# Package 'gtsummary'

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**Title** Presentation-Ready Data Summary and Analytic Result Tables

**Version** 1.4.0

**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, http://www.danieldsjoberg.com/gtsummary/

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

**Depends** R (>= 3.4)

**Imports** broom (>= 0.7.6), broom.helpers (>= 1.3.0), cli (>= 2.3.0), dplyr (>= 1.0.3), forcats (>= 0.5.0), glue (>= 1.4.1), gt (>= 0.2.2), knitr (>= 1.29), lifecycle (>= 0.2.0), purrr (>= 0.3.4), rlang (>= 0.4.10), stringr (>= 1.4.0), survival, tibble (>= 3.0.3), tidyr (>= 1.1.1)

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GGally (>= 2.1.0),
Hmisc,
huxtable (>= 5.0.0),
kableExtra,
lme4,
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mice,
nnet,
officer,
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`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"` 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

### 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 `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

## 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

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

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

## Examples

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

```
}

# Example 2 ---------------------------------
if (requireNamespace("car")) {
  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` *Adds column with N to gtsummary table*

---

## Description

Adds column with N to gtsummary table

## Usage

```
add_n(x, ...)
```

## Arguments

| | |
|---|---|
| `x` | Object created from a gtsummary function |
| `...` | Additional arguments passed to other methods. |

## Author(s)

Daniel D. Sjoberg

## See Also

`add_n.tbl_summary()`, `add_n.tbl_svysummary()`, `add_n.tbl_survfit()`, add_n.tbl_regression, add_n.tbl_uvregression

---

`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:<br>• `"{N}"` total number of observations,<br>• `"{n}"` number of non-missing observations,<br>• `"{n_miss}"` number of missing observations,<br>• `"{p}"` percent non-missing data,<br>• `"{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

Other tbl_summary tools: 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_merge(), tbl_stack(), tbl_summary()

Other tbl_svysummary tools: add_overall(), add_p.tbl_svysummary(), add_q(), add_stat_label(), modify, tbl_merge(), tbl_stack(), 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

**[Experimental]** 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

Other tbl_survfit tools: add_nevent.tbl_survfit(), add_p.tbl_survfit(), modify, tbl_merge(), tbl_stack(), 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 *Add number of events to a regression table*

---

## Description

Adds a column of the number of events to tables created with tbl_regression or tbl_uvregression. Supported model types are among GLMs with binomial distribution family (e.g. stats::glm, `lme4::glmer`, and `geepack::geeglm`) and Cox Proportion Hazards regression models (survival::coxph).

## Usage

```
add_nevent(x, ...)
```

## Arguments

| | |
|---|---|
| `x` | `tbl_regression` or `tbl_uvregression` object |
| `...` | Additional arguments passed to or from other methods. |

## Author(s)

Daniel D. Sjoberg

## See Also

add_nevent.tbl_regression, add_nevent.tbl_uvregression, add_nevent.tbl_survfit

---

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

---

## Description

**[Experimental]** 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_stack(), 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` or `tbl_svysummary`.

## Usage

```
add_overall(x, last, col_label)

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

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

## Arguments

| | |
|---|---|
| `x` | Object with class `tbl_summary` from the tbl_summary function or object with class `tbl_svysummary` from the tbl_svysummary function. |
| `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}"` |

## Value

A `tbl_summary` object or a `tbl_svysummary` object

## Example Output

## Author(s)

Daniel D. Sjoberg

## See Also

Other tbl_summary tools: 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, tbl_merge(), tbl_stack(), tbl_summary()

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

## Examples

```
tbl_overall_ex <-
  trial[c("age", "grade", "trt")] %>%
  tbl_summary(by = trt) %>%
  add_overall()
```

---

# add_p *Adds p-values to gtsummary table*

---

## Description

Adds p-values to gtsummary table

## Usage

```
add_p(x, ...)
```

## Arguments

| | |
|---|---|
| x | Object created from a gtsummary function |
| ... | Additional arguments passed to other methods. |

