t.test"`, `"aov"`, `"wilcox.test"`, `"kruskal.test"`, `"chisq.test"`, `"fisher.test"`, and `"lme4"` (for clustered data). See tests for details, more tests, and instruction for implementing a custom test. Tests default to `"kruskal.test"` for continuous variables (`"wilcox.test"` when "by" variable has two levels), `"chisq.test.no.correct"` for categorical variables with all expected cell counts >=5, and `"fisher.test"` for categorical variables with any expected cell count <5.
`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x,digits = 2)` or equivalently, `purrr::partial(style_pvalue,digits = 2)`).

`group`	Column name (unquoted or quoted) of an ID or grouping variable. The column can be used to calculate p-values with correlated data. Default is `NULL`. See tests for methods that utilize the group= argument.
`include`	Variables to include in output. Input may be a vector of quoted variable names, unquoted variable names, or tidyselect select helper functions. Default is `everything()`.
`test.args`	List of formulas containing additional arguments to pass to tests that accept arguments. For example, add an argument for all t-tests, use `test.args = all_tests("t.test") ~ list(var.equal = TRUE)`
`exclude`	DEPRECATED.
`...`	Not used

Value

A `tbl_summary` object

Example Output

Author(s)

Daniel D. Sjoberg, Emily C. Zabor

See Also

See tbl_summary vignette for detailed examples

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Examples

```
# Example 1 ----------------------------------
add_p_ex1 <-
  trial[c("age", "grade", "trt")] %>%
  tbl_summary(by = trt) %>%
  add_p()

# Example 2 ----------------------------------
add_p_ex2 <-
  trial %>%
  select(trt, age, marker) %>%
  tbl_summary(by = trt, missing = "no") %>%
  add_p(
    # perform t-test for all variables
    test = everything() ~ "t.test",
    # assume equal variance in the t-test
    test.args = all_tests("t.test") ~ list(var.equal = TRUE)
  )
```

`add_p.tbl_survfit` *Adds p-value to survfit table*

Description

[Maturing] Calculate and add a p-value

Usage

```
## S3 method for class 'tbl_survfit'
add_p(
  x,
  test = "logrank",
  test.args = NULL,
  pvalue_fun = style_pvalue,
  include = everything(),
  quiet = NULL,
  ...
)
```

Arguments

`x`	Object of class `"tbl_survfit"`
`test`	string indicating test to use. Must be one of `"logrank"`, `"survdiff"`, `"petopeto_gehanwilcoxon"`, `"coxph_lrt"`, `"coxph_wald"`, "coxph_score". See details below
`test.args`	List of formulas containing additional arguments to pass to tests that accept arguments. For example, add an argument for all t-tests, use `test.args = all_tests("t.test") ~ list(var.equal = TRUE)`
`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x,digits = 2)` or equivalently, `purrr::partial(style_pvalue,digits = 2)`).
`include`	Variables to include in output. Input may be a vector of quoted variable names, unquoted variable names, or tidyselect select helper functions. Default is `everything()`.
`quiet`	Logical indicating whether to print messages in console. Default is `FALSE`
`...`	Not used

test argument

The most common way to specify test= is by using a single string indicating the test name. However, if you need to specify different tests within the same table, the input in flexible using the list notation common throughout the gtsummary package. For example, the following code would call the log-rank test, and a second test of the *G-rho* family.

```
... %>%
  add_p(test = list(trt ~ "logrank", grade ~ "survdiff"),
        test.args = grade ~ list(rho = 0.5))
```

Example Output

See Also

Other tbl_survfit tools: `add_n.tbl_survfit()`, `add_nevent.tbl_survfit()`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_survfit()`

Examples

```
library(survival)

gts_survfit <-
  list(
    survfit(Surv(ttdeath, death) ~ grade, trial),
    survfit(Surv(ttdeath, death) ~ trt, trial)
  ) %>%
  tbl_survfit(times = c(12, 24))

# Example 1 ----------------------------------
add_p_tbl_survfit_ex1 <-
  gts_survfit %>%
  add_p()

# Example 2 ----------------------------------
# Pass `rho=` argument to `survdiff()`
add_p_tbl_survfit_ex2 <-
  gts_survfit %>%
  add_p(test = "survdiff", test.args = list(rho = 0.5))
```

`add_p.tbl_svysummary` *Adds p-values to svysummary tables*

Description

Adds p-values to tables created by `tbl_svysummary` by comparing values across groups.

Usage

```
## S3 method for class 'tbl_svysummary'
add_p(
  x,
  test = NULL,
  pvalue_fun = NULL,
  include = everything(),
  test.args = NULL,
  ...
)
```

Arguments

`x`	Object with class `tbl_svysummary` from the tbl_svysummary function
`test`	List of formulas specifying statistical tests to perform, e.g. `list(all_continuous() ~ "svy.t.test",all_categorical() ~ "svy.wald.test")`. Options include • `"svy.t.test"` for a t-test adapted to complex survey samples (cf. `survey::svyttest`), • `"svy.wilcox.test"` for a Wilcoxon rank-sum test for complex survey samples (cf. `survey::svyranktest`), • `"svy.kruskal.test"` for a Kruskal-Wallis rank-sum test for complex survey samples (cf. `survey::svyranktest`), • `"svy.vanderwaerden.test"` for a van der Waerden's normal-scores test for complex survey samples (cf. `survey::svyranktest`), • `"svy.median.test"` for a Mood's test for the median for complex survey samples (cf. `survey::svyranktest`), • `"svy.chisq.test"` for a Chi-squared test with Rao & Scott's second-order correction (cf. `survey::svychisq`), • `"svy.adj.chisq.test"` for a Chi-squared test adjusted by a design effect estimate (cf. `survey::svychisq`), • `"svy.wald.test"` for a Wald test of independence for complex survey samples (cf. `survey::svychisq`), • `"svy.adj.wald.test"` for an adjusted Wald test of independence for complex survey samples (cf. `survey::svychisq`), • `"svy.lincom.test"` for a test of independence using the exact asymptotic distribution for complex survey samples (cf. `survey::svychisq`), • `"svy.saddlepoint.test"` for a test of independence using a saddlepoint approximation for complex survey samples (cf. `survey::svychisq`), Tests default to `"svy.wilcox.test"` for continuous variables and `"svy.chisq.test"` for categorical variables.
`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x,digits = 2)` or equivalently, `purrr::partial(style_pvalue,digits = 2)`).
`include`	Variables to include in output. Input may be a vector of quoted variable names, unquoted variable names, or tidyselect select helper functions. Default is `everything()`.
`test.args`	List of formulas containing additional arguments to pass to tests that accept arguments. For example, add an argument for all t-tests, use `test.args = all_tests("t.test") ~ list(var.equal = TRUE)`
`...`	Not used

Value

A `tbl_svysummary` object

Example Output

Author(s)

Joseph Larmarange

See Also

Other tbl_svysummary tools: `add_n.tbl_summary()`, `add_overall()`, `add_q()`, `add_stat_label()`, `modify`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_svysummary()`

Examples

```
# Example 1 ----------------------------------
# A simple weighted dataset
add_p_svysummary_ex1 <-
  survey::svydesign(~1, data = as.data.frame(Titanic), weights = ~Freq) %>%
  tbl_svysummary(by = Survived) %>%
  add_p()

# A dataset with a complex design
data(api, package = "survey")
d_clust <- survey::svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc)

# Example 2 ----------------------------------
add_p_svysummary_ex2 <-
  tbl_svysummary(d_clust, by = both, include = c(cname, api00, api99, both)) %>%
  add_p()

# Example 3 ----------------------------------
# change tests to svy t-test and Wald test
add_p_svysummary_ex3 <-
  tbl_svysummary(d_clust, by = both, include = c(cname, api00, api99, both)) %>%
  add_p(
    test = list(
      all_continuous() ~ "svy.t.test",
      all_categorical() ~ "svy.wald.test"
    )
  )
```

`add_q` *Add a column of q-values to account for multiple comparisons*

Description

Adjustments to p-values are performed with stats::p.adjust.

Usage

```
add_q(x, method = "fdr", pvalue_fun = NULL, quiet = NULL)
```

Arguments

`x`	a `gtsummary` object
`method`	String indicating method to be used for p-value adjustment. Methods from stats::p.adjust are accepted. Default is `method = "fdr"`.

`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x, digits = 2)` or equivalently, `purrr::partial(style_pvalue, digits = 2)`).
`quiet`	Logical indicating whether to print messages in console. Default is `FALSE`

Example Output

Author(s)

Esther Drill, Daniel D. Sjoberg

See Also

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit(`
`modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Other tbl_svysummary tools: `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_svysummary()`, `add_stat_label()`, `modify`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_svysummary()`

Other tbl_regression tools: `add_global_p()`, `bold_italicize_labels_levels`, `combine_terms()`, `inline_text.tbl_regression()`, `modify`, `tbl_merge()`, `tbl_regression()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Other tbl_uvregression tools: `add_global_p()`, `bold_italicize_labels_levels`, `inline_text.tbl_uvregression`
`modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_uvregression()`

Examples

```
# Example 1 ----------------------------------
add_q_ex1 <-
  trial[c("trt", "age", "grade", "response")] %>%
  tbl_summary(by = trt) %>%
  add_p() %>%
  add_q()

# Example 2 ----------------------------------
add_q_ex2 <-
  trial[c("trt", "age", "grade", "response")] %>%
  tbl_uvregression(
    y = response,
    method = glm,
    method.args = list(family = binomial),
    exponentiate = TRUE
  ) %>%
  add_global_p() %>%
  add_q()
```

`add_significance_stars`

Add significance stars

Description

[Experimental] Add significance stars to estimates with small p-values

Usage

```
add_significance_stars(
  x,
  pattern = "{estimate}{stars}",
  thresholds = c(0.001, 0.01, 0.05),
  hide_ci = TRUE,
  hide_p = TRUE,
  hide_se = FALSE
)
```

Arguments

`x`	a `'tbl_regression'` or `'tbl_uvregression'` object
`pattern`	glue-syntax string indicating what to display in formatted column. Default is `"{estimate}{stars}"`. Other common patterns are `"{estimate}{stars} ({conf.low},{conf.high})"` and `"{estimate} ({conf.low} to {conf.high}){stars}"`
`thresholds`	thresholds for significance stars. Default is `c(0.001,0.01,0.05)`
`hide_ci`	logical whether to hide confidence interval. Default is `TRUE`
`hide_p`	logical whether to hide p-value. Default is `TRUE`
`hide_se`	logical whether to hide standard error. Default is `FALSE`

Future Updates

There are planned updates to the implementation of this function with respect to the pattern= argument. Currently, this function replaces the numeric estimate column, with a formatted character column following pattern=. Once `gt::cols_merge()` gains the rows= argument the implementation will be updated to use it, which will keep numeric columns numeric. For the *vast majority* of users, *the planned change will be go unnoticed.*

Example Output

Examples

```
tbl <-
  lm(time ~ ph.ecog + sex, survival::lung) %>%
  tbl_regression(label = list(ph.ecog = "ECOG Score", sex = "Sex"))

# Example 1 ----------------------------------
add_significance_stars_ex1 <-
```

```
  tbl %>%
  add_significance_stars(hide_ci = FALSE, hide_p = FALSE)

# Example 2 ----------------------------------
add_significance_stars_ex2 <-
  tbl %>%
  add_significance_stars(
    pattern = "{estimate} ({conf.low}, {conf.high}){stars}",
    hide_ci = TRUE, hide_se = TRUE
  ) %>%
  modify_header(estimate ~ "**Beta (95% CI)**") %>%
  modify_footnote(estimate ~ "CI = Confidence Interval", abbreviation = TRUE)

# Example 3 ----------------------------------
# Use <br> to put a line break between beta and SE in HTML output
add_significance_stars_ex3 <-
  tbl %>%
  add_significance_stars(
    hide_se = TRUE,
    pattern = "{estimate}{stars}<br>({std.error})"
  ) %>%
  modify_header(estimate ~ "**Beta (SE)**") %>%
  modify_footnote(estimate ~ "SE = Standard Error", abbreviation = TRUE) %>%
  as_gt() %>%
  gt::tab_style(
    style = "vertical-align:top",
    locations = gt::cells_body(columns = vars(label))
  )
```

`add_stat` *Add a custom statistic column*

Description

[Maturing] The function allows a user to add a new column (or columns) of statistics to an existing `tbl_summary`, `tbl_svysummary`, or `tbl_continuous` object.

Usage

```
add_stat(x, fns, location = NULL, ...)
```

Arguments

`x`	`tbl_summary`, `tbl_svysummary`, or `tbl_continuous` object
`fns`	list of formulas indicating the functions that create the statistic. See details below.
`location`	list of formulas indicating the location the new statistics are placed. The RHS of the formula must be one of `c("label","level","missing")`. When `"label"`, a single statistic is placed on the variable label row. When `"level"` the statistics are placed on the variable level rows. The length of the vector of statistics returned from the `fns` function must match the dimension of levels. Default is to place the new statistics on the label row.
`...`	DEPRECATED

Details

The returns from custom functions passed in fns= are required to follow a specified format. Each of these function will execute on a single variable.

1. Each function must return a tibble or a vector. If a vector is returned, it will be converted to a tibble with one column and number of rows equal to the length of the vector.
2. When `location = "label"`, the returned statistic from the custom function must be a tibble with one row. When `location = "level"` the tibble must have the same number of rows as there are levels in the variable (excluding the row for unknown values).
3. Each function may take the following arguments: `foo(data,variable,by,tbl,...)`
    - data= is the input data frame passed to `tbl_summary()`
    - variable= is a string indicating the variable to perform the calculation on. This is the variable in the label column of the table.
    - by= is a string indicating the by variable from tbl_summary=, if present
    - tbl= the original `tbl_summary()/tbl_svysummary()` object is also available to utilize

The user-defined does not need to utilize each of these inputs. It's encouraged the user-defined function accept `...` as each of the arguments *will* be passed to the function, even if not all inputs are utilized by the user's function, e.g. `foo(data,variable,by,...)`

- Use `modify_header()` to update the column headers
- Use `modify_fmt_fun()` to update the functions that format the statistics
- Use `modify_footnote()` to add a explanatory footnote

If you return a tibble with column names `p.value` or `q.value`, default p-value formatting will be applied, and you may take advantage of subsequent p-value formatting functions, such as `bold_p()` or `add_q()`.

To access the continuous variable in a `tbl_continuous()` table, use `tbl$inputs$variable`.

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Examples

```
library(dplyr, warn.conflicts = FALSE)
library(stringr)
# Example 1 ----------------------------------
# fn returns t-test pvalue
my_ttest <- function(data, variable, by, ...) {
  t.test(data[[variable]] ~ as.factor(data[[by]]))$p.value
}

add_stat_ex1 <-
  trial %>%
  select(trt, age, marker) %>%
  tbl_summary(by = trt, missing = "no") %>%
  add_stat(fns = everything() ~ my_ttest) %>%
  modify_header(
```

```
    list(
      add_stat_1 ~ "**p-value**",
      all_stat_cols() ~ "**{level}**"
    )
  )

# Example 2 ----------------------------------
# fn returns t-test test statistic and pvalue
my_ttest2 <- function(data, variable, by, ...) {
  t.test(data[[variable]] ~ as.factor(data[[by]])) %>%
    broom::tidy() %>%
    mutate(
    stat = str_glue("t={style_sigfig(statistic)}, {style_pvalue(p.value, prepend_p = TRUE)}")
    ) %>%
    pull(stat)
}

add_stat_ex2 <-
  trial %>%
  select(trt, age, marker) %>%
  tbl_summary(by = trt, missing = "no") %>%
  add_stat(fns = everything() ~ my_ttest2) %>%
  modify_header(add_stat_1 ~ "**Treatment Comparison**")

# Example 3 ----------------------------------
# return test statistic and p-value is separate columns
my_ttest3 <- function(data, variable, by, ...) {
  t.test(data[[variable]] ~ as.factor(data[[by]])) %>%
    broom::tidy() %>%
    select(statistic, p.value)
}

add_stat_ex3 <-
  trial %>%
  select(trt, age, marker) %>%
  tbl_summary(by = trt, missing = "no") %>%
  add_stat(fns = everything() ~ my_ttest3) %>%
  modify_header(
    list(
      statistic ~ "**t-statistic**",
      p.value ~ "**p-value**"
    )
  ) %>%
  modify_fmt_fun(
    list(
      statistic ~ style_sigfig,
      p.value ~ style_pvalue
    )
  )
```

`add_stat_label` *Add statistic labels*

Description

Adds labels describing the summary statistics presented for each variable in the tbl_summary / tbl_svysummary table.

Usage

```
add_stat_label(x, location = NULL, label = NULL)
```

Arguments

`x`	Object with class `tbl_summary` from the tbl_summary function or with class `tbl_svysummary` from the tbl_svysummary function
`location`	location where statistic label will be included. `"row"` (the default) to add the statistic label to the variable label row, and `"column"` adds a column with the statistic label.
`label`	a list of formulas or a single formula updating the statistic label, e.g. `label = all_categorical() ~ "No. (%)"`

Value

A `tbl_summary` or `tbl_svysummary` object

Tips

When using `add_stat_label(location='row')` with subsequent `tbl_merge()`, it's important to have somewhat of an understanding of the underlying structure of the gtsummary table. `add_stat_label(location='ro` works by adding a new column called `"stat_label"` to `x$table_body`. The `"label"` and `"stat_label"` columns are merged when the gtsummary table is printed. The `tbl_merge()` function merges on the `"label"` column (among others), which is typically the first column you see in a gtsummary table. Therefore, when you want to merge a table that has run `add_stat_label(location='row')` you need to match the `"label"` column values before the `"stat_column"` is merged with it.

