

# Package ‘lulab.utils’

September 10, 2024

**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.

**License** Artistic-2.0

**URL** <https://leslie-lu.github.io/>

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

**Encoding** UTF-8

**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

**NeedsCompilation** no

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**Repository** CRAN

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check_cha	<i>check_cha</i>
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### 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))
```

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Table1	<i>Table1</i>
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**Description**

Make Table1

**Usage**

```
Table1(df, ycol, xcol, xlabel, 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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