

# Package ‘jstable’

November 26, 2023

**Title** Create Tables from Different Types of Regression

**Version** 1.1.3

**Date** 2023-11-26

**Description** Create regression tables from generalized linear model(GLM), generalized estimating equation(GEE), generalized linear mixed-effects model(GLMM), Cox proportional hazards model, survey-weighted generalized linear model(svyglm) and survey-weighted Cox model results for publication.

**Depends** R (>= 3.4.0)

**License** Apache License 2.0

**Encoding** UTF-8

**RoxygenNote** 7.2.3

**Imports** geepack, lme4, stats, data.table, labelled, tableone, coxme, survival (>= 3.0.0), survey, methods, dplyr, purrr, magrittr, tibble

**URL** <https://github.com/jinseob2kim/jstable>

**BugReports** <https://github.com/jinseob2kim/jstable/issues>

**Suggests** testthat, knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2023-11-26 05:30:02 UTC

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coefNA	<i>coefNA: make coefficient table with NA</i>
--------	---

---

**Description**

Make coefficient table with NA

**Usage**

coefNA(model)

**Arguments**

model                    glm object (gaussian or binomial)

**Details**

DETAILS

**Value**

coefficient table with NA

**Examples**

```
coefNA(glm(mpg ~ wt + qsec, data = mtcars))
```

---

cox2.display	<i>cox2.display: table for coxph.object with model option: TRUE - allow "frailty" or "cluster" model</i>
--------------	--

---

**Description**

Table for coxph.object with model option: TRUE - allow "frailty" or "cluster" model

**Usage**

```
cox2.display(cox.obj.withmodel, dec = 2)
```

**Arguments**

cox.obj.withmodel                    coxph.object with model option: TRUE

dec                                    Decimal point, Default: 2

**Details**

GEE like - cluster, Mixed effect model like - frailty

**Value**

Table, cluster/frailty info, metrics, caption

**Examples**

```
library(survival)
data(lung)
fit1 <- coxph(Surv(time, status) ~ ph.ecog + age + cluster(inst), data = lung, model = TRUE)
fit2 <- coxph(Surv(time, status) ~ ph.ecog + age + frailty(inst), data = lung, model = TRUE)
cox2.display(fit1)
cox2.display(fit2)
```

---

coxExp	<i>coxExp: transform the unit of coefficients in cox model(internal function)</i>
--------	---

---

**Description**

Transform the unit of coefficients to "HR"

**Usage**

```
coxExp(cox.coef, dec)
```

**Arguments**

cox.coef	cox model coefficients
dec	Decimal point

**Details**

DETAILS

**Value**

The transformed coefficients(95

**Examples**

```
library(coxme)
fit <- coxme(Surv(time, status) ~ ph.ecog + age + (1 | inst), lung)
jstable:::coxExp(jstable:::coxmeTable(fit))
```

---

coxme.display	<i>coxme.display: table for coxme.object (coxme package)</i>
---------------	--

---

**Description**

Make mixed effect model results from coxme.object (coxme package)

**Usage**

```
coxme.display(coxme.obj, dec = 2)
```

**Arguments**

coxme.obj	coxme.object
dec	Decimal point, Default: 2

**Details**

DETAILS

**Value**

Fixed effect table, random effect, metrics, caption

**Examples**

```
library(coxme)
fit <- coxme(Surv(time, status) ~ ph.ecog + age + (1 | inst), lung)
coxme.display(fit)
```

---

`coxmeTable`*coxmeTable: Summary table of coxme.object(internal function)*

---

**Description**Extract fixed effect table in `coxme.object`**Usage**`coxmeTable(mod)`**Arguments**`mod` `coxme.object`**Details**

DETAILS

**Value**

beta, se, z, p of fixed effects

**Examples**

```
library(coxme)
fit <- coxme(Surv(time, status) ~ ph.ecog + age + (1 | inst), lung)
jstable:::coxmeTable(fit)
```

---

CreateTableOne2	<i>CreateTableOne2: Modified CreateTableOne function in tableone package</i>
-----------------	--

---

### Description

Combine CreateTableOne & print function in tableone package

### Usage

```
CreateTableOne2(
  data,
  strata,
  vars,
  factorVars,
  includeNA = F,
  test = T,
  testApprox = chisq.test,
  argsApprox = list(correct = TRUE),
  testExact = fisher.test,
  argsExact = list(workspace = 2 * 10^5),
  testNormal = oneway.test,
  argsNormal = list(var.equal = F),
  testNonNormal = kruskal.test,
  argsNonNormal = list(NULL),
  showAllLevels = T,
  printToggle = F,
  quote = F,
  smd = F,
  Labels = F,
  exact = NULL,
  nonnormal = NULL,
  catDigits = 1,
  contDigits = 2,
  pDigits = 3,
  labeldata = NULL,
  minMax = F,
  showpm = T,
  addOverall = F
)
```

### Arguments

data	A data frame in which these variables exist. All variables (both vars and strata) must be in this data frame.
strata	Stratifying (grouping) variable name(s) given as a character vector. If omitted, the overall results are returned.