For example, the following two tables merge properly

```
tbl1 <- trial %>% select(age, grade) %>% tbl_summary() %>% add_stat_label()
tbl2 <- lm(marker ~ age + grade, trial) %>% tbl_regression()

tbl_merge(list(tbl1, tbl2))
```

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Other tbl_svysummary tools: `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_svysummary()`, `add_q()`, `modify`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_svysummary()`

Examples

```
tbl <- trial %>%
  dplyr::select(trt, age, grade, response) %>%
  tbl_summary(by = trt)

# Example 1 ----------------------------------
# Add statistic presented to the variable label row
add_stat_label_ex1 <-
  tbl %>%
  add_stat_label(
    # update default statistic label for continuous variables
    label = all_continuous() ~ "med. (iqr)"
  )

# Example 2 ----------------------------------
add_stat_label_ex2 <-
  tbl %>%
  add_stat_label(
    # add a new column with statistic labels
    location = "column"
  )

# Example 3 ----------------------------------
add_stat_label_ex3 <-
  trial %>%
  select(age, grade, trt) %>%
  tbl_summary(
    by = trt,
    type = all_continuous() ~ "continuous2",
    statistic = all_continuous() ~ c("{mean} ({sd})", "{min} - {max}"),
  ) %>%
  add_stat_label(label = age ~ c("Mean (SD)", "Min - Max"))
```

`add_vif` *Add Variance Inflation Factor*

Description

[Maturing] Add the variance inflation factor (VIF) or generalized VIF (GVIF) to the regression table. Function uses `car::vif()` to calculate the VIF.

Usage

```
add_vif(x, statistic = NULL, estimate_fun = NULL)
```

Arguments

`x`	`'tbl_regression'` object
`statistic`	`"VIF"` (variance inflation factors, for models with no categorical terms) or one of/combination of `"GVIF"` (generalized variance inflation factors), `"aGVIF"` 'adjusted GVIF, i.e. GVIF^[1/(2*df)] and/or `"df"` (degrees of freedom). See `car::vif()` for details.
`estimate_fun`	Default is `style_sigfig()`.

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Examples

```
# Example 1 ----------------------------------
add_vif_ex1 <-
  lm(age ~ grade + marker, trial) %>%
  tbl_regression() %>%
  add_vif()

# Example 2 ----------------------------------
add_vif_ex2 <-
  lm(age ~ grade + marker, trial) %>%
  tbl_regression() %>%
  add_vif(c("aGVIF", "df"))
```

`as_flex_table` *Convert gtsummary object to a flextable object*

Description

Function converts a gtsummary object to a flextable object. A user can use this function if they wish to add customized formatting available via the flextable functions. The flextable output is particularly useful when combined with R markdown with Word output, since the gt package does not support Word.

Usage

```
as_flex_table(
  x,
  include = everything(),
  return_calls = FALSE,
  strip_md_bold = TRUE
)
```

Arguments

`x`	Object created by a function from the gtsummary package (e.g. tbl_summary or tbl_regression)
`include`	Commands to include in output. Input may be a vector of quoted or unquoted names. tidyselect and gtsummary select helper functions are also accepted. Default is `everything()`.
`return_calls`	Logical. Default is `FALSE`. If `TRUE`, the calls are returned as a list of expressions.
`strip_md_bold`	When TRUE, all double asterisk (markdown language for bold weight) in column labels and spanning headers are removed.

Value

A flextable object

Details

The `as_flex_table()` functions converts the gtsummary object to a flextable, and prints it with the following styling functions.

1. `flextable::flextable()`
2. `flextable::set_header_labels()` to set column labels
3. `flextable::add_header_row()`, if applicable, to set spanning column header
4. `flextable::align()` to set column alignment
5. `flextable::padding()` to indent variable levels
6. `flextable::fontsize()` to set font size
7. `flextable::autofit()` to estimate the column widths
8. `flextable::footnote()` to add table footnotes and source notes
9. `flextable::bold()` to bold cells in data frame
10. `flextable::italic()` to italicize cells in data frame
11. `flextable::border()` to set all border widths to 1
12. `flextable::padding()` to set consistent header padding
13. `flextable::valign()` to ensure label column is top-left justified

Any one of these commands may be omitted using the include= argument.

Pro tip: Use the `flextable::width()` function for exacting control over column width after calling `as_flex_table()`.

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other gtsummary output types: `as_gt()`, `as_hux_table()`, `as_kable_extra()`, `as_kable()`, `as_tibble.gtsummary()`

Examples

```
as_flex_table_ex1 <-
  trial %>%
  select(trt, age, grade) %>%
  tbl_summary(by = trt) %>%
  add_p() %>%
  as_flex_table()
```

`as_gt` *Convert gtsummary object to a gt object*

Description

Function converts a gtsummary object to a `"gt_tbl"` object, that is, a table created with `gt::gt()`. Function is used in the background when the results are printed or knit. A user can use this function if they wish to add customized formatting available via the gt package.

Review the tbl_summary vignette or tbl_regression vignette for detailed examples in the 'Advanced Customization' section.

Usage

```
as_gt(x, include = everything(), return_calls = FALSE, ..., exclude = NULL)
```

Arguments

`x`	Object created by a function from the gtsummary package (e.g. tbl_summary or tbl_regression)
`include`	Commands to include in output. Input may be a vector of quoted or unquoted names. tidyselect and gtsummary select helper functions are also accepted. Default is `everything()`.
`return_calls`	Logical. Default is `FALSE`. If `TRUE`, the calls are returned as a list of expressions.
`...`	Arguments passed on to gt::gt
`exclude`	DEPRECATED.

Value

A `gt_tbl` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other gtsummary output types: `as_flex_table()`, `as_hux_table()`, `as_kable_extra()`, `as_kable()`, `as_tibble.gtsummary()`

Examples

```
as_gt_ex <-
  trial[c("trt", "age", "response", "grade")] %>%
  tbl_summary(by = trt) %>%
  as_gt()
```

`as_hux_table` *Convert gtsummary object to a huxtable object*

Description

Function converts a gtsummary object to a huxtable object. A user can use this function if they wish to add customized formatting available via the huxtable functions. The huxtable package supports output to PDF via LaTeX, as well as HTML and Word.

Usage

```
as_hux_table(
  x,
  include = everything(),
  return_calls = FALSE,
  strip_md_bold = FALSE
)
```

Arguments

`x`	Object created by a function from the gtsummary package (e.g. tbl_summary or tbl_regression)
`include`	Commands to include in output. Input may be a vector of quoted or unquoted names. tidyselect and gtsummary select helper functions are also accepted. Default is `everything()`.
`return_calls`	Logical. Default is `FALSE`. If `TRUE`, the calls are returned as a list of expressions.
`strip_md_bold`	When TRUE, all double asterisk (markdown language for bold weight) in column labels and spanning headers are removed.

Value

A huxtable object

Details

The `as_hux_table()` takes the data frame that will be printed, converts it to a huxtable and formats the table with the following huxtable functions:

1. `huxtable::huxtable()`
2. `huxtable::insert_row()` to insert header rows
3. `huxtable::set_left_padding()` to indent variable levels
4. `huxtable::add_footnote()` to add table footnotes and source notes
5. `huxtable::set_bold()` to bold cells

6. `huxtable::set_italic()` to italicize cells
7. `huxtable::set_top_border()` add horizontal line (when indicated)
8. `huxtable::set_na_string()` to use an em-dash for missing numbers
9. `huxtable::set_markdown()` use markdown for header rows
10. `huxtable::set_align()` to set column alignment

Any one of these commands may be omitted using the include= argument.

Author(s)

David Hugh-Jones

See Also

Other gtsummary output types: `as_flex_table()`, `as_gt()`, `as_kable_extra()`, `as_kable()`, `as_tibble.gtsummary()`

Examples

```
trial %>%
  dplyr::select(trt, age, grade) %>%
  tbl_summary(by = trt) %>%
  add_p() %>%
  as_hux_table()
```

`as_kable` *Convert gtsummary object to a kable object*

Description

Function converts a gtsummary object to a knitr_kable object. This function may be used in the background when the tables are printed or knitted.

Output from knitr::kable is less full featured compared to summary tables produced with gt. For example, kable summary tables do not include indentation, footnotes, or spanning header rows.

Usage

```
as_kable(
  x,
  include = everything(),
  return_calls = FALSE,
  exclude = NULL,
  fmt_missing = TRUE,
  ...
)
```

Arguments

`x`	Object created by a function from the gtsummary package (e.g. tbl_summary or tbl_regression)
`include`	Commands to include in output. Input may be a vector of quoted or unquoted names. tidyselect and gtsummary select helper functions are also accepted. Default is `everything()`.
`return_calls`	Logical. Default is `FALSE`. If `TRUE`, the calls are returned as a list of expressions.
`exclude`	DEPRECATED
`fmt_missing`	Logical argument adding the missing value formats.
`...`	Additional arguments passed to knitr::kable

Details

Tip: To better distinguish variable labels and level labels when indenting is not supported, try `bold_labels()` or `italicize_levels()`.

Value

A `knitr_kable` object

Author(s)

Daniel D. Sjoberg

See Also

Other gtsummary output types: `as_flex_table()`, `as_gt()`, `as_hux_table()`, `as_kable_extra()`, `as_tibble.gtsummary()`

Examples

```
trial %>%
  tbl_summary(by = trt) %>%
  bold_labels() %>%
  as_kable()
```

`as_kable_extra` *Convert gtsummary object to a kableExtra object*

Description

Function converts a gtsummary object to a knitr_kable + kableExtra object. This allows the customized formatting available via knitr::kable and kableExtra; `as_kable_extra()` supports arguments in `knitr::kable()`. `as_kable_extra()` output via gtsummary supports bold and italic cells for table bodies. Users creating pdf output should specify `as_kable_extra(format = "latex")`.

Usage

```
as_kable_extra(
  x,
  include = everything(),
  return_calls = FALSE,
  strip_md_bold = TRUE,
  fmt_missing = TRUE,
  ...
)
```

Arguments

`x`	Object created by a function from the gtsummary package (e.g. tbl_summary or tbl_regression)
`include`	Commands to include in output. Input may be a vector of quoted or unquoted names. tidyselect and gtsummary select helper functions are also accepted. Default is `everything()`.
`return_calls`	Logical. Default is `FALSE`. If `TRUE`, the calls are returned as a list of expressions.
`strip_md_bold`	When TRUE, all double asterisk (markdown language for bold weight) in column labels and spanning headers are removed.
`fmt_missing`	Logical argument adding the missing value formats.
`...`	Additional arguments passed to knitr::kable

Value

A kableExtra object

PDF via LaTeX Tips

This section discusses options intended for use with

- `output: pdf_document` in yaml of `.Rmd`.
- `as_kable_extra(format = "latex")`

Custom column names:

In pdf output, column names do not currently inherit formatting applied in gtsummary tables. However, custom column names can be achieved with the `col.names` argument as shown in Example 2, including attributes such as bold formatting, italic formatting, and line breaks. Doing so requires the `escape = FALSE` argument; however, when using `escape = FALSE` special latex characters like \ and % will need to be escaped prior to entering `as_kable_extra()`. Using `escape = FALSE` when the gtsummary table has special LaTeX characters will result in the error `"LaTeX failed to compile..."`

Additional table styling:

Additional styling is available through `knitr::kable()` and `kableExtra::kable_styling()` as shown in Example 3, which implements row striping and repeated column headers in the presence of page breaks.

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other gtsummary output types: `as_flex_table()`, `as_gt()`, `as_hux_table()`, `as_kable()`, `as_tibble.gtsummary()`

Examples

```
# Example 1 (general) -------------------------------------------------------
as_kable_extra_ex1_gen <-
  trial %>%
  select(trt, age, stage) %>%
  tbl_summary(by = trt) %>%
  bold_labels() %>%
  as_kable_extra()

# Example 2 (PDF via LaTeX) -------------------------------------------------
custom_names <- c(
   "\\textbf{Characteristic}",
   "\\textbf{Drug A}\n\\textit{N = 98}",
   "\\textbf{Drug B}\n\\textit{N = 102}"
)
as_kable_extra_ex2_pdf <-
  trial %>%
  select(trt, age, stage) %>%
  tbl_summary(
     by = trt,
     statistic = list(all_categorical() ~ "{n} ({p}\\%)")
  ) %>%
  bold_labels() %>%
  modify_footnote(
     update = all_stat_cols() ~ "Median (IQR); n (%)"
  ) %>%
  as_kable_extra(
     format = "latex",
     col.names = kableExtra::linebreak(custom_names, align = "c"),
     escape = FALSE
  )

# Example 3 (PDF via LaTeX) -------------------------------------------------
as_kable_extra_ex3_pdf <-
trial %>%
  select(trt, age, stage) %>%
  tbl_summary(by = trt) %>%
  bold_labels() %>%
  as_kable_extra(
    format = "latex",
    booktabs = TRUE,
    longtable = TRUE,
    linesep = ""
  ) %>%
  kableExtra::kable_styling(
    position = "left",
    latex_options = c("striped", "repeat_header"),
```

```
    stripe_color = "gray!15"
  )
```

`as_tibble.gtsummary` *Convert gtsummary object to a tibble*

Description

Function converts a gtsummary object to a tibble.

Usage

```
## S3 method for class 'gtsummary'
as_tibble(
  x,
  include = everything(),
  col_labels = TRUE,
  return_calls = FALSE,
  exclude = NULL,
  fmt_missing = FALSE,
  ...
)
```

Arguments

`x`	Object created by a function from the gtsummary package (e.g. tbl_summary or tbl_regression)
`include`	Commands to include in output. Input may be a vector of quoted or unquoted names. tidyselect and gtsummary select helper functions are also accepted. Default is `everything()`.
`col_labels`	Logical argument adding column labels to output tibble. Default is `TRUE`.
`return_calls`	Logical. Default is `FALSE`. If `TRUE`, the calls are returned as a list of expressions.
`exclude`	DEPRECATED
`fmt_missing`	Logical argument adding the missing value formats.
`...`	Not used

Value

a tibble

Author(s)

Daniel D. Sjoberg

See Also

Other gtsummary output types: `as_flex_table()`, `as_gt()`, `as_hux_table()`, `as_kable_extra()`, `as_kable()`

Examples

```
tbl <-
  trial %>%
  select(trt, age, grade, response) %>%
  tbl_summary(by = trt)

as_tibble(tbl)

# without column labels
as_tibble(tbl, col_labels = FALSE)
```

`bold_italicize_labels_levels` *Bold or Italicize labels or levels in gtsummary tables*

Description

Bold or Italicize labels or levels in gtsummary tables

Usage

```
bold_labels(x)

bold_levels(x)

italicize_labels(x)

italicize_levels(x)
```

Arguments

`x`	Object created using gtsummary functions

Value

Functions return the same class of gtsummary object supplied

Functions

- `bold_labels`: Bold labels in gtsummary tables
- `bold_levels`: Bold levels in gtsummary tables
- `italicize_labels`: Italicize labels in gtsummary tables
- `italicize_levels`: Italicize levels in gtsummary tables

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Other tbl_regression tools: `add_global_p()`, `add_q()`, `combine_terms()`, `inline_text.tbl_regression()`, `modify`, `tbl_merge()`, `tbl_regression()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Other tbl_uvregression tools: `add_global_p()`, `add_q()`, `inline_text.tbl_uvregression()`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_uvregression()`

Examples

```
tbl_bold_ital_ex <-
  trial[c("trt", "age", "grade")] %>%
  tbl_summary() %>%
  bold_labels() %>%
  bold_levels() %>%
  italicize_labels() %>%
  italicize_levels()
```

`bold_p` *Bold significant p-values or q-values*

Description

Bold values below a chosen threshold (e.g. <0.05) in a gtsummary tables.

Usage

```
bold_p(x, t = 0.05, q = FALSE)
```

Arguments

`x`	Object created using gtsummary functions
`t`	Threshold below which values will be bold. Default is 0.05.
`q`	Logical argument. When TRUE will bold the q-value column rather than the p-values. Default is `FALSE`.

Example Output

Author(s)

Daniel D. Sjoberg, Esther Drill

Examples

```
# Example 1 ----------------------------------
bold_p_ex1 <-
  trial[c("age", "grade", "response", "trt")] %>%
  tbl_summary(by = trt) %>%
  add_p() %>%
  bold_p(t = 0.65)

# Example 2 ----------------------------------
bold_p_ex2 <-
  glm(response ~ trt + grade, trial, family = binomial(link = "logit")) %>%
  tbl_regression(exponentiate = TRUE) %>%
  bold_p(t = 0.65)
```

`combine_terms` *Combine terms in a regression model*

Description

The function combines terms from a regression model, and replaces the terms with a single row in the output table. The p-value is calculated using `stats::anova()`.

Usage

```
combine_terms(x, formula_update, label = NULL, quiet = NULL, ...)
```

Arguments

`x`	a `tbl_regression` object
`formula_update`	formula update passed to the stats::update. This updated formula is used to construct a reduced model, and is subsequently passed to `stats::anova()` to calculate the p-value for the group of removed terms. See the stats::update help file for proper syntax. function's formula.= argument
`label`	Option string argument labeling the combined rows
`quiet`	Logical indicating whether to print messages in console. Default is `FALSE`
`...`	Additional arguments passed to stats::anova

Value

`tbl_regression` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_regression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `inline_text.tbl_regress`
`modify`, `tbl_merge()`, `tbl_regression()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Examples

```
# Example 1 ----------------------------------
# Logistic Regression Example, LRT p-value
combine_terms_ex1 <-
  glm(
    response ~ marker + I(marker^2) + grade,
    trial[c("response", "marker", "grade")] %>% na.omit(), # keep complete cases only!
    family = binomial
  ) %>%
  tbl_regression(label = grade ~ "Grade", exponentiate = TRUE) %>%
  # collapse non-linear terms to a single row in output using anova
  combine_terms(
    formula_update = . ~ . - marker - I(marker^2),
    label = "Marker (non-linear terms)",
    test = "LRT"
  )
```

`continuous_summary` *Summarize a continuous variable*

Description

[Experimental] This helper, to be used with `tbl_custom_summary()`, creates a function summarizing a continuous variable.

Usage

```
continuous_summary(variable)
```

Arguments

`variable`	String indicating the name of the variable to be summarized. This variable should be continuous.