## Author(s)

Daniel D. Sjoberg

## See Also

add_p.tbl_summary, add_p.tbl_cross, add_p.tbl_svysummary, add_p.tbl_survfit

`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, ...)
```

## 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. |
| `...` | 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.<br>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

Other tbl_summary tools: add_n.tbl_summary(), add_overall(), add_q(), add_stat_label(), bold_italicize_labels_levels, inline_text.tbl_summary(), inline_text.tbl_survfit(), modify, tbl_merge(), tbl_stack(), 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

**[Experimental]** 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_stack(), 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<br>• `"svy.t.test"` for a t-test adapted to complex survey samples (cf. `survey::svyttest`),<br>• `"svy.wilcox.test"` for a Wilcoxon rank-sum test for complex survey samples (cf. `survey::svyranktest`),<br>• `"svy.kruskal.test"` for a Kruskal-Wallis rank-sum test for complex survey samples (cf. `survey::svyranktest`),<br>• `"svy.vanderwaerden.test"` for a van der Waerden's normal-scores test for complex survey samples (cf. `survey::svyranktest`),<br>• `"svy.median.test"` for a Mood's test for the median for complex survey samples (cf. `survey::svyranktest`),<br>• `"svy.chisq.test"` for a Chi-squared test with Rao & Scott's second-order correction (cf. `survey::svychisq`),<br>• `"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`, `tbl_merge()`, `tbl_stack()`, `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_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, tbl_merge(), tbl_stack(), tbl_summary()

Other tbl_svysummary tools: add_n.tbl_summary(), add_overall(), add_p.tbl_svysummary(), add_stat_label(), modify, tbl_merge(), tbl_stack(), 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_stack()

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

## Examples

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

# Example 2 ----------------------------------
if (requireNamespace("car")) {
  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` or `tbl_svysummary` object.

## Usage

```
add_stat(
  x,
  fns,
  location = NULL,
  fmt_fun = NULL,
  header = NULL,
  footnote = NULL,
  new_col_name = NULL
)
```

## Arguments

| | |
|---|---|
| `x` | `tbl_summary` or `tbl_svysummary` 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. |
| `fmt_fun` | DEPRECATED. |
| `header` | DEPRECATED. |
| `footnote` | DEPRECATED. |
| `new_col_name` | 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 from `tbl_summary()`/`tbl_svysummary()`.

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
    - 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()`.

## Example Output

## 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

Other tbl_summary tools: 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, tbl_merge(), tbl_stack(), tbl_summary()

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

**[Experimental]** 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

## Examples

```
# Example 1 ----------------------------------
if (requireNamespace("car")) {
  add_vif_ex1 <-
    lm(age ~ grade + marker, trial) %>%
    tbl_regression() %>%
    add_vif()
}

# Example 2 ----------------------------------
if (requireNamespace("car")) {
  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. Default is TRUE |

## 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. 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,
  omit = 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. |
| omit | 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 = 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. Default is TRUE |

## 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::align()` to set column alignment
4. `huxtable::set_left_padding()` to indent variable levels
5. `huxtable::add_footnote()` to add table footnotes and source notes
6. `huxtable::set_bold()` to bold cells
7. `huxtable::set_italic()` to italicize cells
8. `huxtable::set_na_string()` to use an em-dash for missing numbers

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 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 knitr::kable.

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, ...)
```

## 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 |
| `...` | 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. A user can use this function if they wish to add customized formatting available via knitr::kable and kableExtra. Note that gtsummary uses the standard markdown ** to bold headers, and they may need to be changed manually with kableExtra output.

## Usage

```
as_kable_extra(
  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. Default is TRUE |
| `...` | Additional arguments passed to knitr::kable |

## Value

A kableExtra object

### 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

```
tbl <-
  trial %>%
  tbl_summary(by = trt) %>%
  as_kable_extra()
```

---

## 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,
  ...
)
```

### 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 |
| ... | 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_n.tbl_summary(), add_overall(), add_p.tbl_summary(), add_q(), add_stat_label(), inline_text.tbl_summary(), inline_text.tbl_survfit(), modify, tbl_merge(), tbl_stack(), tbl_summary()

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

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

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

## 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"
  )
```