vars	Variables to be summarized given as a character vector. Factors are handled as categorical variables, whereas numeric variables are handled as continuous variables. If empty, all variables in the data frame specified in the data argument are used.
factorVars	Numerically coded variables that should be handled as categorical variables given as a character vector. Do not include factors, unless you need to relevel them by removing empty levels. If omitted, only factors are considered categorical variables. The variables specified here must also be specified in the vars argument.
includeNA	If TRUE, NA is handled as a regular factor level rather than missing. NA is shown as the last factor level in the table. Only effective for categorical variables., Default: F
test	If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed, Default: T
testApprox	A function used to perform the large sample approximation based tests. The default is chisq.test. This is not recommended when some of the cell have small counts like fewer than 5, Default: chisq.test
argsApprox	A named list of arguments passed to the function specified in testApprox. The default is list(correct = TRUE), which turns on the continuity correction for chisq.test, Default: list(correct = TRUE)
testExact	A function used to perform the exact tests. The default is fisher.test. If the cells have large numbers, it will fail because of memory limitation. In this situation, the large sample approximation based should suffice., Default: fisher.test
argsExact	A named list of arguments passed to the function specified in testExact. The default is list(workspace = 2 * 10^5), which specifies the memory space allocated for fisher.test, Default: list(workspace = 2 * 10^5)
testNormal	A function used to perform the normal assumption based tests. The default is oneway.test. This is equivalent of the t-test when there are only two groups, Default: oneway.test
argsNormal	A named list of arguments passed to the function specified in testNormal. The default is list(var.equal = TRUE), which makes it the ordinary ANOVA that assumes equal variance across groups., Default: list(var.equal = F)
testNonNormal	A function used to perform the nonparametric tests. The default is kruskal.test (Kruskal-Wallis Rank Sum Test). This is equivalent of the wilcox.test (Mann-Whitney U test) when there are only two groups, Default: kruskal.test
argsNonNormal	A named list of arguments passed to the function specified in testNonNormal. The default is list(NULL), which is just a placeholder., Default: list(NULL)
showAllLevels	Whether to show all levels. FALSE by default, i.e., for 2-level categorical variables, only the higher level is shown to avoid redundant information., Default: T
printToggle	Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned., Default: F
quote	Whether to show everything in quotes. The default is FALSE. If TRUE, everything including the row and column names are quoted so that you can copy it to Excel easily, Default: F

smd	If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated, Default: F
Labels	Use Label, Default: F
exact	A character vector to specify the variables for which the p-values should be those of exact tests. By default all p-values are from large sample approximation tests (chisq.test), Default: NULL
nonnormal	A character vector to specify the variables for which the p-values should be those of nonparametric tests. By default all p-values are from normal assumption-based tests (oneway.test), Default: NULL
catDigits	Number of digits to print for proportions., Default: 1
contDigits	Number of digits to print for continuous variables. Default 2.
pDigits	Number of digits to print for p-values (also used for standardized mean differences), Default: 3
labeldata	labeldata to use, Default: NULL
minMax	Whether to use [min,max] instead of [p25,p75] for nonnormal variables. The default is FALSE.
showpm	Logical, show normal distributed continuous variables as Mean $\pm$ SD. Default: T
addOverall	(optional, only used if strata are supplied) Adds an overall column to the table. Smd and p-value calculations are performed using only the stratified columns. Default: F

## Details

DETAILS

## Value

A matrix object containing what you see is also invisibly returned. This can be assigned a name and exported via write.csv.

## Examples

```
library(survival)
CreateTableOne2(vars = names(lung), strata = "sex", data = lung)
```

---

CreateTableOneJS	<i>CreateTableOneJS: Modified CreateTableOne function in tableone package</i>
------------------	---

---

## Description

Combine CreateTableOne & print function in tableone package



**Usage**

```

CreateTableOneJS(
  vars,
  strata = NULL,
  strata2 = NULL,
  data,
  factorVars = NULL,
  includeNA = F,
  test = T,
  testApprox = chisq.test,
  argsApprox = list(correct = TRUE),
  testExact = fisher.test,
  argsExact = list(workspace = 2 * 10^5),
  testNormal = oneway.test,
  argsNormal = list(var.equal = F),
  testNonNormal = kruskal.test,
  argsNonNormal = list(NULL),
  showAllLevels = T,
  printToggle = F,
  quote = F,
  smd = F,
  Labels = F,
  exact = NULL,
  nonnormal = NULL,
  catDigits = 1,
  contDigits = 2,
  pDigits = 3,
  labeldata = NULL,
  psub = T,
  minMax = F,
  showpm = T,
  addOverall = F
)

```

**Arguments**

<code>vars</code>	Variables to be summarized given as a character vector. Factors are handled as categorical variables, whereas numeric variables are handled as continuous variables. If empty, all variables in the data frame specified in the <code>data</code> argument are used.
<code>strata</code>	Stratifying grouping variable name(s) given as a character vector. If omitted, the overall results are returned.
<code>strata2</code>	Stratifying 2nd grouping variable name(s) given as a character vector. If omitted, the 1 group results are returned.
<code>data</code>	A data frame in which these variables exist. All variables (both <code>vars</code> and <code>strata</code> ) must be in this data frame.

