Package 'gtsummary'

February 12, 2020

Title Presentation-Ready Data Summary and Analytic Result Tables

Version 1.2.6

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. The package is enhanced when the 'gt' package is installed. Use this code to install: 'remotes::install_github(``rstudio/gt'', ref = gtsummary::gt_sha)'.

License MIT + file LICENSE

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

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

Depends R (>= 3.4)

Imports broom (>= 0.5.3), broom.mixed (>= 0.2.4), crayon (>= 1.3.4), dplyr (>= 0.8.3), forcats (>= 0.4.0), glue (>= 1.3.1), knitr (>= 1.26), lifecycle (>= 0.1.0), magrittr (>= 1.5), purrr (>= 0.3.3), rlang (>= 0.4.2), stringr (>= 1.4.0), survival, tibble (>= 2.1.3), tidyr (>= 1.0.0), tidyselect (>= 1.0.0), usethis (>= 1.5.1)

Suggests car,
covr,
geepack,
gt,
Hmisc,
lme4,
pkgdown,
rmarkdown,
spelling,
testthat

VignetteBuilder knitr

RdMacros lifecycle

Additional_repositories http://ddsjoberg.github.io/drat

Encoding UTF-8

Language en-US

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.0.2

R topics documented:

`add_global_p` *Adds the global p-value for a categorical variables*

Description

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

Usage

```
add_global_p(x, ...)
```

Arguments

`x`	`tbl_regression` or `tbl_uvregression` object
`...`	Further arguments passed to or from other methods.

Note

If a needed class of model is not supported by car::Anova, please create a GitHub Issue to request support.

Author(s)

Daniel D. Sjoberg

See Also

`add_global_p.tbl_regression`, `add_global_p.tbl_uvregression`

`add_global_p.tbl_regression` *Adds the global p-value for categorical variables*

Description

This function uses car::Anova with argument `type = "III"` to calculate global p-values for categorical variables.

Usage

```
## S3 method for class 'tbl_regression'
add_global_p(
  x,
  include = x$table_body$variable[x$table_body$var_type %in% c("categorical",
    "interaction")],
  keep = FALSE,
  terms = NULL,
  ...
)
```

Arguments

`x`	Object with class `tbl_regression` from the tbl_regression function
`include`	Variables to calculate global p-value for. Input may be a vector of quoted or unquoted variable names. tidyselect and gtsummary select helper functions are also accepted. Default is `NULL`, which adds global p-values for all categorical and interaction terms.
`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`
`terms`	DEPRECATED. Use include= argument instead.
`...`	Additional arguments to be passed to car::Anova

Value

A `tbl_regression` object

Note

If a needed class of model is not supported by car::Anova, please create a GitHub Issue to request support.

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_regression tools: add_nevent.tbl_regression(), bold_italicize_labels_levels, bold_p.tbl_regression(), bold_p.tbl_stack(), combine_terms(), inline_text.tbl_regression(), modify_header(), sort_p.tbl_regression(), tbl_merge(), tbl_regression(), tbl_stack()

Examples

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

---

add_global_p.tbl_uvregression

Adds the global p-value for categorical variables

Description

This function uses car::Anova with argument `type = "III"` to calculate global p-values for categorical variables.

Usage

```
## S3 method for class 'tbl_uvregression'
add_global_p(x, ...)
```

Arguments

x	Object with class `tbl_uvregression` from the tbl_uvregression function
...	Additional arguments to be passed to car::Anova.

Value

A `tbl_uvregression` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_uvregression tools: add_nevent.tbl_uvregression(), add_q.tbl_uvregression(), bold_italicize_labels_levels, bold_p.tbl_stack(), bold_p.tbl_uvregression(), inline_text.tbl_uvregr modify_header(), sort_p.tbl_uvregression(), tbl_merge(), tbl_stack(), tbl_uvregression()

Examples

```
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 *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

```
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
`statistic`	String indicating the statistic to report. Default is the number of non-missing observation for each variable, `statistic = "{n}"`. Other statistics available to report include: • `"{N}"` total number of observations, • `"{n}"` number of non-missing observations, • `"{n_miss}"` number of missing observations, • `"{p}"` percent non-missing data, • `"{p_miss}"` percent missing data The argument uses glue::glue syntax and multiple statistics may be reported, e.g. `statistic = "{n} / {N} ({p}%)"`
`col_label`	String indicating the column label. Default is `"**N**"`
`footnote`	Logical argument indicating whether to print a footnote clarifying the statistics presented. Default is `FALSE`
`last`	Logical indicator to include N column last in table. Default is `FALSE`, which will display N column first.
`missing`	DEPRECATED. Logical argument indicating whether to print N (`missing = FALSE`), or N missing (`missing = TRUE`). Default is `FALSE`

Value

A tbl_summary object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_summary tools: add_overall(), add_p(), add_q.tbl_summary(), add_stat_label(), bold_italicize_labels_levels, bold_p.tbl_summary(), inline_text.tbl_summary(), modify_header(), sort_p.tbl_summary(), tbl_merge(), tbl_stack(), tbl_summary()

Examples

```
tbl_n_ex <-
  trial[c("trt", "age", "grade", "response")] %>%
  tbl_summary(by = trt) %>%
  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 include 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_regerssion 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, tbl_regression, tbl_uvregression

`add_nevent.tbl_regression` *Add number of events to a regression table*

Description

This function adds a column of the number of events to tables created with tbl_regression. Supported model types include GLMs with binomial distribution family (e.g. stats::glm, lme4::glmer, and geepack::geeglm) and Cox Proportion Hazards regression models (survival::coxph).

The number of events is added to the internal `.$table_body` tibble, and not printed in the default output table (similar to N). The number of events is accessible via the inline_text function for printing in a report.

Usage

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

Arguments

`x`	`tbl_regression` object
`...`	Not used

Value

A `tbl_regression` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_regression tools: `add_global_p.tbl_regression()`, `bold_italicize_labels_levels`, `bold_p.tbl_regression()`, `bold_p.tbl_stack()`, `combine_terms()`, `inline_text.tbl_regression()`, `modify_header()`, `sort_p.tbl_regression()`, `tbl_merge()`, `tbl_regression()`, `tbl_stack()`

Examples