---

# custom_tidiers *Collection of custom tidiers*

---

## Description

**[Experimental]** 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
)

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;<br>• pool_and_tidy_mice(): mice::tidy(x,...)<br>• tidy_standardize(): effectsize::standardize_parameters(x,...)<br>• tidy_bootstrap(): parameters::bootstrap_parameters(x,...) |
| quiet | Logical indicating whether to print messages in console. Default is FALSE |
| 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.
- 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)

if (requireNamespace("effectsize")) {
  tidy_standardize_ex1 <-
    tbl_merge(
      list(tbl_stnd, tbl),
```

```
      tab_spanner = c("**Standardized Model**", "**Original Model**")
    )
}

# Example 2 ----------------------------------
# use "posthoc" method for coef calculation
if (requireNamespace("parameters")) {
  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)
if (requireNamespace("mice")) {
  pool_and_tidy_mice_ex3 <-
    suppressWarnings(mice::mice(trial, m = 2)) %>%
    with(lm(age ~ marker + grade)) %>%
    tbl_regression()
} # mice method called that uses `pool_and_tidy_mice()` as tidier
```

---

`inline_text` *Report statistics from gtsummary tables inline*

---

## Description

Report statistics from gtsummary tables inline

## Usage

```
inline_text(x, ...)
```

## Arguments

| | |
|---|---|
| `x` | Object created from a gtsummary function |
| `...` | Additional arguments passed to other methods. |

## Value

A string reporting results from a gtsummary table

## Author(s)

Daniel D. Sjoberg

## See Also

inline_text.tbl_summary, inline_text.tbl_svysummary, inline_text.tbl_regression, inline_text.tbl_uvregression, inline_text.tbl_survfit, inline_text.tbl_cross, inline_text.gtsummary

## 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

**[Experimental]** 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_stack()

## 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_n.tbl_summary()`, `add_overall()`, `add_p.tbl_summary()`, `add_q()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_survfit()`, `modify`, `tbl_merge()`, `tbl_stack()`, `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

**[Experimental]** 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_n.tbl_summary(), add_overall(), add_p.tbl_summary(), add_q(), add_stat_label(), bold_italicize_labels_levels, inline_text.tbl_summary(), modify, tbl_merge(), tbl_stack(), 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_stack()`, `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, quiet = NULL)
```

## Arguments

| | |
|---|---|
| x | a gtsummary object |
| update | list of formulas or a single formula specifying the updated column header, footnote, or spanning header. The LHS specifies the column(s) to be updated, and the RHS is the updated text. 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` |
| ... | Specify a column and updated column label, e.g. `modify_header(p.value = "Model P-values")`. This is provided as an alternative to the update= argument. They accomplish the same goal of updating column headers. |
| 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 |

## 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=)`, available in gt version >0.2.2
- `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_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(`
`tbl_merge()`, `tbl_stack()`, `tbl_summary()`

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

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

Other tbl_survfit tools: `add_n.tbl_survfit()`, `add_nevent.tbl_survfit()`, `add_p.tbl_survfit()`, `tbl_merge()`, `tbl_stack()`, `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(
    update = list(
      label ~ "**Variable**",
      p.value ~ "**P**"
    )
  ) %>%
  modify_footnote(
    update = 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(update = 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_column_hide` *Modify Hidden Columns*

---

## Description

**[Experimental]** Use these functions to hide or unhide columns in a gtsummary tables.

## 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

Other Advanced modifiers: `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

**[Experimental]** 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

Other Advanced modifiers: `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_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") |
| 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 | 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*.

### See Also

`modify_table_body()`

See gtsummary internals vignette

Other Advanced modifiers: `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

```
if (requireNamespace("GGally")) {
  glm(response ~ marker + grade, trial, family = binomial) %>%
    tbl_regression(
      add_estimate_to_reference_rows = TRUE,
      exponentiate = TRUE
    ) %>%
    plot()
}
```

---

`print_gtsummary` *print and knit_print methods for gtsummary objects*

---

## Description

print and knit_print methods for gtsummary objects

## Usage

```
## S3 method for class 'gtsummary'
print(x, print_engine = NULL, ...)

## S3 method for class 'gtsummary'
knit_print(x, ...)
```

## Arguments

| | |
|---|---|
| `x` | An object created using gtsummary functions |
| `print_engine` | String indicating the print method. Must be one of `"gt"`, `"kable"`, `"kable_extra"`, `"flextable"`, `"tibble"` |
| `...` | Not used |

