

Package: gtsummarytools (via r-universe)

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Title Add the Nobs to gtsummary tables

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Description Add the Nobs to gtsummary tables.

Depends R (>= 4.1.0)

License GPL (>= 2)

Encoding UTF-8

RoxygenNote 7.3.3

Imports gtsummary, tidyr, dplyr, rlang

Suggests knitr, labelled, survival, testthat (>= 3.0.0)

Config/testthat/edition 3

Config/pak/sysreqs cmake make libicu-dev libuv1-dev libxml2-dev libssl-dev libnode-dev

Repository <https://dcr-unibe-ch.r-universe.dev>

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add_nobs

add_nobs

Description

Add Nobs to a gtsummary table of class "tbl_summary". This function adds the Nobs (i.e. number of non-missing data) to a gtsummary table. Depending on the specified location Nobs will be: (i) added in a new column, (ii) displayed as statistics alongside the variable name (iii) added after the variable name within the same cell.

Usage

```
add_nobs(table, location = "col", rm_missing = TRUE, nobs_text = "Nobs")
```

Arguments

table	a gtsummary table of class "tbl_summary"
location	the location for the Nobs. Can take the following values: "col" = Nobs is displayed in new column(s) (default) "row" : Nobs is displayed as statistics alongside the variable name. Stats are presented below "var_name": Nobs is added after the variable name within the same cell. This option is only available if the table is not stratified
rm_missing	if TRUE (default), the presentation of the missing data will be removed from table.
nobs_text	string indicating text shown for the number of missing observation. Default is "Nobs".

Value

a gtsummary table with the Nobs

Examples

```
#Data
library(dplyr)
library(labelled)
library(gtsummary)

data("cancer", package = "survival")#
cancer <-
  cancer |>
  mutate(
    sex.factor = factor(sex, levels = c(1,2), labels = c("Female", "Male") ),
    yn_var = factor(sex, levels = c(1,2), labels = c("Yes", "No") )
  ) |>
  set_variable_labels (
```

```

  yn_var = "Yes/no variable",
  sex.factor = "Gender",
  inst = "Institution code",
  time = "Time",
  age = "Age",
  ph.ecog = "ECOG score")

# Ex1: stratified table
#. gtsummary table
tab <-
  cancer |>
  select(sex.factor, yn_var, inst, time,age, ph.ecog) |>
  tbl_summary(
  by=sex.factor,
  type = all_continuous() ~ "continuous2",
  statistic = all_continuous() ~ c("{median} ({p25}, {p75})", "{min} - {max}"),
  ) |>
  add_overall()

# .Add Nobs gtsummary table
tab |> add_nobs (location = "row", rm_missing = TRUE, nobs_text ="No")
tab |> add_nobs (location = "col")

# Ex2: un-stratified table
#. gtsummary table
tab <-
  cancer |>
  select(sex.factor, yn_var, inst, time,age, ph.ecog) |>
  tbl_summary()

# .Add Nobs gtsummary table
tab |>
  add_nobs(location = "var_name")

```

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