```
tbl_reg_nevent_ex <-
  glm(response ~ trt, trial, family = binomial) %>%
  tbl_regression() %>%
  add_nevent()
```

`add_nevent.tbl_uvregression` *Add number of events to a regression table*

Description

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

Usage

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

Arguments

`x`	`tbl_uvregerssion` object
`...`	Not used

Value

A `tbl_uvregression` object

Reporting Event N

The number of events is added to the internal `.$table_body` tibble, and printed to the right of the N column. The number of events is also accessible via the inline_text function for printing in a report.

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_uvregression tools: `add_global_p.tbl_uvregression()`, `add_q.tbl_uvregression()`, `bold_italicize_labels_levels`, `bold_p.tbl_stack()`, `bold_p.tbl_uvregression()`, `inline_text.tbl_uvregr` `modify_header()`, `sort_p.tbl_uvregression()`, `tbl_merge()`, `tbl_stack()`, `tbl_uvregression()`

Examples

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

add_overall *Add column with overall summary statistics*

Description

Adds a column with overall summary statistics to tables created by `tbl_summary`.

Usage

```
add_overall(x, last = FALSE)
```

Arguments

`x`	Object with class `tbl_summary` from the tbl_summary function
`last`	Logical indicator to display overall column last in table. Default is `FALSE`, which will display overall column first.

Value

A `tbl_summary` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_summary tools: `add_n()`, `add_p()`, `add_q.tbl_summary()`, `add_stat_label()`, `bold_italicize_labels_`
`bold_p.tbl_summary()`, `inline_text.tbl_summary()`, `modify_header()`, `sort_p.tbl_summary()`,
`tbl_merge()`, `tbl_stack()`, `tbl_summary()`

Examples

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

add_p *Adds p-values to summary tables*

Description

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

Usage

```
add_p(
  x,
  test = NULL,
  pvalue_fun = NULL,
  group = NULL,
  include = everything(),
  exclude = NULL
)
```

Arguments

`x`	Object with class `tbl_summary` from the tbl_summary function
`test`	List of formulas specifying statistical tests to perform, e.g. `list(all_continuous() ~ "t.test", all_categorical() ~ "fisher.test")`. Options include • `"t.test"` for a t-test, • `"aov"` for a one-way ANOVA test, • `"wilcox.test"` for a Wilcoxon rank-sum test, • `"kruskal.test"` for a Kruskal-Wallis rank-sum test, • `"chisq.test"` for a chi-squared test of independence, • `"chisq.test.no.correct"` for a chi-squared test of independence without continuity correction, • `"fisher.test"` for a Fisher's exact test, • `"lme4"` for a random intercept logistic regression model to account for clustered data, `lme4::glmer(by ~ variable + (1 | group), family = binomial)`. The by argument must be binary for this option. Tests default to `"kruskal.test"` for continuous variables, `"chisq.test"` for categorical variables with all expected cell counts >=5, and `"fisher.test"` for categorical variables with any expected cell count <5. A custom test function can be added for all or some variables. See below for an example.
`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 (e.g. when the test argument is `"lme4"`). Default is `NULL`. If specified, the row associated with this variable is omitted from the summary table.
`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()`.
`exclude`	DEPRECATED

Value

A `tbl_summary` object

Setting Defaults

If you like to consistently use a different function to format p-values or estimates, you can set options in the script or in the user- or project-level startup file, '.Rprofile'. The default confidence level can also be set. Please note the default option for the estimate is the same as it is for `tbl_regression()`.

- `options(gtsummary.pvalue_fun = new_function)`

Example Output

Author(s)

Emily C. Zabor, Daniel D. Sjoberg

See Also

See tbl_summary vignette for detailed examples

Other tbl_summary tools: `add_n()`, `add_overall()`, `add_q.tbl_summary()`, `add_stat_label()`, `bold_italicize_labels_levels`, `bold_p.tbl_summary()`, `inline_text.tbl_summary()`, `modify_header()`, `sort_p.tbl_summary()`, `tbl_merge()`, `tbl_stack()`, `tbl_summary()`

Examples

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

# Conduct a custom McNemar test for response,
# Function must return a named list of the p-value and the
# test name: list(p = 0.123, test = "McNemar's test")
# The '...' must be included as input
# This feature is experimental, and the API may change in the future
my_mcnemar <- function(data, variable, by, ...) {
  result <- list()
  result$p <- stats::mcnemar.test(data[[variable]], data[[by]])$p.value
  result$test <- "McNemar\\'s test"
  result
}

add_p_ex2 <-
  trial[c("response", "trt")] %>%
  tbl_summary(by = trt) %>%
  add_p(test = response ~ "my_mcnemar")
```

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

Description

Add a column of q values to account for multiple comparisons

Usage

```
add_q(x, ...)
```

Arguments

x	tbl_summary or tbl_uvregression object
...	Additional arguments passed to other methods.