factorVars	Numerically coded variables that should be handled as categorical variables given as a character vector. Do not include factors, unless you need to relevel them by removing empty levels. If omitted, only factors are considered categorical variables. The variables specified here must also be specified in the vars argument.
includeNA	If TRUE, NA is handled as a regular factor level rather than missing. NA is shown as the last factor level in the table. Only effective for categorical variables., Default: F
test	If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed, Default: T
testApprox	A function used to perform the large sample approximation based tests. The default is chisq.test. This is not recommended when some of the cell have small counts like fewer than 5, Default: chisq.test
argsApprox	A named list of arguments passed to the function specified in testApprox. The default is list(correct = TRUE), which turns on the continuity correction for chisq.test, Default: list(correct = TRUE)
testExact	A function used to perform the exact tests. The default is fisher.test. If the cells have large numbers, it will fail because of memory limitation. In this situation, the large sample approximation based should suffice., Default: fisher.test
argsExact	A named list of arguments passed to the function specified in testExact. The default is list(workspace = 2 * 10^5), which specifies the memory space allocated for fisher.test, Default: list(workspace = 2 * 10^5)
testNormal	A function used to perform the normal assumption based tests. The default is oneway.test. This is equivalent of the t-test when there are only two groups, Default: oneway.test
argsNormal	A named list of arguments passed to the function specified in testNormal. The default is list(var.equal = TRUE), which makes it the ordinary ANOVA that assumes equal variance across groups., Default: list(var.equal = F)
testNonNormal	A function used to perform the nonparametric tests. The default is kruskal.test (Kruskal-Wallis Rank Sum Test). This is equivalent of the wilcox.test (Mann-Whitney U test) when there are only two groups, Default: kruskal.test
argsNonNormal	A named list of arguments passed to the function specified in testNonNormal. The default is list(NULL), which is just a placeholder., Default: list(NULL)
showAllLevels	Whether to show all levels. FALSE by default, i.e., for 2-level categorical variables, only the higher level is shown to avoid redundant information., Default: T
printToggle	Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned., Default: F
quote	Whether to show everything in quotes. The default is FALSE. If TRUE, everything including the row and column names are quoted so that you can copy it to Excel easily, Default: F
smd	If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated, Default: F
Labels	Use Label, Default: F

<code>exact</code>	A character vector to specify the variables for which the p-values should be those of exact tests. By default all p-values are from large sample approximation tests ( <code>chisq.test</code> ), Default: NULL
<code>nonnormal</code>	A character vector to specify the variables for which the p-values should be those of nonparametric tests. By default all p-values are from normal assumption-based tests ( <code>oneway.test</code> ), Default: NULL
<code>catDigits</code>	Number of digits to print for proportions. Default: 1
<code>contDigits</code>	Number of digits to print for continuous variables. Default 2.
<code>pDigits</code>	Number of digits to print for p-values (also used for standardized mean differences), Default: 3
<code>labeldata</code>	labeldata to use, Default: NULL
<code>psub</code>	show sub-group p-values, Default: F
<code>minMax</code>	Whether to use [min,max] instead of [p25,p75] for nonnormal variables. The default is FALSE.
<code>showpm</code>	Logical, show normal distributed continuous variables as Mean $\pm$ SD. Default: T
<code>addOverall</code>	(optional, only used if strata are supplied) Adds an overall column to the table. Smd and p-value calculations are performed using only the stratified columns. Default: F

**Details**

DETAILS

**Value**

A matrix object containing what you see is also invisibly returned. This can be assigned a name and exported via `write.csv`.

**Examples**

```
library(survival)
CreateTableOneJS(vars = names(lung), strata = "sex", data = lung)
```

---

```
extractAIC.coxme
```

```
extractAIC.coxme: Extract AIC from coxme.object
```

---

**Description**

Extract AIC from `coxme.object`

**Usage**

```
## S3 method for class 'coxme'
extractAIC(fit, scale = NULL, k = 2, ...)
```

**Arguments**

fit	coxme.object
scale	NULL
k	numeric specifying the 'weight' of the equivalent degrees of freedom (=: edf) part in the AIC formula.
...	further arguments (currently unused in base R).

**Details**

DETAILS

**Value**

AIC(Integreted, Penalized)

**Examples**

```
library(coxme)
fit <- coxme(Surv(time, status) ~ ph.ecog + age + (1 | inst), lung)
extractAIC(fit)
```

---

geeExp

*geeExp: transform the unit of coefficients (internal function)*

---

**Description**

Transform the unit of coefficients to "Coeff", "OR" or "RR"

**Usage**

```
geeExp(gee.coef, family = "binomial", dec)
```

**Arguments**

gee.coef	geeUni object.
family	Family: "gaussian", "binomial", "poisson", "quasipoisson", etc..., Default: 'binomial'
dec	Decimal point

**Details**

DETAILS

**Value**

The transformed coefficients(95

**Examples**

```
library(geepack)
data(dietox)
dietox$Cu <- as.factor(dietox$Cu)
gee.uni <- geeUni("Weight", c("Time", "Cu"),
  data = dietox, id.vec = dietox$Pig,
  family = "gaussian", cor.type = "exchangeable"
)
gee.exp <- geeExp(gee.uni, "binomial", 2)
```

---

geeglm.display      *geeglm.display*

---

**Description**

Make gee results from "geeglm" object

**Usage**

```
geeglm.display(geeglm.obj, decimal = 2)
```

**Arguments**

geeglm.obj	"geeglm" object
decimal	Decimal, Default: 2

**Details**

DETAILS

**Value**

List: caption, main table, metrics table

**See Also**

[data.table-package complete.cases](#)

**Examples**

```
library(geepack)
data(dietox)
dietox$Cu <- as.factor(dietox$Cu)
gee01 <- geeglm(Weight ~ Time + Cu,
  id = Pig, data = dietox,
  family = gaussian, corstr = "ex"
)
geeglm.display(gee01)
```

---

geeUni                      *geeUni: The coefficient of univariate gee (internal function)*

---

### Description

Extract the coefficients of univariate gee using `geeglm` function (geepack package).

