gtsummary :: **CHEAT SHEET**

Summary table and regression model or generate inline reports

Installation

gtsummary requires gt package to work properly
So make sure to install gt before using gtsummary

```
# install gt
install.packages('remotes')
remotes::install_github('rstudio/gt')

# install gtsummary from CRAN
install.packages('gtsummary')

# or development version from github
Remotes::install_github('ddsjoberg/gtsummary')
```

Example data - trial

gtsummary includes results from simulated study of two chemotherapy agents : Drug A / Drug B

```
?trial
```

trt	age	makrer	stage	grade	response	death
chr	dbl	dbl	fct	fct	int	int

Quick Start (tbl_summary)

```
library(dplyr)
library(gtsummary)

trial2 <-
   trial %>% select(trt, age, grade, response)

table1 <- tbl_summary(trial2)

table2 <- tbl_summary(trial2,
  by = trt, # split table by trt group
  missing = "no" # don't list missing data
) %>%
  add_n() %>% # add column with count
  add_p() %>% # add p-value between groups
  bold_labels()
```

Grouped by **trt** and added N, p-value

table1

Characteristic[1]	N = 200
Chemotherapy Treatment	
Drug A	98 (49%)
Drug B	102 (51%)
Age, yrs	47 (38, 57)
Unknown	11
Grade	
I	68 (34%)
II	68 (34%)
III	64 (32%)
Tumor Response	61 (32%)
Unknown	7

[1] Statistics presented: n (%); median (IQR)

table2

Characteristic[1]	N	Drug A, N = 98	Drug B, N = 102	p-value[2]
Age, yrs	189	46 (37, 59)	48 (39, 56)	0.7
Grade	200			0.9
I		35 (36%)	33 (32%)	
II		32 (33%)	36 (35%)	
III		31 (32%)	33 (32%)	
Tumor Response	193	28 (29%)	33 (34%)	0.6

[1] Statistics presented: median (IQR); n (%)

[2] Statistical tests performed: Wilcoxon rank-sum test; chi-square test of independence

Quick Start (tbl_regression)

```
library(survival)
# build regression model
mod1 <- glm(response ~ trt + age + grade, trial,
family = binomial)

t1 <- tbl_regression(mod1, exponentiate = TRUE)

# build survival model table
t2 <- coxph(Surv(ttdeath, death) ~
  trt + grade + age, trial) %>%
  tbl_regression(exponentiate = TRUE)

# merge tables
tbl_merge_ex1 <- tbl_merge(
    tbls = list(t1, t2),
    tab_spanner = c("**Tumor Response**", "**Time to Death**")
  )
```

tbl_merge_ex1

Characteristic	Tumor Response			Time to Death		
	OR[1]	95% CI[1]	p-value	HR[1]	95% CI[1]	p-value
Chemotherapy Treatment						
Drug A	—	—		—	—	
Drug B	1.13	0.60, 2.13	0.7	1.30	0.88, 1.92	0.2
Age, yrs	1.02	1.00, 1.04	0.10	1.01	0.99, 1.02	0.3
Grade						
I	—	—		—	—	
II	0.85	0.39, 1.85	0.7	1.21	0.73, 1.99	0.5
III	1.01	0.47, 2.15	>0.9	1.79	1.12, 2.86	0.014

[1] OR = Odds Ratio, CI = Confidence Interval, HR = Hazard Ratio

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Summary Functions

For create & modify data summary tables

- `tbl_summary()`
- `add_p()`
- `add_overall()`
- `add_n()`
- `add_stat_label()`
- `add_q()` [with tbl_summary]
- `tbl_survival()` [with survfit]