Author(s)

Esther Drill, Daniel D. Sjoberg

See Also

add_q.tbl_summary, add_q.tbl_uvregression, tbl_summary, tbl_uvregression

add_q.tbl_summary — *Add a column of q-values to account for multiple comparisons*

Description

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

Usage

```
## S3 method for class 'tbl_summary'
add_q(x, method = "fdr", pvalue_fun = x$fmt_fun$p.value, ...)
```

Arguments

x	tbl_summary 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)).
...	Additional arguments passed to or from other methods

Value

A tbl_summary object

Example Output

Author(s)

Esther Drill, Daniel D. Sjoberg

See Also

Other tbl_summary tools: add_n(), add_overall(), add_p(), add_stat_label(), bold_italicize_labels_levels, bold_p.tbl_summary(), inline_text.tbl_summary(), modify_header(), sort_p.tbl_summary(), tbl_merge(), tbl_stack(), tbl_summary()

Examples

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

---

add_q.tbl_uvregression

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

Description

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

Usage

```
## S3 method for class 'tbl_uvregression'
add_q(x, method = "fdr", pvalue_fun = x$fmt_fun$p.value, ...)
```

Arguments

x	tbl_uvregression 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)).
...	Additional arguments passed to or from other methods

Value

A tbl_uvregression object

Example Output

Author(s)

Esther Drill, Daniel D. Sjoberg

See Also

Other tbl_uvregression tools: add_global_p.tbl_uvregression(), add_nevent.tbl_uvregression(), bold_italicize_labels_levels, bold_p.tbl_stack(), bold_p.tbl_uvregression(), inline_text.tbl_uvregr modify_header(), sort_p.tbl_uvregression(), tbl_merge(), tbl_stack(), tbl_uvregression()

Examples

```
tbl_uvr_q_ex <-
  trial[c("age", "marker", "grade", "response")] %>%
  tbl_uvregression(
    method = lm,
    y = age
  ) %>%
  add_global_p() %>%
  add_q()
```

---

add_stat_label *Add statistic labels column*

Description

Adds a column with labels describing the summary statistics presented for each variable in the tbl_summary table.

Usage

```
add_stat_label(x)
```

Arguments

x	Object with class tbl_summary from the tbl_summary function

Value

A tbl_summary object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_summary tools: add_n(), add_overall(), add_p(), add_q.tbl_summary(), bold_italicize_labels_lev
bold_p.tbl_summary(), inline_text.tbl_summary(), modify_header(), sort_p.tbl_summary(),
tbl_merge(), tbl_stack(), tbl_summary()

Examples

```
tbl_stat_ex <-
  trial[c("trt", "age", "grade", "response")] %>%
  tbl_summary() %>%
  add_stat_label()
```

---

as_gt *Convert gtsummary object to a gt_tbl 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. You can install gt with `remotes::install_github("rstudio/gt",ref = gtsummary::gt_sha)`.

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

Usage

```
as_gt(x, include = everything(), 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()`, which includes all commands in `x$gt_calls`.
exclude	DEPRECATED.
omit	DEPRECATED.

Value

A `gt_tbl` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

tbl_summary tbl_regression tbl_uvregression tbl_survival

Examples

```
# Requires the gt package
# remotes::install_github("rstudio/gt", ref = gtsummary::gt_sha)

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

---

as_kable *Convert to knitr_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. To use these features, install gt with `remotes::install_github("rstudio/gt",ref = gtsummary::gt_sha)`.

Usage

```
as_kable(x, include = everything(), 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()`, which includes all commands in `x$kable_calls`.
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

tbl_summary tbl_regression tbl_uvregression tbl_survival

Examples

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

---

as_tibbleS3 *Convert gtsummary object to tibble*

Description

Function converts gtsummary objects tibbles. The formatting stored in `x$kable_calls` is applied.

Usage

```
## S3 method for class 'gtsummary'
as_tibble(x, include = everything(), col_labels = TRUE, 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()`, which includes all commands in `x$kable_calls`.
`col_labels`	Logical argument adding column labels to output tibble. Default is `TRUE`.
`exclude`	DEPRECATED
`...`	Not used

Value

a tibble

Author(s)

Daniel D. Sjoberg

See Also

tbl_summary tbl_regression tbl_uvregression tbl_survival

Examples

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

as_tibble(tbl)

# without column labels
as_tibble(tbl, col_names = 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(), add_overall(), add_p(), add_q.tbl_summary(), add_stat_label(), bold_p.tbl_summary(), inline_text.tbl_summary(), modify_header(), sort_p.tbl_summary(), tbl_merge(), tbl_stack(), tbl_summary()

Other tbl_regression tools: add_global_p.tbl_regression(), add_nevent.tbl_regression(), bold_p.tbl_regression(), bold_p.tbl_stack(), combine_terms(), inline_text.tbl_regression(), modify_header(), sort_p.tbl_regression(), tbl_merge(), tbl_regression(), tbl_stack()

Other tbl_uvregression tools: add_global_p.tbl_uvregression(), add_nevent.tbl_uvregression(), add_q.tbl_uvregression(), bold_p.tbl_stack(), bold_p.tbl_uvregression(), inline_text.tbl_uvregressi modify_header(), sort_p.tbl_uvregression(), 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 gtsummary tables.

Usage

```
bold_p(x, ...)
```

Arguments

x	Object created using gtsummary functions
...	Additional arguments passed to other methods.