Details

When using `continuous_summary`, you can specify in the statistic= argument of `tbl_custom_summary()` the same continuous statistics than in `tbl_summary()`. See the *statistic argument* section of the help file of `tbl_summary()`.

Example Output

Author(s)

Joseph Larmarange

See Also

Other tbl_custom_summary tools: `add_overall()`, `proportion_summary()`, `ratio_summary()`, `tbl_custom_summary()`

Examples

```
# Example 1 ----------------------------------
continuous_summary_ex1 <-
  trial %>%
  tbl_custom_summary(
    include = c("stage", "grade"),
    by = "trt",
    stat_fns = ~ continuous_summary("age"),
    statistic = ~ "{median} [{p25}-{p75}]",
    overall_row = TRUE,
    overall_row_label = "All stages & grades"
  ) %>%
  modify_footnote(
    update = all_stat_cols() ~ "Median age (IQR)"
  )
```

`custom_tidiers` *Collection of custom tidiers*

Description

[Maturing] Collection of tidiers that can be passed to `tbl_regression()` and `tbl_uvregression()` to obtain modified results. See examples below.

Usage

```
tidy_standardize(
  x,
  exponentiate = FALSE,
  conf.level = 0.95,
  conf.int = TRUE,
  ...,
  quiet = FALSE
)

tidy_bootstrap(
  x,
  exponentiate = FALSE,
  conf.level = 0.95,
  conf.int = TRUE,
  ...,
  quiet = FALSE
)
```

```
tidy_robust(
  x,
  exponentiate = FALSE,
  conf.level = 0.95,
  conf.int = TRUE,
  vcov_estimation = NULL,
  vcov_type = NULL,
  vcov_args = NULL,
  ...,
  quiet = FALSE
)

pool_and_tidy_mice(x, pool.args = NULL, ..., quiet = FALSE)

tidy_gam(x, conf.int = FALSE, exponentiate = FALSE, conf.level = 0.95, ...)
```

Arguments

`x`	a regression model object
`exponentiate`	Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to `FALSE`.
`conf.level`	The confidence level to use for the confidence interval if `conf.int = TRUE`. Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval.
`conf.int`	Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to `FALSE`.
`...`	arguments passed to method; • `pool_and_tidy_mice()`: `mice::tidy(x,...)` • `tidy_standardize()`: `effectsize::standardize_parameters(x,...)` • `tidy_bootstrap()`: `parameters::bootstrap_parameters(x,...)` • `tidy_robust()`: `parameters::model_parameters(x,...)`
`quiet`	Logical indicating whether to print messages in console. Default is `FALSE`
`vcov_estimation`, `vcov_type`, `vcov_args`	arguments passed to `parameters::model_parameters()`
`pool.args`	named list of arguments passed to `mice::pool()` in `pool_and_tidy_mice()`. Default is `NULL`

Details

- `tidy_standardize()` tidier to report standardized coefficients. The effectsize package includes a wonderful function to estimate standardized coefficients. The tidier uses the output from `effectsize::standardize_parameters()`, and merely takes the result and puts it in `broom::tidy()` format.
- `tidy_bootstrap()` tidier to report bootstrapped coefficients. The parameters package includes a wonderful function to estimate bootstrapped coefficients. The tidier uses the output from `parameters::bootstrap_parameters(test = "p")`, and merely takes the result and puts it in `broom::tidy()` format.

- `tidy_robust()` tidier to report robust standard errors, confidence intervals, and p-values. The parameters package includes a wonderful function to calculate robust standard errors, confidence intervals, and p-values The tidier uses the output from `parameters::model_parameters()`, and merely takes the result and puts it in `broom::tidy()` format. To use this function with `tbl_regression()`, pass a function with the arguments for `tidy_robust()` populated. This is easily done using `purrr::partial()` e.g. `tbl_regression(tidy_fun = partial(tidy_robust,vcov_estima` `= "CL"))`
- `pool_and_tidy_mice()` tidier to report models resulting from multiply imputed data using the mice package. Pass the mice model object *before* the model results have been pooled. See example.

Ensure your model type is compatible with the methods/functions used to estimate the model parameters before attempting to use the tidier with `tbl_regression()`

Example Output

Examples

```
# Example 1 ----------------------------------
mod <- lm(age ~ marker + grade, trial)

tbl_stnd <- tbl_regression(mod, tidy_fun = tidy_standardize)
tbl <- tbl_regression(mod)

tidy_standardize_ex1 <-
  tbl_merge(
    list(tbl_stnd, tbl),
    tab_spanner = c("**Standardized Model**", "**Original Model**")
  )

# Example 2 ----------------------------------
# use "posthoc" method for coef calculation
tidy_standardize_ex2 <-
  tbl_regression(mod, tidy_fun = purrr::partial(tidy_standardize, method = "posthoc"))

# Example 3 ----------------------------------
# Multiple Imputation using the mice package
set.seed(1123)
pool_and_tidy_mice_ex3 <-
  suppressWarnings(mice::mice(trial, m = 2)) %>%
  with(lm(age ~ marker + grade)) %>%
  tbl_regression()
```

`inline_text.gtsummary` *Report statistics from summary tables inline*

Description

Report statistics from summary tables inline

Usage

```
## S3 method for class 'gtsummary'
inline_text(x, variable, level = NULL, column = NULL, pattern = NULL, ...)
```

Arguments

`x`	gtsummary object
`variable`	Variable name of statistic to present
`level`	Level of the variable to display for categorical variables. Default is `NULL`
`column`	Column name to return from `x$table_body`.
`pattern`	String indicating the statistics to return. Uses glue::glue formatting. Default is `NULL`
`...`	Not used

column + pattern

Some gtsummary tables report multiple statistics in a single cell, e.g. `"{mean} ({sd})"` in `tbl_summary()` or `tbl_svysummary()`. We often need to report just the mean or the SD, and that can be accomplished by using both the column= and pattern= arguments. When both of these arguments are specified, the column argument selects the column to report statistics from, and the pattern argument specifies which statistics to report, e.g. `inline_text(x,column = "stat_1",pattern = "{mean}")` reports just the mean from a `tbl_summary()`.

`inline_text.tbl_cross` *Report statistics from cross table inline*

Description

[Maturing] Extracts and returns statistics from a `tbl_cross` object for inline reporting in an R markdown document. Detailed examples in the inline_text vignette

Usage

```
## S3 method for class 'tbl_cross'
inline_text(x, col_level = NULL, row_level = NULL, pvalue_fun = NULL, ...)
```

Arguments

`x`	a `tbl_cross` object
`col_level`	Level of the column variable to display. Default is `NULL` Can also specify `"p.value"` for the p-value and `"stat_0"` for Total column.
`row_level`	Level of the row variable to display. Can also specify the 'Unknown' row. Default is `NULL`
`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x,digits = 2)` or equivalently, `purrr::partial(style_pvalue,digits = 2)`).
`...`	Not used

Value

A string reporting results from a gtsummary table

See Also

Other tbl_cross tools: `add_p.tbl_cross()`, `tbl_cross()`

Examples

```
tbl_cross <-
  tbl_cross(trial, row = trt, col = response) %>%
  add_p()

inline_text(tbl_cross, row_level = "Drug A", col_level = "1")
inline_text(tbl_cross, row_level = "Total", col_level = "1")
inline_text(tbl_cross, col_level = "p.value")
```

`inline_text.tbl_regression`

Report statistics from regression summary tables inline

Description

Takes an object with class `tbl_regression`, and the location of the statistic to report and returns statistics for reporting inline in an R markdown document. Detailed examples in the inline_text vignette

Usage

```
## S3 method for class 'tbl_regression'
inline_text(
  x,
  variable,
  level = NULL,
 pattern = "{estimate} ({conf.level*100}% CI {conf.low}, {conf.high}; {p.value})",
  estimate_fun = NULL,
  pvalue_fun = NULL,
  ...
)
```

Arguments

`x`	Object created from tbl_regression
`variable`	Variable name of statistics to present
`level`	Level of the variable to display for categorical variables. Default is `NULL`, returning the top row in the table for the variable.
`pattern`	String indicating the statistics to return. Uses glue::glue formatting. Default is `"{estimate} ({conf.level }% CI {conf.low}, {conf.high}; {p.value})"`. All columns from `x$table_body` are available to print as well as the confidence level (conf.level). See below for details.

`estimate_fun`	function to style model coefficient estimates. Columns 'estimate', 'conf.low', and 'conf.high' are formatted. Default is `x$inputs$estimate_fun`
`pvalue_fun`	function to style p-values and/or q-values. Default is `function(x) style_pvalue(x,prepend_p = TRUE)`
`...`	Not used

Value

A string reporting results from a gtsummary table

pattern argument

The following items (and more) are available to print. Use `print(x$table_body)` to print the table the estimates are extracted from.

- `{estimate}` coefficient estimate formatted with 'estimate_fun'
- `{conf.low}` lower limit of confidence interval formatted with 'estimate_fun'
- `{conf.high}` upper limit of confidence interval formatted with 'estimate_fun'
- `{p.value}` p-value formatted with 'pvalue_fun'
- `{N}` number of observations in model
- `{label}` variable/variable level label

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_regression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `combine_terms()`, `modify`, `tbl_merge()`, `tbl_regression()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Examples

```
inline_text_ex1 <-
  glm(response ~ age + grade, trial, family = binomial(link = "logit")) %>%
  tbl_regression(exponentiate = TRUE)

inline_text(inline_text_ex1, variable = age)
inline_text(inline_text_ex1, variable = grade, level = "III")
```

`inline_text.tbl_summary`

Report statistics from summary tables inline

Description

Extracts and returns statistics from a `tbl_summary` object for inline reporting in an R markdown document. Detailed examples in the inline_text vignette

Usage

```
## S3 method for class 'tbl_summary'
inline_text(
  x,
  variable,
  column = NULL,
  level = NULL,
  pattern = NULL,
  pvalue_fun = NULL,
  ...
)

## S3 method for class 'tbl_svysummary'
inline_text(
  x,
  variable,
  column = NULL,
  level = NULL,
  pattern = NULL,
  pvalue_fun = NULL,
  ...
)
```

Arguments

`x`	Object created from tbl_summary
`variable`	Variable name of statistic to present
`column`	Column name to return from `x$table_body`. Can also pass the level of a by variable.
`level`	Level of the variable to display for categorical variables. Can also specify the 'Unknown' row. Default is `NULL`
`pattern`	String indicating the statistics to return. Uses glue::glue formatting. Default is pattern shown in `tbl_summary()` output
`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x, digits = 2)` or equivalently, `purrr::partial(style_pvalue, digits = 2)`).
`...`	Not used

Value

A string reporting results from a gtsummary table

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_survfit()`, `modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Examples

```
t1 <- trial[c("trt", "grade")] %>%
  tbl_summary(by = trt) %>%
  add_p()

inline_text(t1, variable = grade, level = "I", column = "Drug A", pattern = "{n}/{N} ({p})%")
inline_text(t1, variable = grade, column = "p.value")
```

`inline_text.tbl_survfit`

Report statistics from survfit tables inline

Description

[Maturing] Extracts and returns statistics from a `tbl_survfit` object for inline reporting in an R markdown document. Detailed examples in the inline_text vignette

Usage

```
## S3 method for class 'tbl_survfit'
inline_text(
  x,
  variable = NULL,
  level = NULL,
  pattern = NULL,
  time = NULL,
  prob = NULL,
  column = NULL,
  estimate_fun = x$inputs$estimate_fun,
  pvalue_fun = NULL,
  ...
)
```

Arguments

`x`	Object created from tbl_survfit
`variable`	Variable name of statistic to present.
`level`	Level of the variable to display for categorical variables. Can also specify the 'Unknown' row. Default is `NULL`
`pattern`	String indicating the statistics to return.
`time`	time for which to return survival probabilities.
`prob`	probability with values in (0,1)

`column`	column to print from `x$table_body`. Columns may be selected with time= or prob= as well.
`estimate_fun`	Function to round and format estimate and confidence limits. Default is the same function used in `tbl_survfit()`
`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x, digits = 2)` or equivalently, `purrr::partial(style_pvalue, digits = 2)`).
`...`	Not used

Value

A string reporting results from a gtsummary table

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Examples

```
library(survival)
# fit survfit
fit1 <- survfit(Surv(ttdeath, death) ~ trt, trial)
fit2 <- survfit(Surv(ttdeath, death) ~ 1, trial)

# sumarize survfit objects
tbl1 <-
  tbl_survfit(
    fit1,
    times = c(12, 24),
    label = "Treatment",
    label_header = "**{time} Month**"
  ) %>%
  add_p()

tbl2 <-
  tbl_survfit(
    fit2,
    probs = 0.5,
    label_header = "**Median Survival**"
  )

# report results inline
inline_text(tbl1, time = 24, level = "Drug B")
inline_text(tbl1, column = p.value)
inline_text(tbl2, prob = 0.5)
```

`inline_text.tbl_uvregression`

Report statistics from regression summary tables inline

Description

Extracts and returns statistics from a table created by the `tbl_uvregression` function for inline reporting in an R markdown document. Detailed examples in the inline_text vignette

Usage

```
## S3 method for class 'tbl_uvregression'
inline_text(
  x,
  variable,
  level = NULL,
  pattern = "{estimate} ({conf.level*100}% CI {conf.low}, {conf.high}; {p.value})",
  estimate_fun = NULL,
  pvalue_fun = NULL,
  ...
)
```

Arguments

`x`	Object created from tbl_uvregression
`variable`	Variable name of statistics to present
`level`	Level of the variable to display for categorical variables. Default is `NULL`, returning the top row in the table for the variable.
`pattern`	String indicating the statistics to return. Uses glue::glue formatting. Default is `"{estimate} ({conf.level }% CI {conf.low},{conf.high}; {p.value})"`. All columns from `x$table_body` are available to print as well as the confidence level (conf.level). See below for details.
`estimate_fun`	function to style model coefficient estimates. Columns 'estimate', 'conf.low', and 'conf.high' are formatted. Default is `x$inputs$estimate_fun`
`pvalue_fun`	function to style p-values and/or q-values. Default is `function(x) style_pvalue(x,prepend_p = TRUE)`
`...`	Not used

Value

A string reporting results from a gtsummary table

pattern argument

The following items (and more) are available to print. Use `print(x$table_body)` to print the table the estimates are extracted from.

- `{estimate}` coefficient estimate formatted with 'estimate_fun'
- `{conf.low}` lower limit of confidence interval formatted with 'estimate_fun'

- `{conf.high}` upper limit of confidence interval formatted with 'estimate_fun'
- `{p.value}` p-value formatted with 'pvalue_fun'
- `{N}` number of observations in model
- `{label}` variable/variable level label

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_uvregression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_uvregression()`

Examples

```
inline_text_ex1 <-
  trial[c("response", "age", "grade")] %>%
  tbl_uvregression(
    method = glm,
    method.args = list(family = binomial),
    y = response,
    exponentiate = TRUE
  )

inline_text(inline_text_ex1, variable = age)
inline_text(inline_text_ex1, variable = grade, level = "III")
```

`modify` *Modify column headers, footnotes, spanning headers, and table captions*

Description

These functions assist with updating or adding column headers (`modify_header()`), footnotes (`modify_footnote()`), spanning headers (`modify_spanning_header()`), and table captions (`modify_caption()`). Use `show_header_names()` to learn the column names.

Usage

```
modify_header(
  x,
  update = NULL,
  ...,
  text_interpret = c("md", "html"),
  quiet = NULL,
  stat_by = NULL
)

modify_footnote(
  x,
```

```
  update = NULL,
  ...,
  abbreviation = FALSE,
  text_interpret = c("md", "html"),
  quiet = NULL
)

modify_spanning_header(
  x,
  update = NULL,
  ...,
  text_interpret = c("md", "html"),
  quiet = NULL
)

modify_caption(x, caption, text_interpret = c("md", "html"))

show_header_names(x = NULL, include_example = TRUE, quiet = NULL)
```

Arguments

`x`	a gtsummary object
`update, ...`	use these arguments to assign updates to headers, spanning headers, and footnotes. See examples below. • `update` expects a list of assignments, with the variable name or selector on the LHS of the formula, and the updated string on the RHS. Also accepts a named list. • `...` pass individual updates outside of a list, e.g, `modify_header(p.value = "**P**",all_stat_cols() ~ "**{level}**")` Use the `show_header_names()` to see the column names that can be modified.
`text_interpret`	String indicates whether text will be interpreted with `gt::md()` or `gt::html()`. Must be `"md"` (default) or `"html"`.
`quiet`	Logical indicating whether to print messages in console. Default is `FALSE`
`stat_by`	DEPRECATED, use `update = all_stat_cols() ~ "<label>"` instead.
`abbreviation`	Logical indicating if an abbreviation is being updated.
`caption`	a string of the table caption/title
`include_example`	logical whether to include print of `modify_header()` example

Value

Updated gtsummary object

tbl_summary(), tbl_svysummary(), and tbl_cross()

When assigning column headers, footnotes, spanning headers, and captions for these gtsummary tables, you may use `{N}` to insert the number of observations. `tbl_svysummary` objects additionally have `{N_unweighted}` available.

When there is a stratifying by= argument present, the following fields are additionally available to stratifying columns: `{level}`, `{n}`, and `{p}` (`{n_unweighted}` and `{p_unweighted}` for `tbl_svysummary` objects)

Syntax follows `glue::glue()`, e.g. `all_stat_cols() ~ "**{level}**, N = {n}"`.

tbl_regression()

When assigning column headers for `tbl_regression` tables, you may use `{N}` to insert the number of observations, and `{N_event}` for the number of events (when applicable).

captions

Captions are assigned based on output type.