For format regression model results

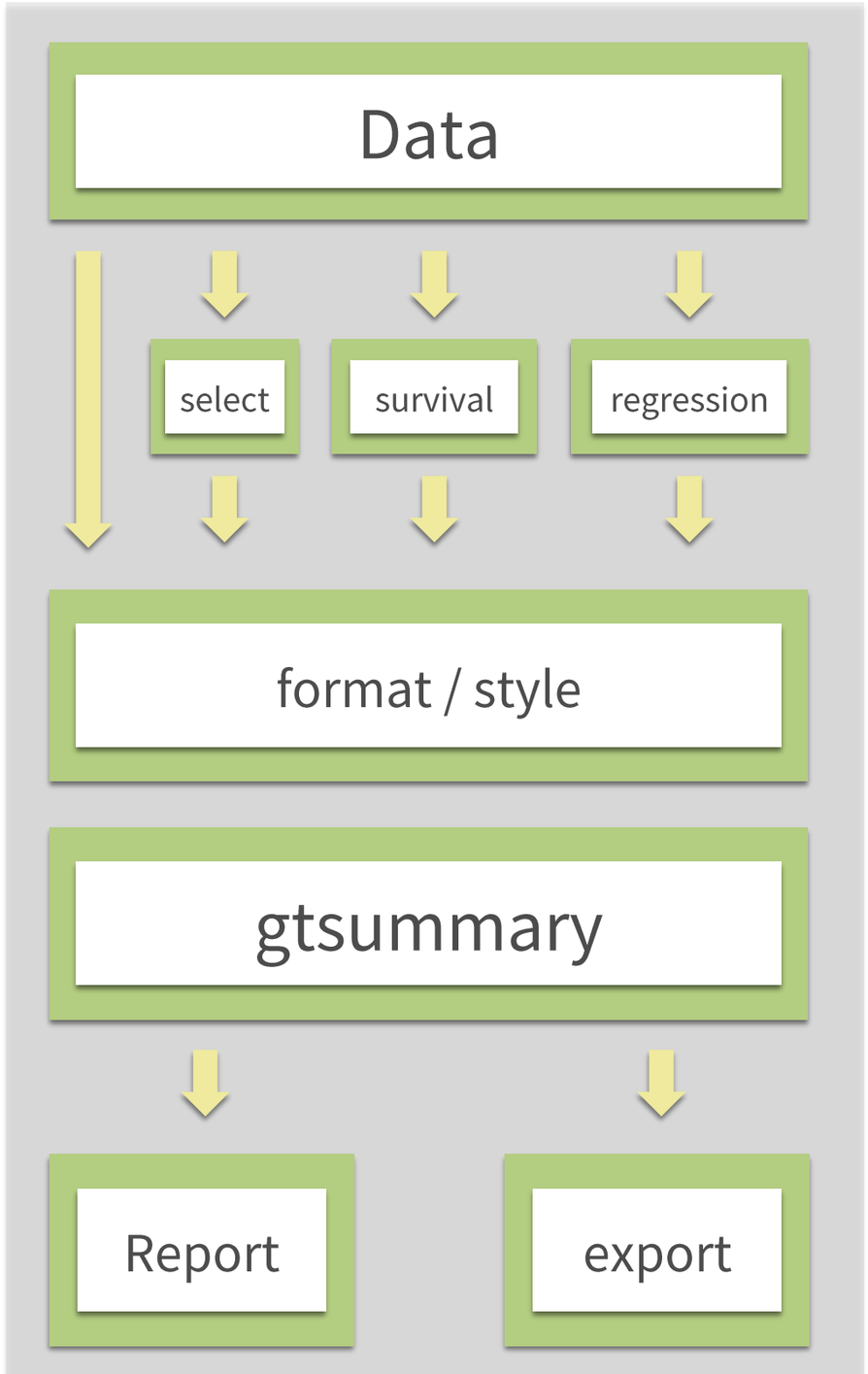
- `tbl_regression()`
- `add_global_p()` [with tbl_regression]
- `add_nevent()` [with tbl_regression]
- `tbl_uvregression()`
- `add_global_p()` [with tbl_uvregression]
- `add_nevent()` [with tbl_uvregression]
- `add_q()` [with tbl_uvregression]

Report Functions

For report result inline in Rmarkdown

- `inline_text` [with tbl_summary]
- `inline_text` [with tbl_survival]
- `inline_text` [with tbl_regression]
- `inline_text` [with tbl_uvregression]

Workflow



General Functions

For modify table view

- `tbl_merge()`
- `tbl_stack()`

- `modify_header()`
- `style_percent()`
- `style_pvalue()`
- `style_sigfig()`
- `style_ratio()`
- `bold_labels()`, `italicize_labels()`
- `bold_levels()`, `italicize_levels()`
- `bold_p()`
- `sort_p()`

- `as_tibble()`
- `as_kable()`
- `as_gt()`

Select Functions

For select group of variables

- `all_*`
  character, integer, double, logical, continuous, categorical, dichotomous