### Usage

```
geeUni(y, x, data, id.vec, family, cor.type = "exchangeable")
```

### Arguments

<code>y</code>	Dependant variable
<code>x</code>	Independent variable
<code>data</code>	Data
<code>id.vec</code>	Vector of id (should be ordered)
<code>family</code>	Family: "gaussian", "binomial", "poisson", "quasipoisson", etc...
<code>cor.type</code>	Correlation structure, Default: 'exchangeable'

### Details

DETAILS

### Value

coefficient, standard error, p-value

### Examples

```
library(geepack)
data(dietox)
dietox$Cu <- as.factor(dietox$Cu)
gee.uni <- geeUni("Weight", "Time",
  data = dietox, id.vec = dietox$Pig,
  family = "gaussian", cor.type = "exchangeable"
)
```

---

glmshow.display	<i>glmshow.display: Show summary table of glm object.</i>
-----------------	---

---

**Description**

Show summary table of glm object(regression, logistic).

**Usage**

```
glmshow.display(glm.object, decimal = 2)
```

**Arguments**

glm.object	glm.object
decimal	digits, Default: 2

**Details**

DETAILS

**Value**

table

**See Also**

[glm](#)

**Examples**

```
glmshow.display(glm(mpg ~ wt + qsec, data = mtcars))
```

---

LabelepiDisplay	<i>LabelepiDisplay: Apply label information to epiDisplay object using label data</i>
-----------------	---

---

**Description**

Apply label information to epiDisplay.object using label data

**Usage**

```
LabelepiDisplay(epiDisplay.obj, label = F, ref)
```

**Arguments**

epiDisplay.obj epiDisplay.object or glmshow.object  
 label Apply label information, Default: F  
 ref Label data made by mk.lev function

**Details**

DETAILS

**Value**

epiDisplay.object with label information

**Examples**

```
fit <- glm(Sepal.Length ~ Sepal.Width + Species, data = iris)
fit.table <- glmshow.display(fit)
iris.label <- mk.lev(iris)
LabelepiDisplay(fit.table, label = TRUE, ref = iris.label)
```

---

LabeljsCox

*LabeljsCox: Apply label information to cox2.display object using label data*

---

**Description**

Apply label information to cox2.display object using label data

**Usage**

```
LabeljsCox(obj, ref)
```

**Arguments**

obj cox2.display object  
 ref Label data made by mk.lev function

**Details**

DETAILS

**Value**

cox2.display object with label information



**Examples**

```

library(survival)
fit <- coxph(Surv(time, status) ~ sex + ph.ecog + ph.karno + cluster(inst),
  data = lung, model = TRUE
)
fit.table <- cox2.display(fit)
lung.label <- mk.lev(lung)
LabeljsCox(fit.table, ref = lung.label)

```

---

LabeljsGeeglm	<i>LabeljsGeeglm: Apply label information to geeglm.display object using label data</i>
---------------	---

---

**Description**

Apply label information to geeglm.display object using label data

**Usage**

```
LabeljsGeeglm(obj, ref)
```

**Arguments**

obj	geeglm.display object
ref	Label data made by mk.lev function

**Details**

DETAILS

**Value**

geeglm.display object with label information

**Examples**

```

library(geepack)
library(jstable)
data(dietox)
dietox$Cu <- as.factor(dietox$Cu)
gee01 <- geeglm(Weight ~ Time + Cu,
  id = Pig, data = dietox,
  family = gaussian, corstr = "ex"
)
g1 <- geeglm.display(gee01)
LabeljsGeeglm(g1, ref = mk.lev(dietox))

```

---

LabeljsMetric	<i>LabeljsMetric: Apply label information to jstable metric object using label data</i>
---------------	---

---

**Description**

Apply label information to metric object of jstable using label data

**Usage**

```
LabeljsMetric(obj.metric, ref)
```

**Arguments**

obj.metric	metric of lmer.display, coxme.display
ref	Label data made by mk.lev function

**Details**

DETAILS

**Value**

metric of lmer.display, coxme.display with label information

**Examples**

```
library(coxme)
fit <- coxme(Surv(time, status) ~ sex + ph.ecog + ph.karno + (1 | inst) + (1 | sex), lung)
fit.table <- coxme.display(fit)
lung.label <- mk.lev(lung)
LabeljsTable(fit.table$table, ref = lung.label)
LabeljsRanef(fit.table$ranef, ref = lung.label)
LabeljsMetric(fit.table$metric, ref = lung.label)
```

---

LabeljsMixed	<i>LabeljsMixed: Apply label information to jstable object using label data</i>
--------------	---

---

**Description**

Apply label information to object of jstable using label data

**Usage**

```
LabeljsMixed(obj, ref)
```

**Arguments**

obj	lmer.display, coxme.display
ref	Label data made by mk.lev function

**Details**

DETAILS

**Value**

lmer.display, coxme.display with label information

**Examples**

```
library(coxme)
fit <- coxme(Surv(time, status) ~ sex + ph.ecog + ph.karno + (1 | inst) + (1 | sex), lung)
fit.table <- coxme.display(fit)
lung.label <- mk.lev(lung)
LabeljsMixed(fit.table, ref = lung.label)
```

---

LabeljsRanef	<i>LabeljsRanef: Apply label information to jstable random effect object using label data</i>
--------------	---