- `gt::gt(caption=)`
- `flextable::set_caption(caption=)`
- `huxtable::set_caption(value=)`
- `knitr::kable(caption=)`

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Other tbl_svysummary tools: `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_svysummary()`, `add_q()`, `add_stat_label()`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_svysummary()`

Other tbl_regression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `combine_terms()`, `inline_text.tbl_regression()`, `tbl_merge()`, `tbl_regression()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Other tbl_uvregression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `inline_text.tbl_uvreg`
`tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_uvregression()`

Other tbl_survfit tools: `add_n.tbl_survfit()`, `add_nevent.tbl_survfit()`, `add_p.tbl_survfit()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_survfit()`

Examples

```
# create summary table
tbl <- trial[c("age", "grade", "trt")] %>%
  tbl_summary(by = trt, missing = "no") %>%
  add_p()

# print the column names that can be modified
show_header_names(tbl)

# Example 1 ----------------------------------
# updating column headers, footnote, and table caption
```

```
modify_ex1 <- tbl %>%
  modify_header(label = "**Variable**", p.value = "**P**") %>%
  modify_footnote(all_stat_cols() ~ "median (IQR) for Age; n (%) for Grade") %>%
  modify_caption("**Patient Characteristics** (N = {N})")

# Example 2 ----------------------------------
# updating headers, remove all footnotes, add spanning header
modify_ex2 <- tbl %>%
  modify_header(all_stat_cols() ~ "**{level}**, N = {n} ({style_percent(p)}%)") %>%
 # use `modify_footnote(everything() ~ NA, abbreviation = TRUE)` to delete abbrev. footnotes
  modify_footnote(update = everything() ~ NA) %>%
  modify_spanning_header(all_stat_cols() ~ "**Treatment Received**")

# Example 3 ----------------------------------
# updating an abbreviation in table footnote
modify_ex3 <-
  glm(response ~ age + grade, trial, family = binomial) %>%
  tbl_regression(exponentiate = TRUE) %>%
  modify_footnote(ci = "CI = Credible Interval", abbreviation = TRUE)
```

`modify_cols_merge` *Modify Column Merging*

Description

[Experimental] Merge two or more columns in a gtsummary table. Use `show_header_names()` to print underlying column names.

Usage

```
modify_cols_merge(x, pattern, rows = NULL)
```

Arguments

`x`	gtsummary object
`pattern`	glue syntax string indicating how to merge columns in `x$table_body`. For example, to construct a confidence interval use `"{conf.low},{conf.high}"`.
`rows`	predicate expression to select rows in `x$table_body`. Can be used to style footnote, formatting functions, missing symbols, and text formatting. Default is `NULL`. See details below.

Value

gtsummary table

Details

1. Calling this function merely records the instructions to merge columns. The actual merging occurs when the gtsummary table is printed or converted with a function like `as_gt()`.
2. Because the column merging is delayed, it is recommended to perform major modifications to the table, such as those with `tbl_merge()` and `tbl_stack()`, before assigning merging instructions. Otherwise, unexpected formatting may occur in the final table.

Future Updates

There are planned updates to the implementation of this function with respect to the pattern= argument. Currently, this function replaces a numeric column with a formatted character column following pattern=. Once `gt::cols_merge()` gains the rows= argument the implementation will be updated to use it, which will keep numeric columns numeric. For the *vast majority* of users, *the planned change will be go unnoticed*.

Example Output

See Also

Other Advanced modifiers: `modify_column_alignment()`, `modify_column_hide()`, `modify_fmt_fun()`, `modify_table_body()`, `modify_table_styling()`

Examples

```
# Example 1 ----------------------------------
modify_cols_merge_ex1 <-
  trial %>%
  select(age, marker, trt) %>%
  tbl_summary(by = trt, missing = "no") %>%
  add_p(all_continuous() ~ "t.test",
        pvalue_fun = ~style_pvalue(., prepend_p = TRUE)) %>%
  modify_fmt_fun(statistic ~ style_sigfig) %>%
  modify_cols_merge(pattern = "t = {statistic}; {p.value}") %>%
  modify_header(statistic ~ "**t-test**")

# Example 2 ----------------------------------
modify_cols_merge_ex2 <-
  lm(marker ~ age + grade, trial) %>%
  tbl_regression() %>%
  modify_cols_merge(
    pattern = "{estimate} ({ci})",
    rows = !is.na(estimate)
  )
```

`modify_column_alignment`

Modify Column Alignment

Description

[Maturing] Update column alignment/justification in a gtsummary table.

Usage

```
modify_column_alignment(x, columns, align = c("left", "right", "center"))
```

Arguments

`x`	gtsummary object
`columns`	vector or selector of columns in `x$table_body`
`align`	string indicating alignment of column, must be one of `c("left","right","center")`

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other Advanced modifiers: `modify_cols_merge()`, `modify_column_hide()`, `modify_fmt_fun()`, `modify_table_body()`, `modify_table_styling()`

Examples

```
# Example 1 ----------------------------------
tbl <-
  lm(age ~ marker + grade, trial) %>%
  tbl_regression() %>%
  modify_column_alignment(columns = everything(), align = "left")
```

`modify_column_hide` *Modify Hidden Columns*

Description

[Maturing] Use these functions to hide or unhide columns in a gtsummary table.

Usage

```
modify_column_hide(x, columns)

modify_column_unhide(x, columns)
```

Arguments

`x`	gtsummary object
`columns`	vector or selector of columns in `x$table_body`

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other Advanced modifiers: `modify_cols_merge()`, `modify_column_alignment()`, `modify_fmt_fun()`, `modify_table_body()`, `modify_table_styling()`

Examples

```
# Example 1 ----------------------------------
# hide 95% CI, and replace with standard error
modify_column_hide_ex1 <-
  lm(age ~ marker + grade, trial) %>%
  tbl_regression() %>%
  modify_column_hide(columns = ci) %>%
  modify_column_unhide(columns = std.error)
```

`modify_fmt_fun` *Modify Formatting Functions*

Description

[Maturing] Use this function to update the way numeric columns and rows of `.$table_body` are formatted

Usage

```
modify_fmt_fun(x, update, rows = NULL)
```

Arguments

`x`	gtsummary object
`update`	list of formulas or a single formula specifying the updated formatting function. The LHS specifies the column(s) to be updated, and the RHS is the updated formatting function.
`rows`	predicate expression to select rows in `x$table_body`. Default is `NULL`. See details below.

Example Output

rows argument

The rows argument accepts a predicate expression that is used to specify rows to apply formatting. The expression must evaluate to a logical when evaluated in `x$table_body`. For example, to apply formatting to the age rows pass `rows = variable == "age"`. A vector of row numbers is NOT acceptable.

A couple of things to note when using the rows= argument.

1. You can use saved objects to create the predicate argument, e.g. `rows = variable == letters[1]`.
2. The saved object cannot share a name with a column in `x$table_body`. The reason for this is that in `tbl_merge()` the columns are renamed, and the renaming process cannot disambiguate the `variable` column from an external object named `variable` in the following expression `rows = .data$variable = .env$variable`.

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other Advanced modifiers: `modify_cols_merge()`, `modify_column_alignment()`, `modify_column_hide()`, `modify_table_body()`, `modify_table_styling()`

Examples

```
# Example 1 ----------------------------------
# show 'grade' p-values to 3 decimal places
modify_fmt_fun_ex1 <-
  lm(age ~ marker + grade, trial) %>%
  tbl_regression() %>%
  modify_fmt_fun(
    update = p.value ~ function(x) style_pvalue(x, digits = 3),
    rows = variable == "grade"
  )
```

`modify_table_body` *Modify Table Body*

Description

[Maturing] Function is for advanced manipulation of gtsummary tables. It allow users to modify the `.$table_body` data frame included in each gtsummary object.

If a new column is added to the table, default printing instructions will then be added to `.$table_styling`. By default, columns are hidden. To show a column, add a column header with `modify_header()`.

Usage

```
modify_table_body(x, fun, ...)
```

Arguments

`x`	gtsummary object
`fun`	A function or formula. If a *function*, it is used as is. If a *formula*, e.g. `fun = ~ .x %>% arrange(variable)`, it is converted to a function. The argument passed to fun= is `x$table_body`.
`...`	Additional arguments passed on to the mapped function

Example Output

See Also

`modify_table_styling()`

See gtsummary internals vignette

Other Advanced modifiers: `modify_cols_merge()`, `modify_column_alignment()`, `modify_column_hide()`, `modify_fmt_fun()`, `modify_table_styling()`

Examples

```
# Example 1 ----------------------------------
# Add number of cases and controls to regression table
modify_table_body_ex1 <-
  trial %>%
  select(response, age, marker) %>%
  tbl_uvregression(
    y = response,
    method = glm,
    method.args = list(family = binomial),
    exponentiate = TRUE,
    hide_n = TRUE
  ) %>%
  # adding number of non-events to table
  modify_table_body(
    ~ .x %>%
      dplyr::mutate(N_nonevent = N_obs - N_event) %>%
      dplyr::relocate(c(N_event, N_nonevent), .before = estimate)
  ) %>%
  # assigning header labels
  modify_header(N_nonevent = "**Control N**", N_event = "**Case N**") %>%
  modify_fmt_fun(c(N_event, N_nonevent) ~ style_number)
```

`modify_table_styling` *Modify Table Styling*

Description

This is a function meant for advanced users to gain more control over the characteristics of the resulting gtsummary table by directly modifying `.$table_styling`

Usage

```
modify_table_styling(
  x,
  columns,
  rows = NULL,
  label = NULL,
  spanning_header = NULL,
  hide = NULL,
  footnote = NULL,
  footnote_abbrev = NULL,
  align = NULL,
  missing_symbol = NULL,
  fmt_fun = NULL,
  text_format = NULL,
  undo_text_format = FALSE,
  text_interpret = c("md", "html"),
  cols_merge_pattern = NULL
)
```

Arguments

`x`	gtsummary object
`columns`	vector or selector of columns in `x$table_body`
`rows`	predicate expression to select rows in `x$table_body`. Can be used to style footnote, formatting functions, missing symbols, and text formatting. Default is `NULL`. See details below.
`label`	string of column label(s)
`spanning_header`	string with text for spanning header
`hide`	logical indicating whether to hide column from output
`footnote`	string with text for footnote
`footnote_abbrev`	string with abbreviation definition, e.g. `"CI = Confidence Interval"`
`align`	string indicating alignment of column, must be one of `c("left","right","center")`
`missing_symbol`	string indicating how missing values are formatted.
`fmt_fun`	function that formats the statistics in the columns/rows in columns= and rows=
`text_format`	string indicated which type of text formatting to apply to the rows and columns. Must be one of `c("bold","italic","indent","indent2")`. Do not assign both `"indent"` and `"indent2"` to the same cell.
`undo_text_format`	rarely used. Logical that undoes the indent, bold, and italic styling when `TRUE`
`text_interpret`	string, must be one of `"md"` or `"html"`
`cols_merge_pattern`	**[Experimental]** glue-syntax string indicating how to merge columns in `x$table_body`. For example, to construct a confidence interval use `"{conf.low},{conf.high}"`. The first column listed in the pattern string must match the single column name passed in columns=.

Details

Review the gtsummary definition vignette for information on `.$table_styling` objects.

rows argument

The rows argument accepts a predicate expression that is used to specify rows to apply formatting. The expression must evaluate to a logical when evaluated in `x$table_body`. For example, to apply formatting to the age rows pass `rows = variable == "age"`. A vector of row numbers is NOT acceptable.

A couple of things to note when using the rows= argument.

1. You can use saved objects to create the predicate argument, e.g. `rows = variable == letters[1]`.
2. The saved object cannot share a name with a column in `x$table_body`. The reason for this is that in `tbl_merge()` the columns are renamed, and the renaming process cannot disambiguate the `variable` column from an external object named `variable` in the following expression `rows = .data$variable = .env$variable`.

cols_merge_pattern argument

There are planned updates to the implementation of column merging. Currently, this function replaces the numeric column with a formatted character column following cols_merge_pattern=. Once `gt::cols_merge()` gains the rows= argument the implementation will be updated to use it, which will keep numeric columns numeric. For the *vast majority* of users, *the planned change will be go unnoticed*.

If this functionality is used in conjunction with `tbl_stack()` (which includes `tbl_uvregression()`), there is potential issue with printing. When columns are stack AND when the column-merging is defined with a quosure, you may run into issues due to the loss of the environment when 2 or more quosures are combined. If the expression version of the quosure is the same as the quosure (i.e. no evaluated objects), there should be no issues. Regardless, this argument is used internally with care, and it is *not* recommended for users.

See Also

`modify_table_body()`

See gtsummary internals vignette

Review list, formula, and selector syntax used throughout gtsummary

Other Advanced modifiers: `modify_cols_merge()`, `modify_column_alignment()`, `modify_column_hide()`, `modify_fmt_fun()`, `modify_table_body()`

`plot` *Plot Regression Coefficients*

Description

The `plot()` function extracts `x$table_body` and passes the it to `GGally::ggcoef_plot()` along with a formatting options.

Usage

```
## S3 method for class 'tbl_regression'
plot(x, remove_header_rows = TRUE, remove_reference_rows = FALSE, ...)

## S3 method for class 'tbl_uvregression'
plot(x, remove_header_rows = TRUE, remove_reference_rows = FALSE, ...)
```

Arguments

`x`	’tbl_regression’ or ’tbl_uvregression’ object
`remove_header_rows`	logical indicating whether to remove header rows for categorical variables. Default is `TRUE`
`remove_reference_rows`	logical indicating whether to remove reference rows for categorical variables. Default is `FALSE`.
`...`	arguments passed to `GGally::ggcoef_plot(...)`

Details

[Experimental]

Value

a ggplot

Examples

```
glm(response ~ marker + grade, trial, family = binomial) %>%
  tbl_regression(
    add_estimate_to_reference_rows = TRUE,
    exponentiate = TRUE
  ) %>%
  plot()
```

`proportion_summary` *Summarize a proportion*

Description

[Experimental] This helper, to be used with `tbl_custom_summary()`, creates a function computing a proportion and its confidence interval.

Usage

```
proportion_summary(
  variable,
  value,
  weights = NULL,
  na.rm = TRUE,
  conf.level = 0.95,
  method = c("wilson", "wilson.no.correct", "exact", "asymptotic")
)
```

Arguments

`variable`	String indicating the name of the variable from which the proportion will be computed.
`value`	Value (or list of values) of `variable` to be taken into account in the numerator.
`weights`	Optional string indicating the name of a weighting variable. If `NULL`, all observations will be assumed to have a weight equal to `1`.
`na.rm`	Should missing values be removed before computing the proportion? (default is `TRUE`)
`conf.level`	Confidence level for the returned confidence interval. Must be strictly greater than 0 and less than 1. Default to 0.95, which corresponds to a 95 percent confidence interval.
`method`	Confidence interval method. Must be one of `c("wilson","wilson.no.correct","exact","asymp` See details below.

Details

Computed statistics:

- `{n}` numerator, (weighted) number of observations equal to `values`
- `{N}` denominator, (weighted) number of observations
- `{prop}` proportion, i.e. `n/N`
- `{conf.low}` lower confidence interval
- `{conf.high}` upper confidence interval

Methods `c("wilson","wilson.no.correct")` are calculated with `stats::prop.test()` (with `correct = c(TRUE,FALSE)`). The default method, `"wilson"`, includes the Yates continuity correction. Methods `c("exact","asymptotic")` are calculated with `Hmisc::binconf()` and the corresponding method.

Example Output

Author(s)

Joseph Larmarange

See Also

Other tbl_custom_summary tools: `add_overall()`, `continuous_summary()`, `ratio_summary()`, `tbl_custom_summary()`

Examples

```
# Example 1 ----------------------------------
proportion_summary_ex1 <-
  Titanic %>%
  as.data.frame() %>%
  tbl_custom_summary(
    include = c("Age", "Class"),
    by = "Sex",
    stat_fns = ~ proportion_summary("Survived", "Yes", weights = "Freq"),
    statistic = ~ "{prop}% ({n}/{N}) [{conf.low}-{conf.high}]",
    digits = ~ list(
      function(x) {style_percent(x, digits = 1)},
      0, 0, style_percent, style_percent
    ),
    overall_row = TRUE,
    overall_row_last = TRUE
  ) %>%
  bold_labels() %>%
  modify_footnote(
    update = all_stat_cols() ~ "Proportion (%) of survivors (n/N) [95% CI]"
  )
```

`ratio_summary` *Summarize the ratio of two variables*

Description

[Experimental] This helper, to be used with `tbl_custom_summary()`, creates a function computing the ratio of two continuous variables and its confidence interval.

Usage

```
ratio_summary(numerator, denominator, na.rm = TRUE, conf.level = 0.95)
```

Arguments

`numerator`	String indicating the name of the variable to be summed for computing the numerator.
`denominator`	String indicating the name of the variable to be summed for computing the denominator.
`na.rm`	Should missing values be removed before summing the numerator and the denominator? (default is `TRUE`)
`conf.level`	Confidence level for the returned confidence interval. Must be strictly greater than 0 and less than 1. Default to 0.95, which corresponds to a 95 percent confidence interval.

Details

Computed statistics:

- `{num}` sum of the variable defined by `numerator`
- `{denom}` sum of the variable defined by `denominator`
- `{ratio}` ratio of `num` by `denom`
- `{conf.low}` lower confidence interval
- `{conf.high}` upper confidence interval

Confidence interval is computed with `stats::poisson.test()`, if and only if `num` is an integer.

Example Output

Author(s)

Joseph Larmarange

See Also

Other tbl_custom_summary tools: `add_overall()`, `continuous_summary()`, `proportion_summary()`, `tbl_custom_summary()`

Examples

```
# Example 1 ----------------------------------
ratio_summary_ex1 <-
  trial %>%
  tbl_custom_summary(
    include = c("stage", "grade"),
    by = "trt",
    stat_fns = ~ ratio_summary("response", "ttdeath"),
    statistic = ~ "{ratio} [{conf.low}; {conf.high}] ({num}/{denom})",
    digits = ~ c(3, 2, 2, 0, 0),
    overall_row = TRUE,
    overall_row_label = "All stages & grades"
  ) %>%
  bold_labels() %>%
  modify_footnote(
    update = all_stat_cols() ~ "Ratio [95% CI] (n/N)"
  )
```

`remove_row_type` *Remove rows by type*

Description

Removes either the header, reference, or missing rows from a gtsummary table.