Author(s)

Daniel D. Sjoberg, Esther Drill

See Also

bold_p.tbl_summary, bold_p.tbl_regression, bold_p.tbl_uvregression

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

Description

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

Usage

```
## S3 method for class 'tbl_regression'
bold_p(x, t = 0.05, ...)
```

Arguments

`x`	Object created using tbl_regression function
`t`	Threshold below which values will be bold. Default is 0.05.
`...`	Not used

Value

A `tbl_regression` object

Example Output

Author(s)

Daniel D. Sjoberg, Esther Drill

See Also

Other tbl_regression tools: `add_global_p.tbl_regression()`, `add_nevent.tbl_regression()`, `bold_italicize_labels_levels`, `bold_p.tbl_stack()`, `combine_terms()`, `inline_text.tbl_regression()`, `modify_header()`, `sort_p.tbl_regression()`, `tbl_merge()`, `tbl_regression()`, `tbl_stack()`

Examples

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

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

Description

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

Usage

```
## S3 method for class 'tbl_stack'
bold_p(x, ...)
```

Arguments

`x`	Object created using tbl_stack function
`...`	arguments passed to bold_p.*() method that matches the first object in the `tbl_stack`

Value

A `tbl_stack` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_uvregression tools: `add_global_p.tbl_uvregression()`, `add_nevent.tbl_uvregression()`, `add_q.tbl_uvregression()`, `bold_italicize_labels_levels`, `bold_p.tbl_uvregression()`, `inline_text.tbl_uvregression()`, `modify_header()`, `sort_p.tbl_uvregression()`, `tbl_merge()`, `tbl_stack()`, `tbl_uvregression()`

Other tbl_regression tools: `add_global_p.tbl_regression()`, `add_nevent.tbl_regression()`, `bold_italicize_labels_levels`, `bold_p.tbl_regression()`, `combine_terms()`, `inline_text.tbl_regression(`
`modify_header()`, `sort_p.tbl_regression()`, `tbl_merge()`, `tbl_regression()`, `tbl_stack()`

Examples

```
t1 <- tbl_regression(lm(age ~ response, trial))
t2 <- tbl_regression(lm(age ~ grade, trial))

bold_p_stack_ex <-
  tbl_stack(list(t1, t2)) %>%
  bold_p(t = 0.10)
```

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

Description

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

Usage

```
## S3 method for class 'tbl_summary'
bold_p(x, t = 0.05, q = FALSE, ...)
```

Arguments

`x`	Object created using `tbl_summary` function
`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`.
`...`	Not used

Value

A `tbl_summary` object

Example Output

Author(s)

Daniel D. Sjoberg, Esther Drill

See Also

Other tbl_summary tools: `add_n()`, `add_overall()`, `add_p()`, `add_q.tbl_summary()`, `add_stat_label()`, `bold_italicize_labels_levels`, `inline_text.tbl_summary()`, `modify_header()`, `sort_p.tbl_summary()`, `tbl_merge()`, `tbl_stack()`, `tbl_summary()`

Examples

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

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

Description

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

Usage

```
## S3 method for class 'tbl_uvregression'
bold_p(x, t = 0.05, q = FALSE, ...)
```

Arguments

`x`	Object created using tbl_uvregression function
`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`.
`...`	Not used

Value

A `tbl_uvregression` object

Example Output

Author(s)

Daniel D. Sjoberg, Esther Drill

See Also

Other tbl_uvregression tools: `add_global_p.tbl_uvregression()`, `add_nevent.tbl_uvregression()`, `add_q.tbl_uvregression()`, `bold_italicize_labels_levels`, `bold_p.tbl_stack()`, `inline_text.tbl_uvregre` `modify_header()`, `sort_p.tbl_uvregression()`, `tbl_merge()`, `tbl_stack()`, `tbl_uvregression()`

Examples

```
tbl_uvglm_bold_p_ex <-
  trial[c("age", "marker", "response", "grade")] %>%
  tbl_uvregression(
    method = glm,
    y = response,
    method.args = list(family = binomial),
    exponentiate = TRUE
  ) %>%
  bold_p(t = 0.25)
```

combine_terms *Combine terms in a regression model*

Description

Experimental 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, ...)
```

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
...	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.tbl_regression()`, `add_nevent.tbl_regression()`, `bold_italicize_labels_levels`, `bold_p.tbl_regression()`, `bold_p.tbl_stack()`, `inline_text.tbl_regressi`
`modify_header()`, `sort_p.tbl_regression()`, `tbl_merge()`, `tbl_regression()`, `tbl_stack()`

Examples

```
# fit model with nonlinear terms for marker
nlmod1 <- lm(
  age ~ marker + I(marker^2) + grade,
  trial[c("age", "marker", "grade")] %>% na.omit() # keep complete cases only!
)

combine_terms_ex1 <-
  tbl_regression(nlmod1, label = grade ~ "Grade") %>%
  # 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)"
  )

# Example with Cubic Splines
library(Hmisc)
mod2 <- lm(
  age ~ rcspline.eval(marker, inclx = TRUE) + grade,
  trial[c("age", "marker", "grade")] %>% na.omit() # keep complete cases only!
)

combine_terms_ex2 <-
  tbl_regression(mod2, label = grade ~ "Grade") %>%
  combine_terms(
    formula_update = . ~ . -rcspline.eval(marker, inclx = TRUE),
    label = "Marker (non-linear terms)"
  )

# Logistic Regression Example, LRT p-value
combine_terms_ex3 <-
  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"
  )
```

`gtsummary_logo` *The gtsummary logo, using ASCII or Unicode characters*

Description

Use `crayon::strip_style()` to get rid of the colors.

Usage

```
gtsummary_logo(unicode = l10n_info()$`UTF-8`)
```

Arguments

`unicode`	Whether to use Unicode symbols. Default is `TRUE` on UTF-8 platforms.

Examples

```
gtsummary_logo()
```

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_regression, inline_text.tbl_uvregression, inline_text.tbl_survival

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 = x$fmt_fun$estimate,
  pvalue_fun = function(x) style_pvalue(x, prepend_p = TRUE),
  ...
)
```

