Package: lulab.utils (via r-universe)

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Title Supporting Functions Maintained by Zhen Lu

Version 0.0.2

Description Miscellaneous functions commonly used by LuLab. This package aims to help more researchers on epidemiology to perform data management and visualization more efficiently.

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URL https://leslie-lu.github.io/

BugReports https://github.com/Leslie-Lu/lulab.utils/issues

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

Imports boot, car, descr, dplyr, magrittr, openxlsx, purrr, stringr, table1

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Repository https://leslie-lu.r-universe.dev

RemoteUrl https://github.com/Leslie-Lu/lulab.utils

RemoteRef HEAD

RemoteSha f5973a312321ba34bd5cd713410622c9aaca5523

Contents

`check_cha` *check_cha*

Description

Check for missing values for character columns

Usage

```
check_cha(col, df, verbose = TRUE)
```

Arguments

`col`	a character variable name
`df`	a data.frame
`verbose`	logical, controlling the output

Details

This function is used to check the distribution of character variables in the data frame.

Value

a distribution table of the character variable in the data frame

Author(s)

Zhen Lu

Examples

```
data("melanoma", package = "boot")
melanoma2 <- melanoma
check_cha('status', melanoma2)
# or
mapply(check_cha,'status', MoreArgs= list(melanoma2))
```

`Table1` *Table1*

Description

Make Table1

Usage

```
Table1(df, ycol, xcol, xlabels, result_dir, verbose = TRUE)
```

Arguments

`df`	a data.frame
`ycol`	a grouping variable
`xcol`	variables to be compared
`xlabels`	levels of ycol
`result_dir`	directory to save the result
`verbose`	logical, controlling the output

Details

This function is used to make Table1 and return excel file.

Value

excel file

Author(s)

Zhen Lu

Examples

```
data("melanoma", package = "boot")
melanoma2 <- melanoma
# Factor the basic variables that
# we're interested in
melanoma2$status <-
  factor(melanoma2$status,
         levels=c(2,1,3),
         labels=c("Alive", # Reference
                  "Melanoma death",
                  "Non-melanoma death"))
test= Table1(
  df= melanoma2,
  xcol= setdiff(names(melanoma2), "status"),
  ycol= "status",
```

```
    result_dir= tempdir()
  )
```

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