Usage

```
remove_row_type(
  x,
  variables = everything(),
  type = c("header", "reference", "missing")
)
```

Arguments

`x`	gtsummary object
`variables`	variables to to remove rows from. Default is `everything()`
`type`	type of row to remove. Must be one of `c("header","reference","missing")`

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Examples

```
# Example 1 ----------------------------------
library(dplyr, warn.conflicts = FALSE, quietly = TRUE)
remove_row_type_ex1 <-
  trial %>%
  select(trt, age) %>%
  mutate(
    age60 = case_when(age < 60 ~ "<60", age >= 60 ~ "60+")
  ) %>%
  tbl_summary(by = trt, missing = "no") %>%
  remove_row_type(age60, type = "header")
```

`select_helpers` *Select helper functions*

Description

Set of functions to supplement the tidyselect set of functions for selecting columns of data frames (and other items as well).

- `all_continuous()` selects continuous variables
- `all_continuous2()` selects only type `"continuous2"`
- `all_categorical()` selects categorical (including `"dichotomous"`) variables
- `all_dichotomous()` selects only type `"dichotomous"`
- `all_tests()` selects variables by the name of the test performed
- `all_stat_cols()` selects columns from `tbl_summary`/`tbl_svysummary` object with summary statistics (i.e. `"stat_0"`, `"stat_1"`, `"stat_2"`, etc.)
- `all_interaction()` selects interaction terms from a regression model
- `all_intercepts()` selects intercept terms from a regression model
- `all_contrasts()` selects variables in regression model based on their type of contrast

Usage

```
all_continuous(continuous2 = TRUE)

all_continuous2()

all_categorical(dichotomous = TRUE)

all_dichotomous()

all_tests(tests = NULL)

all_stat_cols(stat_0 = TRUE)

all_interaction()

all_intercepts()

all_contrasts(contrasts_type = NULL)
```

Arguments

`continuous2`	Logical indicating whether to include continuous2 variables. Default is `TRUE`
`dichotomous`	Logical indicating whether to include dichotomous variables. Default is `TRUE`
`tests`	string indicating the test type of the variables to select, e.g. select all variables being compared with `"t.test"`
`stat_0`	When `FALSE`, will not select the `"stat_0"` column. Default is `TRUE`
`contrasts_type`	type of contrast to select. When `NULL`, all variables with a contrast will be selected. Default is `NULL`. Select among contrast types `c("treatment","sum","poly","helmert","o`

Value

A character vector of column names selected

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Examples

```
select_ex1 <-
  trial %>%
  select(age, response, grade) %>%
  tbl_summary(
    statistic = all_continuous() ~ "{mean} ({sd})",
    type = all_dichotomous() ~ "categorical"
  )
```

`separate_p_footnotes` *Create footnotes for individual p-values*

Description

[Experimental] The usual presentation of footnotes for p-values on a gtsummary table is to have a single footnote that lists all statistical tests that were used to compute p-values on a given table. The `separate_p_footnotes()` function separates aggregated p-value footnotes to individual footnotes that denote the specific test used for each of the p-values.

Usage

```
separate_p_footnotes(x)
```

Arguments

`x`	object with class `"tbl_summary"` or `"tbl_svysummary"`

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `modify`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Other tbl_svysummary tools: `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_svysummary()`, `add_q()`, `add_stat_label()`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_svysummary()`

Examples

```
separate_p_footnotes_ex1 <-
  trial %>%
  select(trt, age, grade) %>%
  tbl_summary(by = trt) %>%
  add_p() %>%
  separate_p_footnotes()
```

`set_gtsummary_theme` *Set a gtsummary theme*

Description

[Maturing] Use this function to set preferences for the display of gtsummary tables. The default formatting and styling throughout the gtsummary package are taken from the published reporting guidelines of the top four urology journals: European Urology, The Journal of Urology, Urology and the British Journal of Urology International. Use this function to change the default reporting style to match another journal, or your own personal style.

Usage

```
set_gtsummary_theme(x)

reset_gtsummary_theme()
```

Arguments

`x`	A gtsummary theme function, e.g. `theme_gtsummary_journal()`, or a named list defining a gtsummary theme. See details below.

Example Output

See Also

Themes vignette

Available gtsummary themes

Examples

```
# Setting JAMA theme for gtsummary
set_gtsummary_theme(theme_gtsummary_journal("jama"))
# Themes can be combined by including more than one
set_gtsummary_theme(theme_gtsummary_compact())

set_gtsummary_theme_ex1 <-
  trial %>%
  dplyr::select(age, grade, trt) %>%
  tbl_summary(by = trt) %>%
  add_stat_label() %>%
  as_gt()

# reset gtsummary theme
reset_gtsummary_theme()
```

`sort_filter_p` *Sort and filter variables in table by p-values*

Description

Sort and filter variables in table by p-values

Usage

```
sort_p(x, q = FALSE)

filter_p(x, q = FALSE, t = 0.05)
```

Arguments

`x`	An object created using gtsummary functions
`q`	Logical argument. When `TRUE` will the q-value column is used
`t`	p-values/q-values less than or equal to this threshold will be retained. Default is 0.05

Example Output

Author(s)

Karissa Whiting, Daniel D. Sjoberg

Examples

```
# Example 1 ----------------------------------
sort_filter_p_ex1 <-
  trial %>%
  select(age, grade, response, trt) %>%
  tbl_summary(by = trt) %>%
  add_p() %>%
```

```
  filter_p(t = 0.8) %>%
  sort_p()

# Example 2 ----------------------------------
sort_p_ex2 <-
  glm(response ~ trt + grade, trial, family = binomial(link = "logit")) %>%
  tbl_regression(exponentiate = TRUE) %>%
  sort_p()
```

`style_number` *Style numbers*

Description

Style numbers

Usage

```
style_number(
  x,
  digits = 0,
  big.mark = NULL,
  decimal.mark = NULL,
  scale = 1,
  ...
)
```

Arguments

`x`	Numeric vector
`digits`	Integer or vector of integers specifying the number of digits to round x=. When vector is passed, each integer is mapped 1:1 to the numeric values in `x`
`big.mark`	Character used between every 3 digits to separate hundreds/thousands/millions/etc. Default is `","`, except when `decimal.mark = ","` when the default is a space.
`decimal.mark`	The character to be used to indicate the numeric decimal point. Default is `"."` or `getOption("OutDec")`
`scale`	A scaling factor: x will be multiplied by scale before formatting.
`...`	Other arguments passed on to `base::format()`

Value

formatted character vector

See Also

Other style tools: `style_percent()`, `style_pvalue()`, `style_ratio()`, `style_sigfig()`

Examples

```
c(0.111, 12.3) %>% style_number(digits = 1)
c(0.111, 12.3) %>% style_number(digits = c(1, 0))
```

`style_percent` *Style percentages*

Description

Style percentages

Usage

```
style_percent(
  x,
  symbol = FALSE,
  digits = 0,
  big.mark = NULL,
  decimal.mark = NULL,
  ...
)
```

Arguments

`x`	numeric vector of percentages
`symbol`	Logical indicator to include percent symbol in output. Default is `FALSE`.
`digits`	number of digits to round large percentages (i.e. greater than 10%). Smaller percentages are rounded to `digits` + 1 places. Default is `0`
`big.mark`	Character used between every 3 digits to separate hundreds/thousands/millions/etc. Default is `","`, except when `decimal.mark = ","` when the default is a space.
`decimal.mark`	The character to be used to indicate the numeric decimal point. Default is `"."` or `getOption("OutDec")`
`...`	Other arguments passed on to `base::format()`

Value

A character vector of styled percentages

Author(s)

Daniel D. Sjoberg

See Also

See Table Gallery vignette for example

Other style tools: `style_number()`, `style_pvalue()`, `style_ratio()`, `style_sigfig()`

Examples

```
percent_vals <- c(-1, 0, 0.0001, 0.005, 0.01, 0.10, 0.45356, 0.99, 1.45)
style_percent(percent_vals)
style_percent(percent_vals, symbol = TRUE, digits = 1)
```

`style_pvalue` *Style p-values*

Description

Style p-values

Usage

```
style_pvalue(
  x,
  digits = 1,
  prepend_p = FALSE,
  big.mark = NULL,
  decimal.mark = NULL,
  ...
)
```

Arguments

`x`	Numeric vector of p-values.
`digits`	Number of digits large p-values are rounded. Must be 1, 2, or 3. Default is 1.
`prepend_p`	Logical. Should 'p=' be prepended to formatted p-value. Default is `FALSE`
`big.mark`	Character used between every 3 digits to separate hundreds/thousands/millions/etc. Default is `","`, except when `decimal.mark = ","` when the default is a space.
`decimal.mark`	The character to be used to indicate the numeric decimal point. Default is `"."` or `getOption("OutDec")`
`...`	Other arguments passed on to `base::format()`

Value

A character vector of styled p-values

Author(s)

Daniel D. Sjoberg

See Also

See tbl_summary vignette for examples

Other style tools: `style_number()`, `style_percent()`, `style_ratio()`, `style_sigfig()`

Examples

```
pvals <- c(
  1.5, 1, 0.999, 0.5, 0.25, 0.2, 0.197, 0.12, 0.10, 0.0999, 0.06,
  0.03, 0.002, 0.001, 0.00099, 0.0002, 0.00002, -1
)
style_pvalue(pvals)
style_pvalue(pvals, digits = 2, prepend_p = TRUE)
```

`style_ratio` *Style significant figure-like rounding for ratios*

Description

When reporting ratios, such as relative risk or an odds ratio, we'll often want the rounding to be similar on each side of the number 1. For example, if we report an odds ratio of 0.95 with a confidence interval of 0.70 to 1.24, we would want to round to two decimal places for all values. In other words, 2 significant figures for numbers less than 1 and 3 significant figures 1 and larger. `style_ratio()` performs significant figure-like rounding in this manner.

Usage

```
style_ratio(x, digits = 2, big.mark = NULL, decimal.mark = NULL, ...)
```

Arguments

`x`	Numeric vector
`digits`	Integer specifying the number of significant digits to display for numbers below 1. Numbers larger than 1 will be be `digits + 1`. Default is `digits = 2`.
`big.mark`	Character used between every 3 digits to separate hundreds/thousands/millions/etc. Default is `","`, except when `decimal.mark = ","` when the default is a space.
`decimal.mark`	The character to be used to indicate the numeric decimal point. Default is `"."` or `getOption("OutDec")`
`...`	Other arguments passed on to `base::format()`

Value

A character vector of styled ratios

Author(s)

Daniel D. Sjoberg

See Also

Other style tools: `style_number()`, `style_percent()`, `style_pvalue()`, `style_sigfig()`

Examples

```
c(
  0.123, 0.9, 1.1234, 12.345, 101.234, -0.123,
  -0.9, -1.1234, -12.345, -101.234
) %>%
  style_ratio()
```

`style_sigfig` *Style significant figure-like rounding*

Description

Converts a numeric argument into a string that has been rounded to a significant figure-like number. Scientific notation output is avoided, however, and additional significant figures may be displayed for large numbers. For example, if the number of significant digits requested is 2, 123 will be displayed (rather than 120 or 1.2x10^2).

Usage

```
style_sigfig(
  x,
  digits = 2,
  scale = 1,
  big.mark = NULL,
  decimal.mark = NULL,
  ...
)
```

Arguments

`x`	Numeric vector
`digits`	Integer specifying the minimum number of significant digits to display
`scale`	A scaling factor: x will be multiplied by scale before formatting.
`big.mark`	Character used between every 3 digits to separate hundreds/thousands/millions/etc. Default is `","`, except when `decimal.mark = ","` when the default is a space.
`decimal.mark`	The character to be used to indicate the numeric decimal point. Default is `"."` or `getOption("OutDec")`
`...`	Other arguments passed on to `base::format()`

Details

If 2 sig figs are input, the number is rounded to 2 decimal places when `abs(x)` < `1`, 1 decimal place when `abs(x)` >= `1` & `abs(x)` < `10`, and to the nearest integer when `abs(x)` >= `10`.

Value

A character vector of styled numbers

Author(s)

Daniel D. Sjoberg

See Also

Other style tools: `style_number()`, `style_percent()`, `style_pvalue()`, `style_ratio()`

Examples

```
c(0.123, 0.9, 1.1234, 12.345, -0.123, -0.9, -1.1234, -132.345, NA, -0.001) %>%
  style_sigfig()
```

`tbl_butcher` *Reduce size of gtsummary objects*

Description

Some gtsummary objects can become large and the size becomes cumbersome when working with the object. The function removes all elements from a gtsummary object, except those required to print the table. This may result in gtsummary functions that add information or modify the table, such as `add_global_p()`, will no longer execute after the excess elements have been removed (aka butchered). Of note, the majority of `inline_text()` calls will continue to execute properly.

Usage

```
tbl_butcher(x)
```

Arguments

`x`	a gtsummary object

Value

a gtsummary object

Examples

```
tbl_large <-
 trial %>%
 tbl_uvregression(
   y = age,
   method = lm
 )

 tbl_butchered <-
   tbl_large %>%
   tbl_butcher()

 # size comparison
 object.size(tbl_large) %>% format(units = "Mb")
 object.size(tbl_butchered) %>% format(units = "Mb")
```

`tbl_continuous` *Summarize a continuous variable*

Description

[Experimental] Summarize a continuous variable by one or more categorical variables

Usage

```
tbl_continuous(
  data,
  variable,
  include = everything(),
  digits = NULL,
  by = NULL,
  statistic = NULL,
  label = NULL
)
```

Arguments

`data`	A data frame
`variable`	Variable name of the continuous column to be summarized
`include`	variables to include in the summary table. Default is `everything()`
`digits`	List of formulas specifying the number of decimal places to round continuous summary statistics. If not specified, an appropriate number of decimals to round statistics will be guessed based on the the variable's distribution.
`by`	A column name (quoted or unquoted) in `data`. Summary statistics will be calculated separately for each level of the `by` variable (e.g. `by = trt`). If `NULL`, summary statistics are calculated using all observations. To stratify a table by two or more variables, use `tbl_strata()`
`statistic`	List of formulas specifying types of summary statistics to display for each variable. The default is `everything() ~ {median} ({p25},{p75})`
`label`	List of formulas specifying variables labels, e.g. `list(age ~ "Age",stage ~ "Path T Stage")`. If a variable's label is not specified here, the label attribute (`attr(data$age,"label")`) is used. If attribute label is `NULL`, the variable name will be used.

Value

a gtsummary table

Example Output

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_continuous tools: `add_overall()`, `add_p.tbl_continuous()`

Examples

```
# Example 1 ----------------------------------
tbl_continuous_ex1 <-
  tbl_continuous(
    data = trial,
    variable = age,
    by = trt,
    include = grade
  )

# Example 2 ----------------------------------
tbl_continuous_ex2 <-
  tbl_continuous(
    data = trial,
    variable = age,
    include = c(trt, grade)
  )
```

`tbl_cross` *Create a cross table of summary statistics*

Description

The function creates a cross table of two categorical variables.

Usage

```
tbl_cross(
  data,
  row = NULL,
  col = NULL,
  label = NULL,
  statistic = NULL,
  digits = NULL,
  percent = c("none", "column", "row", "cell"),
  margin = c("column", "row"),
  missing = c("ifany", "always", "no"),
  missing_text = "Unknown",
  margin_text = "Total"
)
```

Arguments

`data`	A data frame
`row`	A column name in data= to be used for the rows of cross table.
`col`	A column name in data= to be used for the columns of cross table.
`label`	List of formulas specifying variables labels, e.g. `list(age ~ "Age",stage ~ "Path T Stage")`. If a variable's label is not specified here, the label attribute (`attr(data$age,"label")`) is used. If attribute label is `NULL`, the variable name will be used.

`statistic`	A string with the statistic name in curly brackets to be replaced with the numeric statistic (see glue::glue). The default is `{n}`. If percent argument is `"column"`, `"row"`, or `"cell"`, default is `"{n} ({p}%)"`.
`digits`	Specifies the number of decimal places to round the summary statistics. By default integers are shown to the zero decimal places, and percentages are formatted with `style_percent()`. If you would like to modify either of these, pass a vector of integers indicating the number of decimal places to round the statistics. For example, if the statistic being calculated is `"{n} ({p}%)"` and you want the percent rounded to 2 decimal places use `digits = c(0,2)`. User may also pass a styling function: `digits = style_sigfig`
`percent`	Indicates the type of percentage to return. Must be one of "none", "column", "row", or "cell". Default is "cell" when `{N}` or `{p}` is used in statistic.
`margin`	Indicates which margins to add to the table. Default is `c("row","column")`. Use `margin = NULL` to suppress both row and column margins.
`missing`	Indicates whether to include counts of `NA` values in the table. Allowed values are `"no"` (never display NA values), `"ifany"` (only display if any NA values), and `"always"` (includes NA count row for all variables). Default is `"ifany"`.
`missing_text`	String to display for count of missing observations. Default is `"Unknown"`.
`margin_text`	Text to display for margin totals. Default is `"Total"`

Value

A `tbl_cross` object

Example Output

Author(s)

Karissa Whiting, Daniel D. Sjoberg

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_cross tools: `add_p.tbl_cross()`, `inline_text.tbl_cross()`

Examples

```
# Example 1 ----------------------------------
tbl_cross_ex1 <-
  trial %>%
  tbl_cross(row = trt, col = response)

# Example 2 ----------------------------------
tbl_cross_ex2 <-
  trial %>%
  tbl_cross(row = stage, col = trt, percent = "cell") %>%
  add_p()
```

`tbl_custom_summary` *Create a table of summary statistics using a custom summary function*

Description

[Experimental] The `tbl_custom_summary()` function calculates descriptive statistics for continuous, categorical, and dichotomous variables. This function is similar to `tbl_summary()` but allows you to provide a custom function in charge of computing the statistics (see Details).