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 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'
- {ci} confidence interval formatted with x$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.tbl_regression(), add_nevent.tbl_regression(), bold_italicize_labels_levels, bold_p.tbl_regression(), bold_p.tbl_stack(), combine_terms(), modify_header(), sort_p.tbl_regression(), 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 = function(x) style_pvalue(x, prepend_p = TRUE),
  ...
)
```

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(), add_overall(), add_p(), add_q.tbl_summary(), add_stat_label(), bold_italicize_labels_levels, bold_p.tbl_summary(), modify_header(), sort_p.tbl_summary(), tbl_merge(), tbl_stack(), tbl_summary()

Examples

```
t1 <- tbl_summary(trial)
t2 <- tbl_summary(trial, by = trt) %>% add_p()

inline_text(t1, variable = age)
inline_text(t2, variable = grade, level = "I", column = "Drug A",
pattern = "{n}/{N} ({p})%")
inline_text(t2, variable = grade, column = "p.value")
```

---

inline_text.tbl_survival

Report statistics from survival summary tables inline

Description

for inline reporting in an R markdown document.

Usage

```
## S3 method for class 'tbl_survival'
inline_text(
  x,
  strata = NULL,
  time = NULL,
  prob = NULL,
  pattern = "{estimate} ({conf.level*100}% CI {ci})",
  estimate_fun = x$fmt_fun$estimate,
  ...
)
```

Arguments

x	Object created from tbl_survival
strata	If tbl_survival estimates are stratified, level of the stratum to report. Default is NULL when tbl_survival have no specified strata.
time	Time for which to return survival probability
prob	Probability for which to return survival time. For median survival use prob = 0.50
pattern	String indicating the statistics to return. Uses glue::glue formatting. Default is '{estimate} ({conf.level*100}% {ci})'. All columns from x$table_long are available to print as well as the confidence level (conf.level). See below for details.
estimate_fun	function to round/style estimate and lower/upper confidence interval estimates. Note, this does not style the 'ci' column, which is a string. Default is x$estimate_fun
...	Not used

Value

A string reporting results from a gtsummary table

pattern argument

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

- `{label}` 'time' or 'prob' label
- `{estimate}` survival or survival time 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'
- `{ci}` confidence interval formatted with x$estimate_fun (pre-formatted)
- `{time}/{prob}` time or survival quantile (numeric)
- `{n.risk}` number at risk at 'time' (within stratum if applicable)
- `{n.event}` number of observed events at 'time' (within stratum if applicable)
- `{n}` number of observations (within stratum if applicable)
- `{variable}` stratum variable (if applicable)
- `{level}` stratum level (if applicable)
- `{groupname}` label_level from original `tbl_survival()` call

Author(s)

Karissa Whiting

See Also

Other tbl_survival tools: `modify_header()`, `tbl_survival.survfit()`

Examples

```
library(survival)
surv_table <-
  survfit(Surv(ttdeath, death) ~ trt, trial) %>%
  tbl_survival(times = c(12, 24))

inline_text(surv_table,
  strata = "Drug A",
  time = 12
)
```

`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 = x$fmt_fun$estimate,
  pvalue_fun = function(x) style_pvalue(x, prepend_p = TRUE),
  ...
)
```

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 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'
- {ci} confidence interval formatted with x$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.tbl_uvregression(), add_nevent.tbl_uvregression(), add_q.tbl_uvregression(), bold_italicize_labels_levels, bold_p.tbl_stack(), bold_p.tbl_uvregression modify_header(), sort_p.tbl_uvregression(), 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_header *Modify column headers in gtsummary tables*

Description

Column labels can be modified to include calculated statistics; e.g. the N can be dynamically included by wrapping it in curly brackets (following glue::glue syntax).

Usage

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

Arguments

x	gtsummary object, e.g. tbl_summary or tbl_regression
stat_by	String specifying text to include above the summary statistics stratified by a variable. Only use with stratified tbl_summary objects. The following fields are available for use in the headers: • {n} number of observations in each group, • {N} total number of observations, • {p} percentage in each group,

- {level} the 'by' variable level,
- "fisher.test" for a Fisher's exact test,

Syntax follows glue::glue, e.g. stat_by = "**{level}**, N = {n} ({style_percent(p)\%})". The by argument from the parent tbl_summary() cannot be NULL.

... Specifies column label of any other column in .$table_body. Argument is the column name, and the value is the new column header (e.g. p.value = "Model P-values"). Use print(x$table_body) to see columns available.

text_interpret indicates whether text will be interpreted as markdown ("md") or HTML ("html"). The text is interpreted with the gt package's md() or html() functions. The default is "md", and is ignored when the print engine is not gt.

Value

Function return the same class of gtsummary object supplied

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_summary tools: add_n(), add_overall(), add_p(), add_q.tbl_summary(), add_stat_label(), bold_italicize_labels_levels, bold_p.tbl_summary(), inline_text.tbl_summary(), sort_p.tbl_summary() tbl_merge(), tbl_stack(), tbl_summary()

Other tbl_regression tools: add_global_p.tbl_regression(), add_nevent.tbl_regression(), bold_italicize_labels_levels, bold_p.tbl_regression(), bold_p.tbl_stack(), combine_terms(), inline_text.tbl_regression(), sort_p.tbl_regression(), tbl_merge(), tbl_regression(), tbl_stack()

Other tbl_uvregression tools: add_global_p.tbl_uvregression(), add_nevent.tbl_uvregression(), add_q.tbl_uvregression(), bold_italicize_labels_levels, bold_p.tbl_stack(), bold_p.tbl_uvregression inline_text.tbl_uvregression(), sort_p.tbl_uvregression(), tbl_merge(), tbl_stack(), tbl_uvregression()

Other tbl_survival tools: inline_text.tbl_survival(), tbl_survival.survfit()

Examples

```
tbl_col_ex1 <-
  trial[c("age", "grade", "response")] %>%
  tbl_summary() %>%
  modify_header(stat_0 = "**All Patients**, N = {N}")

tbl_col_ex2 <-
  trial[c("age", "grade", "response", "trt")] %>%
  tbl_summary(by = trt) %>%
  modify_header(
    stat_by = "**{level}**, N = {n} ({style_percent(p, symbol = TRUE)})"
  )
```

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, ...)