## Author(s)

Daniel D. Sjoberg

## See Also

tbl_summary tbl_regression tbl_uvregression tbl_merge tbl_stack

## 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

### 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

### Examples

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

---

## set_gtsummary_theme *Set a gtsummary theme*

---

### Description

**[Experimental]** 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, big.mark = NULL, decimal.mark = NULL, ...)
```

## Arguments

| | |
|---|---|
| `x` | Numeric vector |
| `digits` | Integer specifying the minimum number of significant digits to display |
| `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_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,
  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}%)". |
| 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

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_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 |

### 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_stack()

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

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, tbl_stack(), tbl_summary()

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

Other tbl_svysummary tools: add_n.tbl_summary(), add_overall(), add_p.tbl_svysummary(), add_q(), add_stat_label(), modify, tbl_stack(), 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,
  show_yesno = NULL,
  exclude = 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 if 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 |
| show_yesno | DEPRECATED |
| exclude | DEPRECATED |

## 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.

- "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.

## Note

The N reported in the output is the number of observations in the data frame model.frame(x). Depending on the model input, this N may represent different quantities. In most cases, it is the number of people or units in your model. Here are some common exceptions.

1. Survival regression models including time dependent covariates.
2. Random- or mixed-effects regression models with clustered data.
3. GEE regression models with clustered data.

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

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

## 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_regression_methods

*Methods for tbl_regression*

---

## Description

Most regression models are handled by tbl_regression.default(), which uses broom::tidy() to perform initial tidying of results. There are, however, some model types that have modified default printing behavior. Those methods are listed below.

## Usage

```
## S3 method for class 'survreg'
tbl_regression(
  x,
  tidy_fun = function(x, ...) broom::tidy(x, ...) %>% dplyr::filter(.data$term !=
    "Log(scale)"),
  ...
)

## S3 method for class 'mira'
tbl_regression(x, tidy_fun = pool_and_tidy_mice, ...)

## S3 method for class 'mipo'
```

```
tbl_regression(x, ...)

## S3 method for class 'lmerMod'
tbl_regression(
  x,
  tidy_fun = function(x, ...) broom.mixed::tidy(x, ..., effects = "fixed"),
  ...
)

## S3 method for class 'glmerMod'
tbl_regression(
  x,
  tidy_fun = function(x, ...) broom.mixed::tidy(x, ..., effects = "fixed"),
  ...
)

## S3 method for class 'glmmTMB'
tbl_regression(
  x,
  tidy_fun = function(x, ...) broom.mixed::tidy(x, ..., effects = "fixed"),
  ...
)

## S3 method for class 'glmmadmb'
tbl_regression(
  x,
  tidy_fun = function(x, ...) broom.mixed::tidy(x, ..., effects = "fixed"),
  ...
)

## S3 method for class 'stanreg'
tbl_regression(
  x,
  tidy_fun = function(x, ...) broom.mixed::tidy(x, ..., effects = "fixed"),
  ...
)

## S3 method for class 'brmsfit'
tbl_regression(
  x,
  tidy_fun = function(x, ...) broom.mixed::tidy(x, ..., effects = "fixed"),
  ...
)

## S3 method for class 'gam'
tbl_regression(x, tidy_fun = tidy_gam, ...)

## S3 method for class 'multinom'
tbl_regression(x, ...)
```

## Arguments

| | |
|---|---|
| x | Regression model object |

| | |
|---|---|
| tidy_fun | Option to specify a particular tidier function if 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. |
| ... | arguments passed to tbl_regression.default() |

### 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.

- "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.

---

## 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_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_merge(), 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_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()

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

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

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

## Usage

```
tbl_strata(
  data,
  strata,
  .tbl_fun,
  ...,
  .sep = ", ",
  .combine_with = c("tbl_merge", "tbl_stack")
)
```

## 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. |

## 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

## 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()
  )
```

---

# 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(),
  group = 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. |
| 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 continuous 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()` |
| group | DEPRECATED. Migrated to add_p |

## 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(all_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.)

### 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
- {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

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, tbl_merge(), tbl_stack()

## 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

**[Experimental]** 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

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

## 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_survfit_errors` *Common Sources of Error with* `tbl_survfit()`

---

## Description

When functions `add_n()` and `add_p()` are run after `tbl_survfit()`, the original call to `survival::survfit()` is extracted and the formula= and data= arguments are used to calculate the N or p-value.