Usage

```
tbl_custom_summary(
  data,
  by = NULL,
  label = NULL,
  stat_fns,
  statistic,
  digits = NULL,
  type = NULL,
  value = NULL,
  missing = NULL,
  missing_text = NULL,
  include = everything(),
  overall_row = FALSE,
  overall_row_last = FALSE,
  overall_row_label = NULL
)
```

Arguments

`data`	A data frame
`by`	A column name (quoted or unquoted) in `data`. Summary statistics will be calculated separately for each level of the by variable (e.g. `by = trt`). If `NULL`, summary statistics are calculated using all observations. To stratify a table by two or more variables, use `tbl_strata()`
`label`	List of formulas specifying variables labels, e.g. `list(age ~ "Age", stage ~ "Path T Stage")`. If a variable's label is not specified here, the label attribute (`attr(data$age, "label")`) is used. If attribute label is `NULL`, the variable name will be used.
`stat_fns`	Formula or list of formulas specifying the function to be used to compute the statistics (see below for details and examples). You can also use dedicated helpers such as `continuous_summary()`, `ratio_summary()` or `proportion_summary()`.
`statistic`	List of formulas specifying the `glue::glue()` pattern to display the statistics for each variable. The statistics should be returned by the functions specified in `stat_fns` (see below for details and examples).
`digits`	List of formulas specifying the number of decimal places to round summary statistics. If not specified, `tbl_summary` guesses an appropriate number of decimals to round statistics. When multiple statistics are displayed for a single variable, supply a vector rather than an integer. For example, if the statistic being calculated is `"{mean} ({sd})"` and you want the mean rounded to 1 decimal

	place, and the SD to 2 use `digits = list(age ~ c(1,2))`. User may also pass a styling function: `digits = age ~ style_sigfig`
`type`	List of formulas specifying variable types. Accepted values are `c("continuous","continuous2","c` e.g. `type = list(age ~ "continuous", female ~ "dichotomous")`. If type not specified for a variable, the function will default to an appropriate summary type. See below for details.
`value`	List of formulas specifying the value to display for dichotomous variables. See below for details.
`missing`	Indicates whether to include counts of `NA` values in the table. Allowed values are `"no"` (never display NA values), `"ifany"` (only display if any NA values), and `"always"` (includes NA count row for all variables). Default is `"ifany"`.
`missing_text`	String to display for count of missing observations. Default is `"Unknown"`.
`include`	variables to include in the summary table. Default is `everything()`
`overall_row`	Logical indicator to display an overall row. Default is `FALSE`. Use `add_overall()` to add an overall column.
`overall_row_last`	Logical indicator to display overall row last in table. Default is `FALSE`, which will display overall row first.
`overall_row_label`	String indicating the overall row label. Default is `"Overall"`.

Value

A `tbl_custom_summary` and `tbl_summary` object

Similarities with `tbl_summary()`

Please refer to the help file of `tbl_summary()` regarding the use of select helpers, and arguments `include`, `by`, `type`, `value`, `digits`, `missing` and `missing_text`.

`stat_fns` argument

The `stat_fns` argument specify the custom function(s) to be used for computing the summary statistics. For example, `stat_fns = everything() ~ foo`.

Each function may take the following arguments: `foo(data, full_data, variable, by, type, ...)`

- data= is the input data frame passed to `tbl_custom_summary()`, subset according to the level of by or `variable` if any, excluding `NA` values of the current `variable`
- full_data= is the full input data frame passed to `tbl_custom_summary()`
- variable= is a string indicating the variable to perform the calculation on
- by= is a string indicating the by variable from tbl_custom_summary=, if present
- type= is a string indicating the type of variable (continuous, categorical, ...)
- stat_display= a string indicating the statistic to display (for the `statistic` argument, for that variable)

The user-defined does not need to utilize each of these inputs. It's encouraged the user-defined function accept `...` as each of the arguments *will* be passed to the function, even if not all inputs are utilized by the user's function, e.g. `foo(data, ...)` (see examples).

The user-defined function should return a one row `dplyr::tibble()` with one column per summary statistics (see examples).

statistic argument

The statistic argument specifies the statistics presented in the table. The input is a list of formulas that specify the statistics to report. For example, `statistic = list(age ~ "{mean} ({sd})")`. A statistic name that appears between curly brackets will be replaced with the numeric statistic (see `glue::glue()`). All the statistics indicated in the statistic argument should be returned by the functions defined in the `stat_fns` argument.

When the summary type is `"continuous2"`, pass a vector of statistics. Each element of the vector will result in a separate row in the summary table.

For both categorical and continuous variables, statistics on the number of missing and non-missing observations and their proportions are also available to display.

- `{N_obs}` total number of observations
- `{N_miss}` number of missing observations
- `{N_nonmiss}` number of non-missing observations
- `{p_miss}` percentage of observations missing
- `{p_nonmiss}` percentage of observations not missing

Note that for categorical variables, `{N_obs}`, `{N_miss}` and `{N_nonmiss}` refer to the total number, number missing and number non missing observations in the denominator, not at each level of the categorical variable.

It is recommended to use `modify_footnote()` to properly describe the displayed statistics (see examples).

Caution

The returned table is compatible with all `gtsummary` features applicable to a `tbl_summary` object, like `add_overall()`, `modify_footnote()` or `bold_labels()`.

However, some of them could be inappropriate in such case. In particular, `add_p()` do not take into account the type of displayed statistics and always return the p-value of a comparison test of the current variable according to the by groups, which may be incorrect if the displayed statistics refer to a third variable.

Example Output

Author(s)

Joseph Larmarange

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `modify`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Other tbl_custom_summary tools: `add_overall()`, `continuous_summary()`, `proportion_summary()`, `ratio_summary()`

Examples

```
# Example 1 ----------------------------------
my_stats <- function(data, ...) {
  marker_sum = sum(data$marker, na.rm = TRUE)
  mean_age = mean(data$age, na.rm = TRUE)
  dplyr::tibble(
    marker_sum = marker_sum,
    mean_age = mean_age
  )
}

my_stats(trial)

tbl_custom_summary_ex1 <-
  trial %>%
  tbl_custom_summary(
    include = c("stage", "grade"),
    by = "trt",
    stat_fns = everything() ~ my_stats,
    statistic = everything() ~ "A: {mean_age} - S: {marker_sum}",
    digits = everything() ~ c(1, 0),
    overall_row = TRUE,
    overall_row_label = "All stages & grades"
  ) %>%
  add_overall(last = TRUE) %>%
  modify_footnote(
    update = all_stat_cols() ~ "A: mean age - S: sum of marker"
  ) %>%
  bold_labels()

# Example 2 ----------------------------------
# Use `data[[variable]]` to access the current variable
mean_ci <- function(data, variable, ...) {
  test <- t.test(data[[variable]])
  dplyr::tibble(
    mean = test$estimate,
    conf.low = test$conf.int[1],
    conf.high = test$conf.int[2]
  )
}

tbl_custom_summary_ex2 <-
  trial %>%
  tbl_custom_summary(
    include = c("marker", "ttdeath"),
    by = "trt",
    stat_fns = ~ mean_ci,
    statistic = ~ "{mean} [{conf.low}; {conf.high}]"
  ) %>%
  add_overall(last = TRUE) %>%
  modify_footnote(
    update = all_stat_cols() ~ "mean [95% CI]"
  )

# Example 3 ----------------------------------
# Use `full_data` to access the full datasets
```

```
# Returned statistic can also be a character
diff_to_great_mean <- function(data, full_data, ...) {
  mean <- mean(data$marker, na.rm = TRUE)
  great_mean <- mean(full_data$marker, na.rm = TRUE)
  diff <- mean - great_mean
  dplyr::tibble(
    mean = mean,
    great_mean = great_mean,
    diff = diff,
    level = ifelse(diff > 0, "high", "low")
  )
}

tbl_custom_summary_ex3 <-
  trial %>%
  tbl_custom_summary(
    include = c("grade", "stage"),
    by = "trt",
    stat_fns = ~ diff_to_great_mean,
    statistic = ~ "{mean} ({level}, diff: {diff})",
    overall_row = TRUE
  ) %>%
  bold_labels()
```

`tbl_merge` *Merge two or more gtsummary objects*

Description

Merges two or more `tbl_regression`, `tbl_uvregression`, `tbl_stack`, `tbl_summary`, or `tbl_svysummary` objects and adds appropriate spanning headers.

Usage

```
tbl_merge(tbls, tab_spanner = NULL)
```

Arguments

`tbls`	List of gtsummary objects to merge
`tab_spanner`	Character vector specifying the spanning headers. Must be the same length as `tbls`. The strings are interpreted with `gt::md`. Must be same length as `tbls` argument. Default is `NULL`, and places a default spanning header. If `FALSE`, no header will be placed.

Value

A `tbl_merge` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

tbl_stack

Other tbl_regression tools: add_global_p(), add_q(), bold_italicize_labels_levels, combine_terms(), inline_text.tbl_regression(), modify, tbl_regression(), tbl_split(), tbl_stack(), tbl_strata()

Other tbl_uvregression tools: add_global_p(), add_q(), bold_italicize_labels_levels, inline_text.tbl_uvreg modify, tbl_split(), tbl_stack(), tbl_strata(), tbl_uvregression()

Other tbl_summary tools: add_ci(), add_n.tbl_summary(), add_overall(), add_p.tbl_summary(), add_q(), add_stat_label(), bold_italicize_labels_levels, inline_text.tbl_summary(), inline_text.tbl_survfit(), modify, separate_p_footnotes(), tbl_custom_summary(), tbl_split(), tbl_stack(), tbl_strata(), tbl_summary()

Other tbl_survfit tools: add_n.tbl_survfit(), add_nevent.tbl_survfit(), add_p.tbl_survfit(), modify, tbl_split(), tbl_stack(), tbl_strata(), tbl_survfit()

Other tbl_svysummary tools: add_n.tbl_summary(), add_overall(), add_p.tbl_svysummary(), add_q(), add_stat_label(), modify, separate_p_footnotes(), tbl_split(), tbl_stack(), tbl_strata(), tbl_svysummary()

Examples

```
# Example 1 ----------------------------------
# Side-by-side Regression Models
library(survival)
t1 <-
  glm(response ~ trt + grade + age, trial, family = binomial) %>%
  tbl_regression(exponentiate = TRUE)
t2 <-
  coxph(Surv(ttdeath, death) ~ trt + grade + age, trial) %>%
  tbl_regression(exponentiate = TRUE)
tbl_merge_ex1 <-
  tbl_merge(
    tbls = list(t1, t2),
    tab_spanner = c("**Tumor Response**", "**Time to Death**")
  )

# Example 2 ----------------------------------
# Descriptive statistics alongside univariate regression, with no spanning header
t3 <-
  trial[c("age", "grade", "response")] %>%
  tbl_summary(missing = "no") %>%
  add_n() %>%
  modify_header(stat_0 ~ "**Summary Statistics**")
t4 <-
  tbl_uvregression(
    trial[c("ttdeath", "death", "age", "grade", "response")],
    method = coxph,
    y = Surv(ttdeath, death),
    exponentiate = TRUE,
    hide_n = TRUE
  )
```

```
tbl_merge_ex2 <-
  tbl_merge(tbls = list(t3, t4)) %>%
  modify_spanning_header(everything() ~ NA_character_)
```

`tbl_regression` *Display regression model results in table*

Description

This function takes a regression model object and returns a formatted table that is publication-ready. The function is highly customizable allowing the user to obtain a bespoke summary table of the regression model results. Review the tbl_regression vignette for detailed examples.

Usage

```
tbl_regression(x, ...)

## Default S3 method:
tbl_regression(
  x,
  label = NULL,
  exponentiate = FALSE,
  include = everything(),
  show_single_row = NULL,
  conf.level = NULL,
  intercept = FALSE,
  estimate_fun = NULL,
  pvalue_fun = NULL,
  tidy_fun = NULL,
  add_estimate_to_reference_rows = FALSE,
  conf.int = NULL,
  ...
)
```

Arguments

`x`	Regression model object
`...`	Not used
`label`	List of formulas specifying variables labels, e.g. `list(age ~ "Age",stage ~ "Path T Stage")`
`exponentiate`	Logical indicating whether to exponentiate the coefficient estimates. Default is `FALSE`.
`include`	Variables to include in output. Input may be a vector of quoted variable names, unquoted variable names, or tidyselect select helper functions. Default is `everything()`.
`show_single_row`	By default categorical variables are printed on multiple rows. If a variable is dichotomous (e.g. Yes/No) and you wish to print the regression coefficient on a single row, include the variable name(s) here–quoted and unquoted variable name accepted.

`conf.level`	Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval.
`intercept`	Logical argument indicating whether to include the intercept in the output. Default is `FALSE`
`estimate_fun`	Function to round and format coefficient estimates. Default is style_sigfig when the coefficients are not transformed, and style_ratio when the coefficients have been exponentiated.
`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x,digits = 2)` or equivalently, `purrr::partial(style_pvalue,digits = 2)`).
`tidy_fun`	Option to specify a particular tidier function for the model. Default is to use `broom::tidy`, but if an error occurs then tidying of the model is attempted with `parameters::model_parameters()`, if installed.
`add_estimate_to_reference_rows`	add a reference value. Default is FALSE
`conf.int`	Logical indicating whether or not to include a confidence interval in the output. Defaults to `TRUE`.

Value

A `tbl_regression` object

Methods

The default method for `tbl_regression()` model summary uses `broom::tidy(x)` to perform the initial tidying of the model object. There are, however, a few models that use modifications.

- `"parsnip/workflows"`: If the model was prepared using parsnip/workflows, the original model fit is extracted and the original x= argument is replaced with the model fit. This will typically go unnoticed; however,if you've provided a custom tidier in tidy_fun= the tidier will be applied to the model fit object and not the parsnip/workflows object.
- `"survreg"`: The scale parameter is removed, `broom::tidy(x) %>% dplyr::filter(term != "Log(scale)")`
- `"multinom"`: This multinomial outcome is complex, with one line per covariate per outcome (less the reference group)
- `"gam"`: Uses the internal tidier `tidy_gam()` to print both parametric and smooth terms.
- `"lmerMod"`, `"glmerMod"`, `"glmmTMB"`, `"glmmadmb"`, `"stanreg"`, `"brmsfit"`: These mixed effects models use `broom.mixed::tidy(x,effects = "fixed")`. Specify `tidy_fun = broom.mixed::tidy` to print the random components.

This list is not exhaustive, and care should be taken for each number reported.

Example Output

Author(s)

Daniel D. Sjoberg

See Also

See tbl_regression vignette for detailed examples

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_regression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `combine_terms()`, `inline_text.tbl_regression()`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Examples

```
# Example 1 ----------------------------------
library(survival)
tbl_regression_ex1 <-
  coxph(Surv(ttdeath, death) ~ age + marker, trial) %>%
  tbl_regression(exponentiate = TRUE)

# Example 2 ----------------------------------
tbl_regression_ex2 <-
  glm(response ~ age + grade, trial, family = binomial(link = "logit")) %>%
  tbl_regression(exponentiate = TRUE)

# Example 3 ----------------------------------
suppressMessages(library(lme4))
tbl_regression_ex3 <-
  glmer(am ~ hp + (1 | gear), mtcars, family = binomial) %>%
  tbl_regression(exponentiate = TRUE)
```

`tbl_split` *Split gtsummary table*

Description

[Experimental] The `tbl_split` function splits a single gtsummary table into multiple tables. Updates to the print method are expected.

Usage

```
tbl_split(x, ...)

## S3 method for class 'gtsummary'
tbl_split(x, variables, ...)

## S3 method for class 'tbl_split'
print(x, ...)
```

Arguments

`x`	gtsummary table
`...`	not used
`variables`	variables at which to split the gtsummary table rows (tables will be separated after each of these variables)

Value

`tbl_split` object

See Also

Other tbl_regression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `combine_terms()`, `inline_text.tbl_regression()`, `modify`, `tbl_merge()`, `tbl_regression()`, `tbl_stack()`, `tbl_strata()`

Other tbl_uvregression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `inline_text.tbl_uvreg` `modify`, `tbl_merge()`, `tbl_stack()`, `tbl_strata()`, `tbl_uvregression()`

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_stack()`, `tbl_strata()`, `tbl_summary()`

Other tbl_survfit tools: `add_n.tbl_survfit()`, `add_nevent.tbl_survfit()`, `add_p.tbl_survfit()`, `modify`, `tbl_merge()`, `tbl_stack()`, `tbl_strata()`, `tbl_survfit()`

Other tbl_svysummary tools: `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_svysummary()`, `add_q()`, `add_stat_label()`, `modify`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_stack()`, `tbl_strata()`, `tbl_svysummary()`

Examples

```
tbl <-
  tbl_summary(trial) %>%
  tbl_split(variables = c(marker, grade))
```

`tbl_stack` *Stacks two or more gtsummary objects*

Description

Assists in patching together more complex tables. `tbl_stack()` appends two or more `tbl_regression`, `tbl_summary`, `tbl_svysummary`, or `tbl_merge` objects. Column attributes, including number formatting and column footnotes, are retained from the first passed gtsummary object.