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

Arguments

x	An object created using gtsummary functions
...	Not used

Author(s)

Daniel D. Sjoberg

See Also

tbl_summary tbl_regression tbl_uvregression tbl_merge tbl_stack

select_helpers *Select helper functions*

Description

Set of functions to supplement the tidyselect set of functions for selecting columns of data frames. `all_continuous()`, `all_categorical()`, and `all_dichotomous()` may only be used with `tbl_summary()`, where each variable has been classified into one of these three groups. All other helpers are available throughout the package.

Usage

```
all_numeric()

all_character()

all_integer()

all_double()

all_logical()
```

```
all_factor()

all_continuous()

all_categorical(dichotomous = TRUE)

all_dichotomous()
```

Arguments

dichotomous	Logical indicating whether to include dichotomous variables. Default is TRUE

Value

A character vector of column names selected

---

sort_p.tbl_regression *Sort variables in table by ascending p-values*

Description

Sort variables in tables created by tbl_regression by ascending p-values

Usage

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

Arguments

x	An object created using tbl_regression function
...	Not used

Value

A tbl_regression object

Example Output

Author(s)

Karissa Whiting

See Also

Other tbl_regression tools: add_global_p.tbl_regression(), add_nevent.tbl_regression(), bold_italicize_labels_levels, bold_p.tbl_regression(), bold_p.tbl_stack(), combine_terms(), inline_text.tbl_regression(), modify_header(), tbl_merge(), tbl_regression(), tbl_stack()

Examples

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

`sort_p.tbl_summary` *Sort variables in table by ascending p-values*

Description

Sort variables in tables created by tbl_summary by ascending p-values

Usage

```
## S3 method for class 'tbl_summary'
sort_p(x, q = FALSE, ...)
```

Arguments

`x`	An object created using `tbl_summary` function
`q`	Logical argument. When `TRUE` will sort by the q-value column rather than the p-values
`...`	Not used

Value

A `tbl_summary` object

Example Output

Author(s)

Karissa Whiting

See Also

Other tbl_summary tools: `add_n()`, `add_overall()`, `add_p()`, `add_q.tbl_summary()`, `add_stat_label()`, `bold_italicize_labels_levels`, `bold_p.tbl_summary()`, `inline_text.tbl_summary()`, `modify_header()`, `tbl_merge()`, `tbl_stack()`, `tbl_summary()`

Examples

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

`sort_p.tbl_uvregression` *Sort variables in table by ascending p-values*

Description

Sort variables in tables created by tbl_uvregression by ascending p-values

Usage

```
## S3 method for class 'tbl_uvregression'
sort_p(x, q = FALSE, ...)
```

Arguments

x	an object created using `tbl_uvregression` function
q	logical argument. When `TRUE` will sort by the q-value column rather than the p-values
...	Not used

Value

A `tbl_uvregression` object

Example Output

Author(s)

Karissa Whiting

See Also

Other tbl_uvregression tools: `add_global_p.tbl_uvregression()`, `add_nevent.tbl_uvregression()`, `add_q.tbl_uvregression()`, `bold_italicize_labels_levels`, `bold_p.tbl_stack()`, `bold_p.tbl_uvregression` `inline_text.tbl_uvregression()`, `modify_header()`, `tbl_merge()`, `tbl_stack()`, `tbl_uvregression()`

Examples

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

style_percent *Style percentages to be displayed in tables or text*

Description

Style percentages to be displayed in tables or text

Usage

```
style_percent(x, symbol = FALSE)
```

Arguments

x	numeric vector of percentages
symbol	Logical indicator to include percent symbol in output. Default is FALSE.

Value

A character vector of styled percentages

Author(s)

Daniel D. Sjoberg

See Also

See Table Gallery vignette for example

Other style tools: 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)
```

style_pvalue *Style p-values to be displayed in tables or text*

Description

Style p-values to be displayed in tables or text

Usage

```
style_pvalue(x, digits = 1, prepend_p = FALSE)
```

Arguments

x	Numeric vector of p-values.
digits	Number of digits large p-values are rounded. Must be 1 or 2. Default is 1.
prepend_p	Logical. Should 'p=' be prepended to formatted p-value. Default is FALSE

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_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 *Implement 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)
```

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`.

Value

A character vector of styled ratios

Author(s)

Daniel D. Sjoberg

See Also

Other style tools: `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` *Implement 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)
```

Arguments

`x`	Numeric vector
`digits`	Integer specifying the minimum number of significant digits to display

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_percent()`, `style_pvalue()`, `style_ratio()`

Examples

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

`tbl_merge` *Merge two or more gtsummary objects*

Description

Merges two or more `tbl_regression`, `tbl_uvregression`, `tbl_stack`, or `tbl_summary` 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.tbl_regression()`, `add_nevent.tbl_regression()`, `bold_italicize_labels_levels`, `bold_p.tbl_regression()`, `bold_p.tbl_stack()`, `combine_terms()`, `inline_text.tbl_regression()`, `modify_header()`, `sort_p.tbl_regression()`, `tbl_regression()`, `tbl_stack()`

Other tbl_uvregression tools: `add_global_p.tbl_uvregression()`, `add_nevent.tbl_uvregression()`, `add_q.tbl_uvregression()`, `bold_italicize_labels_levels`, `bold_p.tbl_stack()`, `bold_p.tbl_uvregression` `inline_text.tbl_uvregression()`, `modify_header()`, `sort_p.tbl_uvregression()`, `tbl_stack()`, `tbl_uvregression()`

Other tbl_summary tools: `add_n()`, `add_overall()`, `add_p()`, `add_q.tbl_summary()`, `add_stat_label()`, `bold_italicize_labels_levels`, `bold_p.tbl_summary()`, `inline_text.tbl_summary()`, `modify_header()`, `sort_p.tbl_summary()`, `tbl_stack()`, `tbl_summary()`

Examples