---

**Description**

Apply label information to ranef object of jstable using label data

**Usage**

```
LabeljsRanef(obj.ranef, ref)
```

**Arguments**

obj.ranef	ranef of lmer.display, coxme.display, cox2.display
ref	Label data made by mk.lev function

**Details**

DETAILS

**Value**

ranef of lmer.display, coxme.display, cox2.display with label information

**Examples**

```
library(coxme)
fit <- coxme(Surv(time, status) ~ sex + ph.ecog + ph.karno + (1 | inst) + (1 | sex), lung)
fit.table <- coxme.display(fit)
lung.label <- mk.lev(lung)
LabeljsTable(fit.table$table, ref = lung.label)
LabeljsRanef(fit.table$ranef, ref = lung.label)
```

---

LabeljsTable	<i>LabeljsTable: Apply label information to jstable object using label data</i>
--------------	---

---

**Description**

Apply label information to table of `geeglm.display`, `lmer.display`, `coxme.display` using label data

**Usage**

```
LabeljsTable(obj.table, ref)
```

**Arguments**

<code>obj.table</code>	table of <code>geeglm.display</code> , <code>lmer.display</code> , <code>coxme.display</code>
<code>ref</code>	Label data made by <code>mk.lev</code> function

**Details**

DETAILS

**Value**

table of `geeglm.display`, `lmer.display`, `coxme.display` with label information

**Examples**

```
library(coxme)
fit <- coxme(Surv(time, status) ~ sex + ph.ecog + ph.karno + (1 | inst) + (1 | sex), lung)
fit.table <- coxme.display(fit)
lung.label <- mk.lev(lung)
LabeljsTable(fit.table$table, ref = lung.label)
```

---

lmer.display	<i>lmer.display: table for "lmerMod" or "glmerMod" object (lme4 package)</i>
--------------	--

---

**Description**

Make mixed effect model results from "lmerMod" or "glmerMod" object (lme4 package)

**Usage**

```
lmer.display(lmerMod.obj, dec = 2, ci.ranef = F)
```

**Arguments**

lmerMod.obj	"lmerMod" or "glmerMod" object
dec	Decimal, Default: 2
ci.ranef	Show confidence interval of random effects?, Default: F

**Details**

DETAILS

**Value**

Table: fixed & random effect

**Examples**

```
library(geepack)
data(dietox)
dietox$Cu <- as.factor(dietox$Cu)
l1 <- lme4::lmer(Weight ~ Time + Cu + (1 | Pig) + (1 | Evit), data = dietox)
lmer.display(l1)
```

---

lmerExp	<i>lmerExp: transform the unit of coefficients (internal function)</i>
---------	--

---

**Description**

Transform the unit of coefficients to "Coeff", "OR" or "RR"

**Usage**

```
lmerExp(lmer.coef, family = "binomial", dec)
```

**Arguments**

lmer.coef	lmer coefficients.
family	Family: "gaussian", "binomial", "poisson", "quasipoisson", etc..., Default: 'binomial'
dec	Decimal point

**Details**

DETAILS

**Value**

The transformed coefficients(95

**Examples**

```
# EXAMPLE1
```

---

```
mk.lev
```

*Export label and level: multiple variable*

---

**Description**

Export label and level: multiple variable

**Usage**

```
mk.lev(data)
```

**Arguments**

data	data
------	------

**Details**

DETAILS

**Value**

default label and level data

**Examples**

```
mk.lev(iris)
```

---

mk.lev.var	<i>Export label and level: one variable</i>
------------	---

---

**Description**

Export label and level: one variable

**Usage**

```
mk.lev.var(data, vname)
```

**Arguments**

data	data
vname	variable to export label and level

**Details**

DETAILS

**Value**

if continuous variable - (label, NA), categorical variable - (label, level)

**Examples**

```
lapply(names(iris), function(x) {
  jstable::mk.lev.var(iris, x)
})
```

---

opt.data	<i>datable option for data(DT package)</i>
----------	--

---

**Description**

DT::datatable option for data

**Usage**

```
opt.data(fname)
```

**Arguments**

fname	File name to download
-------	-----------------------

**Details**

DETAILS

**Value**

datatable option object

**Examples**

```
opt.data("mtcars")
```

---

`opt.roc`*datable option for ROC result(DT package)*

---

**Description**

DT::datatable option for ROC result

**Usage**

```
opt.roc(fname)
```

**Arguments**

fname	File name to download
-------	-----------------------

**Details**

DETAILS

**Value**

datatable option object

**Examples**

```
options <- opt.roc("mtcars")
```



---

opt.simplifiedown      *databale option for simple download(DT package)*

---

**Description**

Simple download DT::datatable option - No filter, No page

**Usage**

opt.simplifiedown(fname)

**Arguments**

fname              File name to download

**Details**

DETAILS

**Value**

datatable option object

**Examples**

```
options <- opt.simplifiedown("mtcars")
```

---

opt.tb1              *databale option for table 1(DT package)*

---

**Description**

DT::datatable option for table 1

**Usage**

opt.tb1(fname)

**Arguments**

fname              File name to download

**Details**

DETAILS

**Value**

datatable option object

**Examples**

```
options <- opt.tb1("mtcars")
```

---

opt.tbreg	<i>datable option for regression table(DT package)</i>
-----------	--

---

**Description**

DT::datatable option for glm, gee(geepack package), lmer/glmer(lme4 package)

**Usage**

```
opt.tbreg(fname)
```

**Arguments**

fname	File name to download
-------	-----------------------

**Details**

DETAILS

**Value**

datatable option object

**Examples**

```
options <- opt.tbreg("mtcars")
```

---

svycox.display	<i>svycoxph.display: table for svycoxph.object in survey package.</i>
----------------	---

---

**Description**

Table for complex design cox model.