When the values of the formula= and data= are unavailable, the functions cannot execute. Below are some tips to modify your code to ensure all functions run without issue.

1. Let `tbl_survfit()` construct the `survival::survfit()` for you by passing a data frame to `tbl_survfit()`. The survfit model will be constructed in a manner ensuring the formula and data are available. This only works if you have a stratified model.

   Instead of the following line

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

   Use this code

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

2. Construct an expression of the `survival::survfit()` before evaluating it. Ensure the formula and data are available in the call by using the tidyverse bang-bang operator, !!.

   Use this code

```
formula_arg <- Surv(ttdeath, death) ~ 1
data_arg <- trial
rlang::expr(survfit(!!formula_arg, !!data_arg)) %>%
  eval() %>%
  tbl_survfit(times = c(12, 24))
```

---

`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 continuous 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(all_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.)

## Author(s)

Joseph Larmarange

## See Also

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

## Examples

```
# Example 1 ----------------------------------
# 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,
  show_yesno = NULL,
  exclude = 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 if 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 |
| show_yesno | DEPRECATED |
| exclude | DEPRECATED |

## 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.

- "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.

## Note

The N reported in the output is the number of observations in the data frame model.frame(x). Depending on the model input, this N may represent different quantities. In most cases, it is the number of people or units in your model. Here are some common exceptions.

1. Survival regression models including time dependent covariates.
2. Random- or mixed-effects regression models with clustered data.
3. GEE regression models with clustered data.

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

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

## 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)
  )
```

---

# tests *Tests/methods available in* add_p() *and* add_difference()

---

## Description

Below is a listing of tests available internally within gtsummary.

Tests listed with ... may have additional arguments passed to them using add_p(test.args=). For example, to calculate a p-value from t.test() assuming equal variance, use tbl_summary(trial,by = trt) %>% add_p(age ~ "t.test",test.args = age ~ list(var.equal = TRUE))

### tbl_summary() %>% add_p()

| alias | description | pseudo-code |
|---|---|---|
| "t.test" | t-test | t.test(variable ~ as.factor(by), data = data |
| "aov" | One-way ANOVA | aov(variable ~ as.factor(by), data = data) %> |
| "kruskal.test" | Kruskal-Wallis test | kruskal.test(data[[variable]], as.factor(d |
| "wilcox.test" | Wilcoxon rank-sum test | wilcox.test(variable ~ as.factor(by), data = |
| "chisq.test" | chi-square test of independence | chisq.test(x = data[[variable]], y = as.fact |
| "chisq.test.no.correct" | chi-square test of independence | chisq.test(x = data[[variable]], y = as.fact |
| "fisher.test" | Fisher's exact test | fisher.test(data[[variable]], as.factor(da |
| "mcnemar.test" | McNemar's test | mcnemar.test(data[[variable]], data[[by]], |
| "lme4" | random intercept logistic regression | lme4::glmer(by ~ (1 \UFF5C group), data, family = |

| | | |
|---|---|---|
| "paired.t.test" | Paired t-test | tidyr::pivot_wider(id_cols = group, ...); t.test(by_1, |
| "paired.wilcox.test" | Paired Wilcoxon rank-sum test | tidyr::pivot_wider(id_cols = group, ...); wilcox.test( |
| "prop.test" | Test for equality of proportions | prop.test(x, n, conf.level = 0.95, ...) |
| "ancova" | ANCOVA | lm(variable ~ by + adj.vars) |

**tbl_svysummary() %>% add_p()**

| alias | description |
|---|---|
| "svy.t.test" | t-test adapted to complex survey samples |
| "svy.wilcox.test" | Wilcoxon rank-sum test for complex survey samples |
| "svy.kruskal.test" | Kruskal-Wallis rank-sum test for complex survey samples |
| "svy.vanderwaerden.test" | van der Waerden's normal-scores test for complex survey samples |
| "svy.median.test" | Mood's test for the median for complex survey samples |
| "svy.chisq.test" | chi-squared test with Rao & Scott's second-order correction |
| "svy.adj.chisq.test" | chi-squared test adjusted by a design effect estimate |
| "svy.wald.test" | Wald test of independence for complex survey samples |
| "svy.adj.wald.test" | adjusted Wald test of independence for complex survey samples |
| "svy.lincom.test" | test of independence using the exact asymptotic distribution for complex survey samples |
| "svy.saddlepoint.test" | test of independence using a saddlepoint approximation for complex survey samples |