Usage

```
tbl_stack(tbls, group_header = NULL, quiet = NULL)
```

Arguments

`tbls`	List of gtsummary objects
`group_header`	Character vector with table headers where length matches the length of tbls=
`quiet`	Logical indicating whether to print messages in console. Default is `FALSE`

Value

A `tbl_stack` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

tbl_merge

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_strata()`, `tbl_summary()`

Other tbl_svysummary tools: `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_svysummary()`, `add_q()`, `add_stat_label()`, `modify`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_split()`, `tbl_strata()`, `tbl_svysummary()`

Other tbl_regression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `combine_terms()`, `inline_text.tbl_regression()`, `modify`, `tbl_merge()`, `tbl_regression()`, `tbl_split()`, `tbl_strata()`

Other tbl_uvregression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `inline_text.tbl_uvreg` `modify`, `tbl_merge()`, `tbl_split()`, `tbl_strata()`, `tbl_uvregression()`

Other tbl_survfit tools: `add_n.tbl_survfit()`, `add_nevent.tbl_survfit()`, `add_p.tbl_survfit()`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_strata()`, `tbl_survfit()`

Examples

```
# Example 1 ----------------------------------
# stacking two tbl_regression objects
t1 <-
  glm(response ~ trt, trial, family = binomial) %>%
  tbl_regression(
    exponentiate = TRUE,
    label = list(trt ~ "Treatment (unadjusted)")
  )

t2 <-
  glm(response ~ trt + grade + stage + marker, trial, family = binomial) %>%
  tbl_regression(
    include = "trt",
    exponentiate = TRUE,
    label = list(trt ~ "Treatment (adjusted)")
  )

tbl_stack_ex1 <- tbl_stack(list(t1, t2))

# Example 2 ----------------------------------
# stacking two tbl_merge objects
library(survival)
t3 <-
  coxph(Surv(ttdeath, death) ~ trt, trial) %>%
  tbl_regression(
    exponentiate = TRUE,
    label = list(trt ~ "Treatment (unadjusted)")
```

```
  )

t4 <-
  coxph(Surv(ttdeath, death) ~ trt + grade + stage + marker, trial) %>%
  tbl_regression(
    include = "trt",
    exponentiate = TRUE,
    label = list(trt ~ "Treatment (adjusted)")
  )


# first merging, then stacking
row1 <- tbl_merge(list(t1, t3), tab_spanner = c("Tumor Response", "Death"))
row2 <- tbl_merge(list(t2, t4))
tbl_stack_ex2 <-
  tbl_stack(list(row1, row2), group_header = c("Unadjusted Analysis", "Adjusted Analysis"))
```

`tbl_strata` *Stratified gtsummary tables*

Description

[Maturing] Build a stratified gtsummary table. Any gtsummary table that accepts a data frame as its first argument can be stratified.

- In `tbl_strata()`, the stratified or subset data frame is passed to the function in .tbl_fun=, e.g. `purrr::map(data,.tbl_fun)`.
- In `tbl_strata2()`, both the stratified data frame and the strata level are passed to .tbl_fun=, e.g. `purrr::map2(data,strata,.tbl_fun)`

Usage

```
tbl_strata(
  data,
  strata,
  .tbl_fun,
  ...,
  .sep = ", ",
  .combine_with = c("tbl_merge", "tbl_stack"),
  .combine_args = NULL,
  .header = ifelse(.combine_with == "tbl_merge", "**{strata}**", "{strata}"),
  .stack_group_header = NULL,
  .quiet = NULL
)

tbl_strata2(
  data,
  strata,
  .tbl_fun,
  ...,
  .sep = ", ",
```

```
  .combine_with = c("tbl_merge", "tbl_stack"),
  .combine_args = NULL,
  .header = ifelse(.combine_with == "tbl_merge", "**{strata}**", "{strata}"),
  .stack_group_header = NULL,
  .quiet = NULL
)
```

Arguments

`data`	a data frame or survey object
`strata`	character vector or tidy-selector of columns in data to stratify results by
`.tbl_fun`	A function or formula. If a *function*, it is used as is. If a formula, e.g. `~ .x %>% tbl_summary() %>% add_p()`, it is converted to a function. The stratified data frame is passed to this function.
`...`	Additional arguments passed on to the `.tbl_fun` function.
`.sep`	when more than one stratifying variable is passed, this string is used to separate the levels in the spanning header. Default is `", "`
`.combine_with`	One of `c("tbl_merge","tbl_stack")`. Names the function used to combine the stratified tables.
`.combine_args`	named list of arguments that are passed to function specified in .combine_with=
`.header`	String indicating the headers that will be placed. Default is `"**{strata}**"` when `.combine_with = "tbl_merge"` and `"{strata}"` when `.combine_with = "tbl_stack"`. Items placed in curly brackets will be evaluated according to `glue::glue()` syntax. • `strata` stratum levels • `n` N within stratum • `N` Overall N The evaluated value of .header= is also available within `tbl_strata2(.tbl_fun=)`
`.stack_group_header`	DEPRECATED.
`.quiet`	Logical indicating whether to print messages in console. Default is `FALSE`

Tips

- `tbl_summary()`
  - The number of digits continuous variables are rounded to is determined separately within each stratum of the data frame. Set the digits= argument to ensure continuous variables are rounded to the same number of decimal places.
  - If some levels of a categorical variable are unobserved within a stratum, convert the variable to a factor to ensure all levels appear in each stratum's summary table.

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_regression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `combine_terms()`, `inline_text.tbl_regression()`, `modify`, `tbl_merge()`, `tbl_regression()`, `tbl_split()`, `tbl_stack()`

Other tbl_uvregression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `inline_text.tbl_uvreg`
`modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_uvregression()`

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_summary()`

Other tbl_survfit tools: `add_n.tbl_survfit()`, `add_nevent.tbl_survfit()`, `add_p.tbl_survfit()`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_survfit()`

Other tbl_svysummary tools: `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_svysummary()`, `add_q()`, `add_stat_label()`, `modify`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_svysummary()`

Examples

```
# Example 1 ----------------------------------
tbl_strata_ex1 <-
  trial %>%
  select(age, grade, stage, trt) %>%
  mutate(grade = paste("Grade", grade)) %>%
  tbl_strata(
    strata = grade,
    .tbl_fun =
      ~ .x %>%
        tbl_summary(by = trt, missing = "no") %>%
        add_n(),
    .header = "**{strata}**, N = {n}"
  )

# Example 2 ----------------------------------
tbl_strata_ex2 <-
  trial %>%
  select(grade, response) %>%
  mutate(grade = paste("Grade", grade)) %>%
  tbl_strata2(
    strata = grade,
    .tbl_fun =
      ~.x %>%
      tbl_summary(
        label = list(response = .y),
        missing = "no",
        statistic = response ~ "{p}%"
      ) %>%
      add_ci(pattern = "{stat} ({ci})") %>%
     modify_header(stat_0 = "**Rate (95% CI)**") %>%
     modify_footnote(stat_0 = NA),
    .combine_with = "tbl_stack",
    .combine_args = list(group_header = NULL),
    .quiet = TRUE
  ) %>%
  modify_caption("**Response Rate by Grade**")
```

`tbl_summary` *Create a table of summary statistics*

Description

The `tbl_summary` function calculates descriptive statistics for continuous, categorical, and dichotomous variables. Review the tbl_summary vignette for detailed examples.

Usage

```
tbl_summary(
  data,
  by = NULL,
  label = NULL,
  statistic = NULL,
  digits = NULL,
  type = NULL,
  value = NULL,
  missing = NULL,
  missing_text = NULL,
  sort = NULL,
  percent = NULL,
  include = everything()
)
```

Arguments

`data`	A data frame
`by`	A column name (quoted or unquoted) in `data`. Summary statistics will be calculated separately for each level of the by variable (e.g. `by = trt`). If `NULL`, summary statistics are calculated using all observations. To stratify a table by two or more variables, use `tbl_strata()`
`label`	List of formulas specifying variables labels, e.g. `list(age ~ "Age", stage ~ "Path T Stage")`. If a variable's label is not specified here, the label attribute (`attr(data$age, "label")`) is used. If attribute label is `NULL`, the variable name will be used.
`statistic`	List of formulas specifying types of summary statistics to display for each variable. The default is `list(all_continuous() ~ "{median} ({p25}, {p75})", all_categorical() ~ "{n} ({p}%)")`. See below for details.
`digits`	List of formulas specifying the number of decimal places to round summary statistics. If not specified, `tbl_summary` guesses an appropriate number of decimals to round statistics. When multiple statistics are displayed for a single variable, supply a vector rather than an integer. For example, if the statistic being calculated is `"{mean} ({sd})"` and you want the mean rounded to 1 decimal place, and the SD to 2 use `digits = list(age ~ c(1, 2))`. User may also pass a styling function: `digits = age ~ style_sigfig`
`type`	List of formulas specifying variable types. Accepted values are `c("continuous", "continuous2", "` e.g. `type = list(age ~ "continuous", female ~ "dichotomous")`. If type not specified for a variable, the function will default to an appropriate summary type. See below for details.

`value`	List of formulas specifying the value to display for dichotomous variables. See below for details.
`missing`	Indicates whether to include counts of `NA` values in the table. Allowed values are `"no"` (never display NA values), `"ifany"` (only display if any NA values), and `"always"` (includes NA count row for all variables). Default is `"ifany"`.
`missing_text`	String to display for count of missing observations. Default is `"Unknown"`.
`sort`	List of formulas specifying the type of sorting to perform for categorical data. Options are `frequency` where results are sorted in descending order of frequency and `alphanumeric`, e.g. `sort = list(everything() ~ "frequency")`
`percent`	Indicates the type of percentage to return. Must be one of `"column"`, `"row"`, or `"cell"`. Default is `"column"`.
`include`	variables to include in the summary table. Default is `everything()`

Value

A `tbl_summary` object

select helpers

Select helpers from the \tidyselect\ package and \gtsummary\ package are available to modify default behavior for groups of variables. For example, by default continuous variables are reported with the median and IQR. To change all continuous variables to mean and standard deviation use `statistic = list(all_continuous() ~ "{mean} ({sd})")`.

All columns with class logical are displayed as dichotomous variables showing the proportion of events that are `TRUE` on a single row. To show both rows (i.e. a row for `TRUE` and a row for `FALSE`) use `type = list(where(is.logical) ~ "categorical")`.

The select helpers are available for use in any argument that accepts a list of formulas (e.g. `statistic`, `type`, `digits`, `value`, `sort`, etc.)

Read more on the syntax used through the package.

type argument

The `tbl_summary()` function has four summary types:

- `"continuous"` summaries are shown on a *single row*. Most numeric variables default to summary type continuous.
- `"continuous2"` summaries are shown on *2 or more rows*
- `"categorical"` *multi-line* summaries of nominal data. Character variables, factor variables, and numeric variables with fewer than 10 unique levels default to type categorical. To change a numeric variable to continuous that defaulted to categorical, use `type = list(varname ~ "continuous")`
- `"dichotomous"` categorical variables that are displayed on a *single row*, rather than one row per level of the variable. Variables coded as `TRUE`/`FALSE`, `0`/`1`, or `yes`/`no` are assumed to be dichotomous, and the `TRUE`, `1`, and `yes` rows are displayed. Otherwise, the value to display must be specified in the `value` argument, e.g. `value = list(varname ~ "level to show")`

statistic argument

The statistic argument specifies the statistics presented in the table. The input is a list of formulas that specify the statistics to report. For example, `statistic = list(age ~ "{mean} ({sd})")` would report the mean and standard deviation for age; `statistic = list(all_continuous() ~ "{mean} ({sd})")` would report the mean and standard deviation for all continuous variables. A statistic name that appears between curly brackets will be replaced with the numeric statistic (see glue::glue).

For categorical variables the following statistics are available to display.

- `{n}` frequency
- `{N}` denominator, or cohort size
- `{p}` formatted percentage

For continuous variables the following statistics are available to display.

- `{median}` median
- `{mean}` mean
- `{sd}` standard deviation
- `{var}` variance
- `{min}` minimum
- `{max}` maximum
- `{sum}` sum
- {p##} any integer percentile, where ## is an integer from 0 to 100
- `{foo}` any function of the form `foo(x)` is accepted where `x` is a numeric vector

When the summary type is `"continuous2"`, pass a vector of statistics. Each element of the vector will result in a separate row in the summary table.

For both categorical and continuous variables, statistics on the number of missing and non-missing observations and their proportions are available to display.

- `{N_obs}` total number of observations
- `{N_miss}` number of missing observations
- `{N_nonmiss}` number of non-missing observations
- `{p_miss}` percentage of observations missing
- `{p_nonmiss}` percentage of observations not missing

Note that for categorical variables, `{N_obs}`, `{N_miss}` and `{N_nonmiss}` refer to the total number, number missing and number non missing observations in the denominator, not at each level of the categorical variable.

Example Output

Author(s)

Daniel D. Sjoberg

See Also

See tbl_summary vignette for detailed tutorial

See table gallery for additional examples

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_summary tools: `add_ci()`, `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `inline_text.tbl_survfit()`, `modify`, `separate_p_footnotes()`, `tbl_custom_summary()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Examples

```
# Example 1 ----------------------------------
tbl_summary_ex1 <-
  trial %>%
  select(age, grade, response) %>%
  tbl_summary()

# Example 2 ----------------------------------
tbl_summary_ex2 <-
  trial %>%
  select(age, grade, response, trt) %>%
  tbl_summary(
    by = trt,
    label = list(age ~ "Patient Age"),
    statistic = list(all_continuous() ~ "{mean} ({sd})"),
    digits = list(age ~ c(0, 1))
  )

# Example 3 ----------------------------------
# for convenience, you can also pass named lists to any arguments
# that accept formulas (e.g label, digits, etc.)
tbl_summary_ex3 <-
  trial %>%
  select(age, trt) %>%
  tbl_summary(
    by = trt,
    label = list(age = "Patient Age")
  )

# Example 4 ----------------------------------
# multi-line summaries of continuous data with type 'continuous2'
tbl_summary_ex4 <-
  trial %>%
  select(age, marker) %>%
  tbl_summary(
    type = all_continuous() ~ "continuous2",
    statistic = all_continuous() ~ c("{median} ({p25}, {p75})", "{min}, {max}"),
    missing = "no"
  )
```

`tbl_survfit` *Creates table of survival probabilities*

Description

[Maturing] Function takes a `survfit` object as an argument, and provides a formatted summary table of the results

Usage

```
tbl_survfit(x, ...)

## S3 method for class 'list'
tbl_survfit(
  x,
  times = NULL,
  probs = NULL,
  statistic = NULL,
  label = NULL,
  label_header = NULL,
  estimate_fun = NULL,
  missing = NULL,
  conf.level = 0.95,
  reverse = FALSE,
  quiet = NULL,
  ...
)

## S3 method for class 'survfit'
tbl_survfit(x, ...)

## S3 method for class 'data.frame'
tbl_survfit(x, y, include = everything(), ...)
```

Arguments

`x`	a survfit object, list of survfit objects, or a data frame. If a data frame is passed, a list of survfit objects is constructed using each variable as a stratifying variable.
`...`	For `tbl_survfit.data.frame()` and `tbl_survfit.survfit()` the arguments are passed to `tbl_survfit.list()`. They are not used when `tbl_survfit.list()` is called directly.
`times`	numeric vector of times for which to return survival probabilities.
`probs`	numeric vector of probabilities with values in (0,1) specifying the survival quantiles to return
`statistic`	string defining the statistics to present in the table. Default is `"{estimate} ({conf.low},{conf.high})"`
`label`	List of formulas specifying variables labels, e.g. `list(age ~ "Age, yrs", stage ~ "Path T Stage")`, or a string for a single variable table.

`label_header`	string specifying column labels above statistics. Default is `"{prob} Percentile"` for survival percentiles, and `"Time {time}"` for n-year survival estimates
`estimate_fun`	function to format the Kaplan-Meier estimates. Default is `style_percent()` for survival probabilities and style_sigfig for survival times
`missing`	text to fill when estimate is not estimable. Default is `"--"`
`conf.level`	Confidence level for confidence intervals. Default is 0.95
`reverse`	Flip the probability reported, i.e. `1 -estimate`. Default is `FALSE`. Does not apply to survival quantile requests
`quiet`	Logical indicating whether to print messages in console. Default is `FALSE`
`y`	outcome call, e.g. `y = Surv(ttdeath,death)`
`include`	Variable to include as stratifying variables.

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_survfit tools: `add_n.tbl_survfit()`, `add_nevent.tbl_survfit()`, `add_p.tbl_survfit()`, `modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Examples

```
library(survival)

# Example 1 ----------------------------------
# Pass single survfit() object
tbl_survfit_ex1 <- tbl_survfit(
  survfit(Surv(ttdeath, death) ~ trt, trial),
  times = c(12, 24),
  label_header = "**{time} Month**"
)

# Example 2 ----------------------------------
# Pass a data frame
tbl_survfit_ex2 <- tbl_survfit(
  trial,
  y = Surv(ttdeath, death),
  include = c(trt, grade),
  probs = 0.5,
  label_header = "**Median Survival**"
)

# Example 3 ----------------------------------
# Pass a list of survfit() objects
tbl_survfit_ex3 <-
  list(
    survfit(Surv(ttdeath, death) ~ 1, trial),
```

```
    survfit(Surv(ttdeath, death) ~ trt, trial)
  ) %>%
  tbl_survfit(times = c(12, 24))

# Example 4 Competing Events Example ---------
# adding a competing event for death (cancer vs other causes)
set.seed(1123)
library(dplyr, warn.conflicts = FALSE, quietly = TRUE)
trial2 <- trial %>%
  mutate(
    death_cr = case_when(
      death == 0 ~ "censor",
      runif(n()) < 0.5 ~ "death from cancer",
      TRUE ~ "death other causes"
    ) %>% factor()
  )

survfit_cr_ex4 <-
  survfit(Surv(ttdeath, death_cr) ~ grade, data = trial2) %>%
  tbl_survfit(times = c(12, 24), label = "Tumor Grade")
```

`tbl_svysummary` *Create a table of summary statistics from a survey object*

Description

The `tbl_svysummary` function calculates descriptive statistics for continuous, categorical, and dichotomous variables taking into account survey weights and design. It is similar to `tbl_summary()`.