**Usage**

```
svycox.display(svycoxph.obj, decimal = 2)
```

**Arguments**

svycoxph.obj	svycoxph.object
decimal	digit, Default: 2

**Details**

DETAILS

**Value**

List including table, metric, caption

**See Also**

[svycoxph AIC](#)

**Examples**

```
library(survival)
data(pbc)
pbc$sex <- factor(pbc$sex)
pbc$stage <- factor(pbc$stage)
pbc$randomized <- with(pbc, !is.na(trt) & trt > 0)
biasmodel <- glm(randomized ~ age * edema, data = pbc, family = binomial)
pbc$randprob <- fitted(biasmodel)

if (is.null(pbc$albumin)) pbc$albumin <- pbc$alb ## pre2.9.0

dpsc <- survey::svydesign(
  id = ~1, prob = ~randprob, strata = ~edema,
  data = subset(pbc, randomized)
)

model <- survey::svycoxph(Surv(time, status > 0) ~ sex + protime + albumin + stage,
  design = dpsc
)
svycox.display(model)
```

---

svyCreateTableOne2     *svyCreateTableOne2: Modified svyCreateTableOne function in tableone package*

---

### Description

Combine svyCreateTableOne & print function in tableone package

### Usage

```
svyCreateTableOne2(
  data,
  strata,
  vars,
  factorVars,
  includeNA = F,
  test = T,
  showAllLevels = T,
  printToggle = F,
  quote = F,
  smd = F,
  nonnormal = NULL,
  catDigits = 1,
  contDigits = 2,
  pDigits = 3,
  Labels = F,
  labeldata = NULL,
  minMax = F,
  showpm = T,
  addOverall = F
)
```

### Arguments

data	A data frame in which these variables exist. All variables (both vars and strata) must be in this data frame.
strata	Stratifying (grouping) variable name(s) given as a character vector. If omitted, the overall results are returned.
vars	Variables to be summarized given as a character vector. Factors are handled as categorical variables, whereas numeric variables are handled as continuous variables. If empty, all variables in the data frame specified in the data argument are used.
factorVars	Numerically coded variables that should be handled as categorical variables given as a character vector. Do not include factors, unless you need to relevel them by removing empty levels. If omitted, only factors are considered categorical variables. The variables specified here must also be specified in the vars argument.

includeNA	If TRUE, NA is handled as a regular factor level rather than missing. NA is shown as the last factor level in the table. Only effective for categorical variables., Default: F
test	If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed, Default: T
showAllLevels	Whether to show all levels. FALSE by default, i.e., for 2-level categorical variables, only the higher level is shown to avoid redundant information., Default: T
printToggle	Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned., Default: F
quote	Whether to show everything in quotes. The default is FALSE. If TRUE, everything including the row and column names are quoted so that you can copy it to Excel easily, Default: F
smd	If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated, Default: F
nonnormal	A character vector to specify the variables for which the p-values should be those of nonparametric tests. By default all p-values are from normal assumption-based tests (oneway.test)., Default: NULL
catDigits	Number of digits to print for proportions., Default: 1
contDigits	Number of digits to print for continuous variables. Default 2.
pDigits	Number of digits to print for p-values (also used for standardized mean differences), Default: 3
Labels	Use Label, Default: F
labeldata	labeldata to use, Default: NULL
minMax	Whether to use [min,max] instead of [p25,p75] for nonnormal variables. The default is FALSE.
showpm	Logical, show normal distributed continuous variables as Mean $\pm$ SD. Default: T
addOverall	(optional, only used if strata are supplied) Adds an overall column to the table. Smd and p-value calculations are performed using only the stratified columns. Default: F

## Details

DETAILS

## Value

A matrix object containing what you see is also invisibly returned. This can be assigned a name and exported via write.csv.

**Examples**

```

library(survey)
data(nhanes)
nhanes$SDMVPSU <- as.factor(nhanes$SDMVPSU)
nhanesSvy <- svydesign(
  ids = ~SDMVPSU, strata = ~SDMVSTRA, weights = ~WTMEC2YR,
  nest = TRUE, data = nhanes
)
svyCreateTableOne2(
  vars = c("HI_CHOL", "race", "agecat", "RIAGENDR"),
  strata = "RIAGENDR", data = nhanesSvy,
  factorVars = c("HI_CHOL", "race", "RIAGENDR")
)

```

---

svyCreateTableOneJS	<i>svyCreateTableOneJS: Modified CreateTableOne function in tableone package</i>
---------------------	--

---

**Description**

Combine svyCreateTableOne & print function in tableone package

**Usage**

```

svyCreateTableOneJS(
  vars,
  strata = NULL,
  strata2 = NULL,
  data,
  factorVars = NULL,
  includeNA = F,
  test = T,
  showAllLevels = T,
  printToggle = F,
  quote = F,
  smd = F,
  Labels = F,
  nonnormal = NULL,
  catDigits = 1,
  contDigits = 2,
  pDigits = 3,
  labeldata = NULL,
  psub = T,
  minMax = F,
  showpm = T,
  addOverall = F
)