```
# 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**")
  )

# Descriptive statistics alongside univariate regression, with no spanning header
t3 <-
  trial[c("age", "grade", "response")] %>%
  tbl_summary(missing = "no") %>%
  add_n()
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)) %>%
  as_gt(include = -tab_spanner) %>%
  gt::cols_label(stat_0_1 = gt::md("**Summary Statistics**"))
```

`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,
  label = NULL,
  exponentiate = FALSE,
  include = everything(),
  show_single_row = NULL,
  conf.level = NULL,
```

```
  intercept = FALSE,
  estimate_fun = NULL,
  pvalue_fun = NULL,
  tidy_fun = NULL,
  show_yesno = NULL,
  exclude = NULL
)
```

Arguments

x	Regression model object
label	List of formulas specifying variables labels, e.g. `list(age ~ "Age,yrs",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 is not a vetted model or you need to implement a custom method. Default is NULL
show_yesno	DEPRECATED
exclude	DEPRECATED

Value

A `tbl_regression` object

Setting Defaults

If you prefer to consistently use a different function to format p-values or estimates, you can set options in the script or in the user- or project-level startup file, '.Rprofile'. The default confidence level can also be set.

- `options(gtsummary.pvalue_fun = new_function)`
- `options(gtsummary.tbl_regression.estimate_fun = new_function)`
- `options(gtsummary.conf.level = 0.90)`

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.tbl_regression()`, `add_nevent.tbl_regression()`, `bold_italicize_labels_levels`, `bold_p.tbl_regression()`, `bold_p.tbl_stack()`, `combine_terms()`, `inline_text.tbl_regression()`, `modify_header()`, `sort_p.tbl_regression()`, `tbl_merge()`, `tbl_stack()`

Examples

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

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

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

# for convenience, you can also pass named lists to any arguments
# that accept formulas (e.g label, etc.)
glm(response ~ age + grade, trial, family = binomial(link = "logit")) %>%
  tbl_regression(exponentiate = TRUE, label = list(age = "Patient Age"))
```

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`, or `tbl_merge` objects. gt attributes from the first regression object are utilized for output table.

Usage

```
tbl_stack(tbls)
```

Arguments

`tbls`	List of gtsummary objects

Value

A `tbl_stack` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

tbl_merge

Other tbl_summary tools: `add_n()`, `add_overall()`, `add_p()`, `add_q.tbl_summary()`, `add_stat_label()`, `bold_italicize_labels_levels`, `bold_p.tbl_summary()`, `inline_text.tbl_summary()`, `modify_header()`, `sort_p.tbl_summary()`, `tbl_merge()`, `tbl_summary()`

Other tbl_regression tools: `add_global_p.tbl_regression()`, `add_nevent.tbl_regression()`, `bold_italicize_labels_levels`, `bold_p.tbl_regression()`, `bold_p.tbl_stack()`, `combine_terms()`, `inline_text.tbl_regression()`, `modify_header()`, `sort_p.tbl_regression()`, `tbl_merge()`, `tbl_regression()`

Other tbl_uvregression tools: `add_global_p.tbl_uvregression()`, `add_nevent.tbl_uvregression()`, `add_q.tbl_uvregression()`, `bold_italicize_labels_levels`, `bold_p.tbl_stack()`, `bold_p.tbl_uvregression`, `inline_text.tbl_uvregression()`, `modify_header()`, `sort_p.tbl_uvregression()`, `tbl_merge()`, `tbl_uvregression()`

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))
```

`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 = c("ifany", "always", "no"),
  missing_text = "Unknown",
  sort = NULL,
  percent = c("column", "row", "cell"),
  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.
label	List of formulas specifying variables labels, e.g. list(age ~ "Age,yrs",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)).
type	List of formulas specifying variable types. Accepted values are c("continuous","categorical","c e.g. type = list(starts_with(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".
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.)

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

type argument

tbl_summary displays summary statistics for three types of data: continuous, categorical, and dichotomous. If the type is not specified, tbl_summary will do its best to guess the type. Dichotomous variables are categorical variables that are displayed on a single row in the output table, 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")`

Example Output

Author(s)

Daniel D. Sjoberg

See Also

See tbl_summary vignette for detailed examples

Other tbl_summary tools: add_n(), add_overall(), add_p(), add_q.tbl_summary(), add_stat_label(), bold_italicize_labels_levels, bold_p.tbl_summary(), inline_text.tbl_summary(), modify_header(), sort_p.tbl_summary(), tbl_merge(), tbl_stack()

Examples

```
tbl_summary_ex1 <-
  trial[c("age", "grade", "response")] %>%
  tbl_summary()

tbl_summary_ex2 <-
  trial[c("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))
  )

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

---

tbl_survival *Creates table of univariate summary statistics for time-to-event endpoints*

Description

Questioning Questioning whether gtsummary is the place for our univariate survival functions to live. This may be exported to another package in the future.

Usage

```
tbl_survival(x, ...)
```

Arguments

x	A survfit object
...	Additional arguments passed to other methods

See Also

tbl_survival.survfit

`tbl_survival.survfit` *Creates table of survival probabilities*

Description

Questioning Questioning whether gtsummary is the place for our univariate survival functions to live. This may be exported to another package in the future. Function takes a `survfit` object as an argument, and provides a formatted summary of the results

Usage