**tbl_survfit() %>% add_p()**

| alias | description | pseudo-code |
|---|---|---|
| "logrank" | Log-rank test | survival::survdiff(Surv(.) ~ v |
| "petopeto_gehanwilcoxon" | Peto & Peto modification of Gehan-Wilcoxon test | survival::survdiff(Surv(.) ~ v |
| "survdiff" | G-rho family test | survival::survdiff(Surv(.) ~ v |
| "coxph_lrt" | Cox regression (LRT) | survival::coxph(Surv(.) ~ vari |
| "coxph_wald" | Cox regression (Wald) | survival::coxph(Surv(.) ~ vari |
| "coxph_score" | Cox regression (Score) | survival::coxph(Surv(.) ~ vari |

**tbl_summary() %>% add_difference()**

| alias | description | difference statistic | pseudo-code |
|---|---|---|---|
| "t.test" | t-test | mean difference | t.test(variable ~ as.f |
| "paired.t.test" | Paired t-test | mean difference | tidyr::pivot_wider(id_cols |
| "paired.wilcox.test" | Paired Wilcoxon rank-sum test | rate difference | tidyr::pivot_wider(id_cols |
| "prop.test" | Test for equality of proportions | rate difference | prop.test(x, n, conf.l |
| "ancova" | ANCOVA | mean difference | lm(variable ~ by + adj. |
| "ancova_lme4" | ANCOVA with random intercept | mean difference | lme4::lmer(variable ~ by + |
| "cohens_d" | Cohen's D | standardized mean difference | effectsize::cohens_d( |

### Custom Functions

To report a p-value (or difference) for a test not available in gtsummary, you can create a custom function. The output is a data frame that is one line long. The structure is similar to the output of `broom::tidy()` of a typical statistical test. The `add_p()` and `add_comparison()` functions will look for columns called `"p.value"`, `"estimate"`, `"conf.low"`, `"conf.high"`, and `"method"` for the p-value, difference, confidence interval, and the test name used in the footnote.

Example calculating a p-value from a t-test assuming a common variance between groups.

```
ttest_common_variance <- function(data, variable, by, ...) {
  data <- data[c(variable, by)] %>% dplyr::filter(complete.cases(.))
  t.test(data[[variable]] ~ factor(data[[by]]), var.equal = TRUE) %>%
  broom::tidy()
}

trial[c("age", "trt")] %>%
  tbl_summary(by = trt) %>%
  add_p(test = age ~ "ttest_common_variance")
```

A custom `add_difference()` is similar, and accepts arguments conf.level= and adj.vars= as well.

```
ttest_common_variance <- function(data, variable, by, conf.level, ...) {
  data <- data[c(variable, by)] %>% dplyr::filter(complete.cases(.))
 t.test(data[[variable]] ~ factor(data[[by]]), conf.level = conf.level, var.equal = TRUE) %>%
  broom::tidy()
}
```

#### Function Arguments:

For `tbl_summary()` objects, the custom function will be passed the following arguments: `custom_pvalue_fun(data=`
While your function may not utilize each of these arguments, these arguments are passed and the function must accept them. We recommend including `...` to future-proof against updates where additional arguments are added.

The following table describes the argument inputs for each gtsummary table type.

| argument | tbl_summary | tbl_svysummary | tbl_survfi |
|---|---|---|---|
| data= | A data frame | A survey object | A survfi |
| variable= | String variable name | String variable name | NA |
| by= | String variable name | String variable name | NA |
| group= | String variable name | NA | NA |
| type= | Summary type | Summary type | NA |
| conf.level= | Confidence interval level | NA | NA |
| adj.vars= | Character vector of adjustment variable names (e.g. used in ANCOVA) | NA | NA |

---

`theme_gtsummary` *Available gtsummary themes*

---

## Description

**[Experimental]** 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)

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 |
| `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)<br>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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