```

**Arguments**

vars	Variables to be summarized given as a character vector. Factors are handled as categorical variables, whereas numeric variables are handled as continuous variables. If empty, all variables in the data frame specified in the data argument are used.
strata	Stratifying grouping variable name(s) given as a character vector. If omitted, the overall results are returned.
strata2	Stratifying 2nd grouping variable name(s) given as a character vector. If omitted, the 1 group results are returned.
data	A data frame in which these variables exist. All variables (both vars and strata) must be in this data frame.
factorVars	Numerically coded variables that should be handled as categorical variables given as a character vector. Do not include factors, unless you need to relevel them by removing empty levels. If omitted, only factors are considered categorical variables. The variables specified here must also be specified in the vars argument.
includeNA	If TRUE, NA is handled as a regular factor level rather than missing. NA is shown as the last factor level in the table. Only effective for categorical variables., Default: F
test	If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed, Default: T
showAllLevels	Whether to show all levels. FALSE by default, i.e., for 2-level categorical variables, only the higher level is shown to avoid redundant information., Default: T
printToggle	Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned., Default: F
quote	Whether to show everything in quotes. The default is FALSE. If TRUE, everything including the row and column names are quoted so that you can copy it to Excel easily, Default: F
smd	If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated, Default: F
Labels	Use Label, Default: F
nonnormal	A character vector to specify the variables for which the p-values should be those of nonparametric tests. By default all p-values are from normal assumption-based tests (oneway.test), Default: NULL
catDigits	Number of digits to print for proportions., Default: 1
contDigits	Number of digits to print for continuous variables. Default 2.
pDigits	Number of digits to print for p-values (also used for standardized mean differences), Default: 3
labeldata	labeldata to use, Default: NULL
psub	show sub-group p-values, Default: F
minMax	Whether to use [min,max] instead of [p25,p75] for nonnormal variables. The default is FALSE.

showpm	Logical, show normal distributed continuous variables as Mean $\pm$ SD. Default: T
addOverall	(optional, only used if strata are supplied) Adds an overall column to the table. Smd and p-value calculations are performed using only the stratified columns. Default: F

**Details**

DETAILS

**Value**

A matrix object containing what you see is also invisibly returned. This can be assigned a name and exported via write.csv.

**Examples**

```
library(survey)
data(nhanes)
nhanes$SDMVPSU <- as.factor(nhanes$SDMVPSU)
nhanesSvy <- svydesign(
  ids = ~SDMVPSU, strata = ~SDMVSTRA, weights = ~WTMEC2YR,
  nest = TRUE, data = nhanes
)
svyCreateTableOneJS(
  vars = c("HI_CHOL", "race", "agecat", "RIAGENDR"),
  strata = "RIAGENDR", data = nhanesSvy,
  factorVars = c("HI_CHOL", "race", "RIAGENDR")
)
```

---

svyregress.display      *svyregress.display: table for svyglm.object*

---

**Description**

table for svyglm.object (survey package).

**Usage**

```
svyregress.display(svyglm.obj, decimal = 2)
```

**Arguments**

svyglm.obj	svyglm.object
decimal	digit, Default: 2

**Details**

DETAILS



**Value**

table

**Examples**

```

library(survey)
data(api)
apistrat$tt <- c(rep(1, 20), rep(0, nrow(apistrat) - 20))
dstrat <- svydesign(id = ~1, strata = ~stype, weights = ~pw, data = apistrat, fpc = ~fpc)
ds <- svyglm(api00 ~ ell + meals + cname + mobility, design = dstrat)
ds2 <- svyglm(tt ~ ell + meals + cname + mobility, design = dstrat, family = quasibinomial())
svyregress.display(ds)
svyregress.display(ds2)

```

TableSubgroupCox

*TableSubgroupCox: Sub-group analysis table for Cox/svycox model.***Description**

Sub-group analysis table for Cox/svycox model.

**Usage**

```

TableSubgroupCox(
  formula,
  var_subgroup = NULL,
  var_cov = NULL,
  data,
  time_eventrate = 3 * 365,
  decimal.hr = 2,
  decimal.percent = 1,
  decimal.pvalue = 3
)

```

**Arguments**

formula	formula with survival analysis.
var_subgroup	1 sub-group variable for analysis, Default: NULL
var_cov	Variables for additional adjust, Default: NULL
data	Data or svydesign in survey package.
time_eventrate	Time for kaplan-meier based event rate calculation, Default = 365 * 3
decimal.hr	Decimal for hazard ratio, Default: 2
decimal.percent	Decimal for percent, Default: 1
decimal.pvalue	Decimal for pvalue, Default: 3

**Details**

This result is used to make forestplot.

**Value**

Sub-group analysis table.

**See Also**

[safely](#), [map](#), [map2](#) [coxph](#) [svycoxph](#) [confint](#)

**Examples**

```
library(survival)
library(dplyr)
lung %>%
  mutate(
    status = as.integer(status == 1),
    sex = factor(sex),
    kk = factor(as.integer(pat.karno >= 70))
  ) -> lung
TableSubgroupCox(Surv(time, status) ~ sex, data = lung, time_eventrate = 100)
TableSubgroupCox(Surv(time, status) ~ sex,
  var_subgroup = "kk", data = lung,
  time_eventrate = 100
)

## survey design
library(survey)
data.design <- svydesign(id = ~1, data = lung)
TableSubgroupCox(Surv(time, status) ~ sex, data = data.design, time_eventrate = 100)
TableSubgroupCox(Surv(time, status) ~ sex,
  var_subgroup = "kk", data = data.design,
  time_eventrate = 100
)
```

---

TableSubgroupGLM

*TableSubgroupGLM: Sub-group analysis table for GLM.*

---

**Description**

Sub-group analysis table for GLM.