```
## S3 method for class 'survfit'
tbl_survival(
  x,
  times = NULL,
  probs = NULL,
  label = ifelse(is.null(probs), "{time}", "{prob*100}%"),
  level_label = "{level}, N = {n}",
  header_label = NULL,
  header_estimate = NULL,
  failure = FALSE,
  missing = "-",
  estimate_fun = NULL,
  ...
)
```

Arguments

`x`	A survfit object with a no stratification (e.g. `survfit(Surv(ttdeath,death) ~ 1,trial)`), or a single stratifying variable (e.g. `survfit(Surv(ttdeath,death) ~ trt,trial)`)
`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
`label`	String defining the label shown for the time or prob column. Default is `"{time}"` or `"{prob*100}%"`. The input uses glue::glue notation to convert the string into a label. A common label may be `"{time} Months"`, which would resolve to "6 Months" or "12 Months" depending on specified `times`.
`level_label`	Used when survival results are stratified. It is a string defining the label shown. The input uses glue::glue notation to convert the string into a label. The default is `"{level},N = {n}"`. Other information available to call are `'{n}'`, `'{level}'`, `'{n.event.tot}'`, `'{n.event.strata}'`, and `'{strata}'`. See below for details.
`header_label`	String to be displayed as column header. Default is `'**Time**'` when `time` is specified, and `'**Quantile**'` when `probs` is specified.

header_estimate
: String to be displayed as column header of the Kaplan-Meier estimate. Default is `'**Probability**'` when `time` is specified, and `'**Time**'` when `probs` is specified.

failure
: Calculate failure probabilities rather than survival probabilities. Default is `FALSE`. Does NOT apply to survival quantile requests

missing
: String indicating what to replace missing confidence limits with in output. Default is `missing = "-"`

estimate_fun
: Function used to format the estimate and confidence limits. The default is `style_percent(x, symbol = TRUE)` for survival probabilities, and `style_sigfig(x, digits = 3)` for time estimates.

...
: Not used

Value

A `tbl_survival` object

level_label argument

The `level_label` is used to modify the stratum labels. The default is `level_label = "{level}, N = {n}"`. The quantities in the curly brackets evaluate to stratum-specific values. For example, in the trial data set, there is a column called `trt` with levels 'Drug A' and 'Drug B'. In this example, `{level}` would evaluate to either 'Drug A' or 'Drug B' depending on the stratum. Other quantities available to print are:

- `{level}` level of the stratification variable
- `{level_label}` label of level for the stratification variable
- `{n}` number of observations, or number within stratum
- `{n.event.tot}` total number of events (total across stratum, if applicable)
- `{n.event.strata}` total number of events within stratum, if applicable
- `{strata}` raw stratum specification from `survfit` object

Example Output

Author(s)

Daniel D. Sjoberg

See Also

Other tbl_survival tools: `inline_text.tbl_survival()`, `modify_header()`

Examples

```
library(survival)
fit1 <- survfit(Surv(ttdeath, death) ~ trt, trial)
tbl_strata_ex1 <-
  tbl_survival(
    fit1,
    times = c(12, 24),
```

```
    label = "{time} Months"
  )

fit2 <- survfit(Surv(ttdeath, death) ~ 1, trial)
tbl_nostrata_ex2 <-
  tbl_survival(
    fit2,
    probs = c(0.1, 0.2),
    header_estimate = "**Months**"
  )
```

`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,
  formula = "{y} ~ {x}",
  exponentiate = FALSE,
  label = NULL,
  include = everything(),
  exclude = NULL,
  hide_n = FALSE,
  show_single_row = NULL,
  conf.level = NULL,
  estimate_fun = NULL,
  pvalue_fun = NULL,
  show_yesno = NULL,
  tidy_fun = NULL
)
```

Arguments

data	Data frame to be used in univariate regression modeling. Data frame includes the outcome variable(s) and the independent variables.
method	Regression method (e.g. lm, glm, survival::coxph, 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.
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)".
exponentiate	Logical indicating whether to exponentiate the coefficient estimates. Default is FALSE.
label	List of formulas specifying variables labels, e.g. list(age ~ "Age,yrs",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().
exclude	DEPRECATED
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)).
show_yesno	DEPRECATED
tidy_fun	Option to specify a particular tidier function if the model is not a vetted model or you need to implement a custom method. Default is NULL

Value

A tbl_uvregression object

Example Output

Setting Defaults

If you prefer to consistently use a different function to format p-values or estimates, you can set options in the script or in the user- or project-level startup file, '.Rprofile'. The default confidence level can also be set.

- `options(gtsummary.pvalue_fun = new_function)`
- `options(gtsummary.tbl_regression.estimate_fun = new_function)`
- `options(gtsummary.conf.level = 0.90)`

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.tbl_uvregression()`, `add_nevent.tbl_uvregression()`, `add_q.tbl_uvregression()`, `bold_italicize_labels_levels`, `bold_p.tbl_stack()`, `bold_p.tbl_uvregression`, `inline_text.tbl_uvregression()`, `modify_header()`, `sort_p.tbl_uvregression()`, `tbl_merge()`, `tbl_stack()`

Examples

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

# 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)
  )

# for convenience, you can also pass named lists to any arguments
# that accept formulas (e.g label, etc.)
library(survival)
trial[c("ttdeath", "death", "age", "grade", "response")] %>%
  tbl_uvregression(
    method = coxph,
    y = Surv(ttdeath, death),
    exponentiate = TRUE
  )
```

`trial` *Results from a simulated study of two chemotherapy agents: Drug A and Drug B*

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, yrs

marker Marker Level, ng/mL

stage T Stage

grade Grade

response Tumor Response

death Patient Died

ttdeath Months to Death/Censor

Index