Usage

```
tbl_svysummary(
  data,
  by = NULL,
  label = NULL,
  statistic = NULL,
  digits = NULL,
  type = NULL,
  value = NULL,
  missing = NULL,
  missing_text = NULL,
  sort = NULL,
  percent = NULL,
  include = everything()
)
```

Arguments

`data`	A survey object created with created with `survey::svydesign()`
`by`	A column name (quoted or unquoted) in `data`. Summary statistics will be calculated separately for each level of the `by` variable (e.g. `by = trt`). If `NULL`, summary statistics are calculated using all observations. To stratify a table by two or more variables, use `tbl_strata()`

`label`	List of formulas specifying variables labels, e.g. `list(age ~ "Age",stage ~ "Path T Stage")`. If a variable's label is not specified here, the label attribute (`attr(data$age,"label")`) is used. If attribute label is `NULL`, the variable name will be used.
`statistic`	List of formulas specifying types of summary statistics to display for each variable. The default is `list(all_continuous() ~ "{median} ({p25},{p75})",all_categorical() ~ "{n} ({p}%)")`. See below for details.
`digits`	List of formulas specifying the number of decimal places to round summary statistics. If not specified, `tbl_summary` guesses an appropriate number of decimals to round statistics. When multiple statistics are displayed for a single variable, supply a vector rather than an integer. For example, if the statistic being calculated is `"{mean} ({sd})"` and you want the mean rounded to 1 decimal place, and the SD to 2 use `digits = list(age ~ c(1,2))`. User may also pass a styling function: `digits = age ~ style_sigfig`
`type`	List of formulas specifying variable types. Accepted values are `c("continuous","continuous2","` e.g. `type = list(age ~ "continuous",female ~ "dichotomous")`. If type not specified for a variable, the function will default to an appropriate summary type. See below for details.
`value`	List of formulas specifying the value to display for dichotomous variables. See below for details.
`missing`	Indicates whether to include counts of `NA` values in the table. Allowed values are `"no"` (never display NA values), `"ifany"` (only display if any NA values), and `"always"` (includes NA count row for all variables). Default is `"ifany"`.
`missing_text`	String to display for count of missing observations. Default is `"Unknown"`.
`sort`	List of formulas specifying the type of sorting to perform for categorical data. Options are `frequency` where results are sorted in descending order of frequency and `alphanumeric`, e.g. `sort = list(everything() ~ "frequency")`
`percent`	Indicates the type of percentage to return. Must be one of `"column"`, `"row"`, or `"cell"`. Default is `"column"`.
`include`	variables to include in the summary table. Default is `everything()`

Value

A `tbl_svysummary` object

statistic argument

The statistic argument specifies the statistics presented in the table. The input is a list of formulas that specify the statistics to report. For example, `statistic = list(age ~ "{mean} ({sd})")` would report the mean and standard deviation for age; `statistic = list(all_continuous() ~ "{mean} ({sd})")` would report the mean and standard deviation for all continuous variables. A statistic name that appears between curly brackets will be replaced with the numeric statistic (see glue::glue).

For categorical variables the following statistics are available to display.

- `{n}` frequency
- `{N}` denominator, or cohort size
- `{p}` formatted percentage
- `{n_unweighted}` unweighted frequency

- `{N_unweighted}` unweighted denominator
- `{p_unweighted}` unweighted formatted percentage

For continuous variables the following statistics are available to display.

- `{median}` median
- `{mean}` mean
- `{sd}` standard deviation
- `{var}` variance
- `{min}` minimum
- `{max}` maximum
- {p##} any integer percentile, where ## is an integer from 0 to 100
- `{sum}` sum

Unlike `tbl_summary()`, it is not possible to pass a custom function.

For both categorical and continuous variables, statistics on the number of missing and non-missing observations and their proportions are available to display.

- `{N_obs}` total number of observations
- `{N_miss}` number of missing observations
- `{N_nonmiss}` number of non-missing observations
- `{p_miss}` percentage of observations missing
- `{p_nonmiss}` percentage of observations not missing
- `{N_obs_unweighted}` unweighted total number of observations
- `{N_miss_unweighted}` unweighted number of missing observations
- `{N_nonmiss_unweighted}` unweighted number of non-missing observations
- `{p_miss_unweighted}` unweighted percentage of observations missing
- `{p_nonmiss_unweighted}` unweighted percentage of observations not missing

Note that for categorical variables, `{N_obs}`, `{N_miss}` and `{N_nonmiss}` refer to the total number, number missing and number non missing observations in the denominator, not at each level of the categorical variable.

Example Output

type argument

The `tbl_summary()` function has four summary types:

- `"continuous"` summaries are shown on a *single row*. Most numeric variables default to summary type continuous.
- `"continuous2"` summaries are shown on *2 or more rows*
- `"categorical"` *multi-line* summaries of nominal data. Character variables, factor variables, and numeric variables with fewer than 10 unique levels default to type categorical. To change a numeric variable to continuous that defaulted to categorical, use `type = list(varname ~ "continuous")`
- `"dichotomous"` categorical variables that are displayed on a *single row*, rather than one row per level of the variable. Variables coded as `TRUE`/`FALSE`, `0`/`1`, or `yes`/`no` are assumed to be dichotomous, and the `TRUE`, `1`, and `yes` rows are displayed. Otherwise, the value to display must be specified in the `value` argument, e.g. `value = list(varname ~ "level to show")`

select helpers

Select helpers from the \tidyselect\ package and \gtsummary\ package are available to modify default behavior for groups of variables. For example, by default continuous variables are reported with the median and IQR. To change all continuous variables to mean and standard deviation use `statistic = list(all_continuous() ~ "{mean} ({sd})")`.

All columns with class logical are displayed as dichotomous variables showing the proportion of events that are `TRUE` on a single row. To show both rows (i.e. a row for `TRUE` and a row for `FALSE`) use `type = list(where(is.logical) ~ "categorical")`.

The select helpers are available for use in any argument that accepts a list of formulas (e.g. `statistic`, `type`, `digits`, `value`, `sort`, etc.)

Read more on the syntax used through the package.

Author(s)

Joseph Larmarange

See Also

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_svysummary tools: `add_n.tbl_summary()`, `add_overall()`, `add_p.tbl_svysummary()`, `add_q()`, `add_stat_label()`, `modify`, `separate_p_footnotes()`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Examples

```
# A simple weighted dataset
tbl_svysummary_ex1 <-
  survey::svydesign(~1, data = as.data.frame(Titanic), weights = ~Freq) %>%
  tbl_svysummary(by = Survived, percent = "row")

# Example 2 ----------------------------------
# A dataset with a complex design
data(api, package = "survey")
tbl_svysummary_ex2 <-
  survey::svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc) %>%
  tbl_svysummary(by = "both", include = c(cname, api00, api99, both))
```

`tbl_uvregression` *Display univariate regression model results in table*

Description

This function estimates univariate regression models and returns them in a publication-ready table. It can create univariate regression models holding either a covariate or outcome constant.

For models holding outcome constant, the function takes as arguments a data frame, the type of regression model, and the outcome variable y=. Each column in the data frame is regressed on the specified outcome. The `tbl_uvregression` function arguments are similar to the tbl_regression arguments. Review the tbl_uvregression vignette for detailed examples.

You may alternatively hold a single covariate constant. For this, pass a data frame, the type of regression model, and a single covariate in the x= argument. Each column of the data frame will serve as the outcome in a univariate regression model. Take care using the `x` argument that each of the columns in the data frame are appropriate for the same type of model, e.g. they are all continuous variables appropriate for lm, or dichotomous variables appropriate for logistic regression with glm.

Usage

```
tbl_uvregression(
  data,
  method,
  y = NULL,
  x = NULL,
  method.args = NULL,
  exponentiate = FALSE,
  label = NULL,
  include = everything(),
  tidy_fun = NULL,
  hide_n = FALSE,
  show_single_row = NULL,
  conf.level = NULL,
  estimate_fun = NULL,
  pvalue_fun = NULL,
  formula = "{y} ~ {x}",
  add_estimate_to_reference_rows = NULL,
  conf.int = NULL,
  ...
)
```

Arguments

`data`	Data frame to be used in univariate regression modeling. Data frame includes the outcome variable(s) and the independent variables. Survey design objects are also accepted.
`method`	Regression method (e.g. lm, glm, survival::coxph, `survey::svyglm`, and more).
`y`	Model outcome (e.g. `y = recurrence` or `y = Surv(time,recur)`). All other column in `data` will be regressed on `y`. Specify one and only one of `y` or `x`
`x`	Model covariate (e.g. `x = trt`). All other columns in `data` will serve as the outcome in a regression model with `x` as a covariate. Output table is best when `x` is a continuous or dichotomous variable displayed on a single row. Specify one and only one of `y` or `x`
`method.args`	List of additional arguments passed on to the regression function defined by `method`.
`exponentiate`	Logical indicating whether to exponentiate the coefficient estimates. Default is `FALSE`.
`label`	List of formulas specifying variables labels, e.g. `list(age ~ "Age",stage ~ "Path T Stage")`
`include`	Variables to include in output. Input may be a vector of quoted variable names, unquoted variable names, or tidyselect select helper functions. Default is `everything()`.

`tidy_fun`	Option to specify a particular tidier function for the model. Default is to use `broom::tidy`, but if an error occurs then tidying of the model is attempted with `parameters::model_parameters()`, if installed.
`hide_n`	Hide N column. Default is `FALSE`
`show_single_row`	By default categorical variables are printed on multiple rows. If a variable is dichotomous (e.g. Yes/No) and you wish to print the regression coefficient on a single row, include the variable name(s) here–quoted and unquoted variable name accepted.
`conf.level`	Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval.
`estimate_fun`	Function to round and format coefficient estimates. Default is style_sigfig when the coefficients are not transformed, and style_ratio when the coefficients have been exponentiated.
`pvalue_fun`	Function to round and format p-values. Default is style_pvalue. The function must have a numeric vector input (the numeric, exact p-value), and return a string that is the rounded/formatted p-value (e.g. `pvalue_fun = function(x) style_pvalue(x, digits = 2)` or equivalently, `purrr::partial(style_pvalue, digits = 2)`).
`formula`	String of the model formula. Uses glue::glue syntax. Default is `"{y} ~ {x}"`, where `{y}` is the dependent variable, and `{x}` represents a single covariate. For a random intercept model, the formula may be `formula = "{y} ~ {x} + (1 | gear)"`.
`add_estimate_to_reference_rows`	add a reference value. Default is FALSE
`conf.int`	Logical indicating whether or not to include a confidence interval in the output. Defaults to `TRUE`.
`...`	Not used

Value

A `tbl_uvregression` object

Example Output

Methods

The default method for `tbl_regression()` model summary uses `broom::tidy(x)` to perform the initial tidying of the model object. There are, however, a few models that use modifications.

- `"parsnip/workflows"`: If the model was prepared using parsnip/workflows, the original model fit is extracted and the original x= argument is replaced with the model fit. This will typically go unnoticed; however,if you've provided a custom tidier in tidy_fun= the tidier will be applied to the model fit object and not the parsnip/workflows object.
- `"survreg"`: The scale parameter is removed, `broom::tidy(x) %>% dplyr::filter(term != "Log(scale)")`
- `"multinom"`: This multinomial outcome is complex, with one line per covariate per outcome (less the reference group)

- `"gam"`: Uses the internal tidier `tidy_gam()` to print both parametric and smooth terms.
- `"lmerMod"`, `"glmerMod"`, `"glmmTMB"`, `"glmmadmb"`, `"stanreg"`, `"brmsfit"`: These mixed effects models use `broom.mixed::tidy(x,effects = "fixed")`. Specify `tidy_fun = broom.mixed::tidy` to print the random components.

This list is not exhaustive, and care should be taken for each number reported.

Author(s)

Daniel D. Sjoberg

See Also

See tbl_regression vignette for detailed examples

Review list, formula, and selector syntax used throughout gtsummary

Other tbl_uvregression tools: `add_global_p()`, `add_q()`, `bold_italicize_labels_levels`, `inline_text.tbl_uvreg`
`modify`, `tbl_merge()`, `tbl_split()`, `tbl_stack()`, `tbl_strata()`

Examples

```
# Example 1 ----------------------------------
tbl_uv_ex1 <-
  tbl_uvregression(
    trial[c("response", "age", "grade")],
    method = glm,
    y = response,
    method.args = list(family = binomial),
    exponentiate = TRUE
  )

# Example 2 ----------------------------------
# rounding pvalues to 2 decimal places
library(survival)
tbl_uv_ex2 <-
  tbl_uvregression(
    trial[c("ttdeath", "death", "age", "grade", "response")],
    method = coxph,
    y = Surv(ttdeath, death),
    exponentiate = TRUE,
    pvalue_fun = function(x) style_pvalue(x, digits = 2)
  )
```

`theme_gtsummary` *Available gtsummary themes*

Description

[Maturing] The following themes are available to use within the gtsummary package. Print theme elements with `theme_gtsummary_journal(set_theme = FALSE) %>% print()`. Review the themes vignette for details.

Usage

```
theme_gtsummary_journal(
  journal = c("jama", "lancet", "nejm", "qjecon"),
  set_theme = TRUE
)

theme_gtsummary_compact(set_theme = TRUE, font_size = NULL)

theme_gtsummary_printer(
  print_engine = c("gt", "kable", "kable_extra", "flextable", "huxtable", "tibble"),
  set_theme = TRUE
)

theme_gtsummary_language(
  language = c("de", "en", "es", "fr", "gu", "hi", "is", "ja", "kr", "mr", "pt", "se",
    "zh-cn", "zh-tw"),
  decimal.mark = NULL,
  big.mark = NULL,
  iqr.sep = NULL,
  ci.sep = NULL,
  set_theme = TRUE
)

theme_gtsummary_continuous2(
  statistic = "{median} ({p25, {p75})",
  set_theme = TRUE
)

theme_gtsummary_mean_sd(set_theme = TRUE)

theme_gtsummary_eda(set_theme = TRUE)
```

Arguments

`journal`	String indicating the journal theme to follow. One of `c("jama","lancet","nejm","qjecon")`. Details below.
`set_theme`	Logical indicating whether to set the theme. Default is `TRUE`. When `FALSE` the named list of theme elements is returned invisibly
`font_size`	Numeric font size for compact theme. Default is 13 for gt tables, and 8 for all other output types
`print_engine`	String indicating the print method. Must be one of `"gt"`, `"kable"`, `"kable_extra"`, `"flextable"`, `"tibble"`
`language`	String indicating language. Must be one of `"de"` (German), `"en"` (English), `"es"` (Spanish), `"fr"` (French), `"gu"` (Gujarati), `"hi"` (Hindi), `"is"` (Icelandic),`"ja"` (Japanese), `"kr"` (Korean), `"mr"` (Marathi), `"pt"` (Portuguese), `"se"` (Swedish), `"zh-c,n"` (Chinese Simplified), `"zh-tw"` (Chinese Traditional) If a language is missing a translation for a word or phrase, please feel free to reach out on GitHub with the translated text!
`decimal.mark`	The character to be used to indicate the numeric decimal point. Default is `"."` or `getOption("OutDec")`

`big.mark`	Character used between every 3 digits to separate hundreds/thousands/millions/etc. Default is `","`, except when `decimal.mark = ","` when the default is a space.
`iqr.sep`	string indicating separator for the default IQR in `tbl_summary()`. If decimal.mark= is NULL, iqr.sep= is `","`. The comma separator, however, can look odd when `decimal.mark = ","`. In this case the argument will default to an en dash
`ci.sep`	string indicating separator for confidence intervals. If decimal.mark= is NULL, ci.sep= is `","`. The comma separator, however, can look odd when `decimal.mark = ","`. In this case the argument will default to an en dash
`statistic`	Default statistic continuous variables

Themes

- `theme_gtsummary_journal(journal=)`
  - `"jama"` *The Journal of the American Medical Association*
    - Round large p-values to 2 decimal places; separate confidence intervals with `"ll to ul"`.
    - `tbl_summary()` Doesn't show percent symbol; use em-dash to separate IQR; run `add_stat_label()`
    - `tbl_regression()`/`tbl_uvregression()` show coefficient and CI in same column
  - `"lancet"` *The Lancet*
    - Use mid-point as decimal separator; round large p-values to 2 decimal places; separate confidence intervals with `"ll to ul"`.
    - `tbl_summary()` Doesn't show percent symbol; use em-dash to separate IQR
  - `"nejm"` *The New England Journal of Medicine*
    - Round large p-values to 2 decimal places; separate confidence intervals with `"ll to ul"`.
    - `tbl_summary()` Doesn't show percent symbol; use em-dash to separate IQR
  - `"qjecon"` *The Quarterly Journal of Economics* **Under Development**
    - `tbl_summary()` all percentages rounded to one decimal place
    - `tbl_regression()`/`tbl_uvregression()` add significance stars with `add_significance_stars()`; hides CI and p-value from output
- `theme_gtsummary_compact()`
  - tables printed with gt, flextable, kableExtra, or huxtable will be compact with smaller font size and reduced cell padding
- `theme_gtsummary_printer(print_engine=)`
  - Use this theme to permanently change the default printer.
- `theme_gtsummary_continuous2()`
  - Set all continuous variables to summary type `"continuous2"` by default
- `theme_gtsummary_mean_sd()`
  - Set default summary statistics to mean and standard deviation in `tbl_summary()`
  - Set default continuous tests in `add_p()` to t-test and ANOVA
- `theme_gtsummary_eda()`
  - Set all continuous variables to summary type `"continuous2"` by default
  - In `tbl_summary()` show the median, mean, IQR, SD, and Range by default

Use `reset_gtsummary_theme()` to restore the default settings

Review the themes vignette to create your own themes.

Example Output

See Also

Themes vignette

`set_gtsummary_theme()`, `reset_gtsummary_theme()`

Examples

```
# Setting JAMA theme for gtsummary
theme_gtsummary_journal("jama")
# Themes can be combined by including more than one
theme_gtsummary_compact()

set_gtsummary_theme_ex1 <-
  trial %>%
  select(age, grade, trt) %>%
  tbl_summary(by = trt) %>%
  as_gt()

# reset gtsummary themes
reset_gtsummary_theme()
```

`trial` *Results from a simulated study of two chemotherapy agents*

Description

A dataset containing the baseline characteristics of 200 patients who received Drug A or Drug B. Dataset also contains the outcome of tumor response to the treatment.

Usage

```
trial
```

Format

A data frame with 200 rows–one row per patient

trt Chemotherapy Treatment

age Age

marker Marker Level (ng/mL)

stage T Stage

grade Grade

response Tumor Response

death Patient Died

ttdeath Months to Death/Censor

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