**Usage**

```
TableSubgroupGLM(
  formula,
  var_subgroup = NULL,
  var_cov = NULL,
```

```

    data,
    family = "binomial",
    decimal.estimate = 2,
    decimal.percent = 1,
    decimal.pvalue = 3
  )

```

### Arguments

formula	formula with survival analysis.
var_subgroup	1 sub-group variable for analysis, Default: NULL
var_cov	Variables for additional adjust, Default: NULL
data	Data or svydesign in survey package.
family	family, "gaussian" or "binomial"
decimal.estimate	Decimal for estimate, Default: 2
decimal.percent	Decimal for percent, Default: 1
decimal.pvalue	Decimal for pvalue, Default: 3

### Details

This result is used to make forestplot.

### Value

Sub-group analysis table.

### See Also

[safely.map](#), [map2](#) [glm](#) [svyglm](#) [confint](#)

### Examples

```

library(survival)
library(dplyr)
lung %>%
  mutate(
    status = as.integer(status == 1),
    sex = factor(sex),
    kk = factor(as.integer(pat.karno >= 70))
  ) -> lung
TableSubgroupGLM(status ~ sex, data = lung, family = "binomial")
TableSubgroupGLM(status ~ sex, var_subgroup = "kk", data = lung, family = "binomial")

## survey design
library(survey)
data.design <- svydesign(id = ~1, data = lung)
TableSubgroupGLM(status ~ sex, data = data.design, family = "binomial")
TableSubgroupGLM(status ~ sex, var_subgroup = "kk", data = data.design, family = "binomial")

```

---

TableSubgroupMultiCox *TableSubgroupMultiCox: Multiple sub-group analysis table for Cox/svycox model.*

---

### Description

Multiple sub-group analysis table for Cox/svycox model.

### Usage

```
TableSubgroupMultiCox(
  formula,
  var_subgroups = NULL,
  var_cov = NULL,
  data,
  time_eventrate = 3 * 365,
  decimal.hr = 2,
  decimal.percent = 1,
  decimal.pvalue = 3,
  line = F
)
```

### Arguments

formula	formula with survival analysis.
var_subgroups	Multiple sub-group variables for analysis, Default: NULL
var_cov	Variables for additional adjust, Default: NULL
data	Data or svydesign in survey package.
time_eventrate	Time for kaplan-meier based event rate calculation, Default = 365 * 3
decimal.hr	Decimal for hazard ratio, Default: 2
decimal.percent	Decimal for percent, Default: 1
decimal.pvalue	Decimal for pvalue, Default: 3
line	Include new-line between sub-group variables, Default: F

### Details

This result is used to make forestplot.

### Value

Multiple sub-group analysis table.

### See Also

[map bind](#)

**Examples**

```

library(survival)
library(dplyr)
lung %>%
  mutate(
    status = as.integer(status == 1),
    sex = factor(sex),
    kk = factor(as.integer(pat.karno >= 70)),
    kk1 = factor(as.integer(pat.karno >= 60))
  ) -> lung
TableSubgroupMultiCox(Surv(time, status) ~ sex,
  var_subgroups = c("kk", "kk1"),
  data = lung, time_eventrate = 100, line = TRUE
)

## survey design
library(survey)
data.design <- svydesign(id = ~1, data = lung)
TableSubgroupMultiCox(Surv(time, status) ~ sex,
  var_subgroups = c("kk", "kk1"),
  data = data.design, time_eventrate = 100
)

```

---

TableSubgroupMultiGLM *TableSubgroupMultiGLM: Multiple sub-group analysis table for GLM.*

---

**Description**

Multiple sub-group analysis table for GLM.

**Usage**

```

TableSubgroupMultiGLM(
  formula,
  var_subgroups = NULL,
  var_cov = NULL,
  data,
  family = "binomial",
  decimal.estimate = 2,
  decimal.percent = 1,
  decimal.pvalue = 3,
  line = F
)

```

**Arguments**

formula            formula with survival analysis.

var\_subgroups Multiple sub-group variables for analysis, Default: NULL  
 var\_cov Variables for additional adjust, Default: NULL  
 data Data or svydesign in survey package.  
 family family, "gaussian" or "binomial"  
 decimal.estimate Decimal for estimate, Default: 2  
 decimal.percent Decimal for percent, Default: 1  
 decimal.pvalue Decimal for pvalue, Default: 3  
 line Include new-line between sub-group variables, Default: F

### Details

This result is used to make forestplot.

### Value

Multiple sub-group analysis table.

### See Also

[map bind](#)

### Examples

```

library(survival)
library(dplyr)
lung %>%
  mutate(
    status = as.integer(status == 1),
    sex = factor(sex),
    kk = factor(as.integer(pat.karno >= 70)),
    kk1 = factor(as.integer(pat.karno >= 60))
  ) -> lung
TableSubgroupMultiGLM(status ~ sex,
  var_subgroups = c("kk", "kk1"),
  data = lung, line = TRUE, family = "binomial"
)

## survey design
library(survey)
data.design <- svydesign(id = ~1, data = lung)
TableSubgroupMultiGLM(status ~ sex,
  var_subgroups = c("kk", "kk1"),
  data = data.design, family = "binomial"
)

```

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