

# Package ‘jstable’

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

**Version** 1.3.0

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**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** 7.3.2

**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

**LazyData** true

**NeedsCompilation** no

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**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**

<code>coxme.obj</code>	<code>coxme.object</code>
<code>dec</code>	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	<i>coxmeTable: Summary table of coxme.object(internal function)</i>
------------	---

---

**Description**

Extract fixed effect table in `coxme.object`

**Usage**

```
coxmeTable(mod)
```

**Arguments**

<code>mod</code>	<code>coxme.object</code>
------------------	---------------------------

**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 &amp; 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

<code>data</code>	A data frame in which these variables exist. All variables (both vars and strata) must be in this data frame.
<code>strata</code>	Stratifying (grouping) variable name(s) given as a character vector. If omitted, the overall results are returned.
<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 data argument are used.
<code>factorVars</code>	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.
<code>includeNA</code>	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
<code>test</code>	If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed, Default: T
<code>testApprox</code>	A function used to perform the large sample approximation based tests. The default is <code>chisq.test</code> . This is not recommended when some of the cell have small counts like fewer than 5, Default: <code>chisq.test</code>
<code>argsApprox</code>	A named list of arguments passed to the function specified in <code>testApprox</code> . The default is <code>list(correct = TRUE)</code> , which turns on the continuity correction for <code>chisq.test</code> , Default: <code>list(correct = TRUE)</code>
<code>testExact</code>	A function used to perform the exact tests. The default is <code>fisher.test</code> . If the cells have large numbers, it will fail because of memory limitation. In this situation, the large sample approximation based should suffice., Default: <code>fisher.test</code>
<code>argsExact</code>	A named list of arguments passed to the function specified in <code>testExact</code> . The default is <code>list(workspace = 2 * 10^5)</code> , which specifies the memory space allocated for <code>fisher.test</code> , Default: <code>list(workspace = 2 * 10^5)</code>
<code>testNormal</code>	A function used to perform the normal assumption based tests. The default is <code>oneway.test</code> . This is equivalent of the t-test when there are only two groups, Default: <code>oneway.test</code>
<code>argsNormal</code>	A named list of arguments passed to the function specified in <code>testNormal</code> . The default is <code>list(var.equal = TRUE)</code> , which makes it the ordinary ANOVA that assumes equal variance across groups., Default: <code>list(var.equal = F)</code>

<code>testNonNormal</code>	A function used to perform the nonparametric tests. The default is <code>kruskal.test</code> (Kruskal-Wallis Rank Sum Test). This is equivalent of the <code>wilcox.test</code> (Mann-Whitney U test) when there are only two groups, Default: <code>kruskal.test</code>
<code>argsNonNormal</code>	A named list of arguments passed to the function specified in <code>testNonNormal</code> . The default is <code>list(NULL)</code> , which is just a placeholder., Default: <code>list(NULL)</code>
<code>showAllLevels</code>	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
<code>printToggle</code>	Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned., Default: F
<code>quote</code>	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
<code>smd</code>	If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated, Default: F
<code>Labels</code>	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>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)
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,
  normalityTest = 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.
<code>factorVars</code>	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 <code>vars</code> argument.
<code>includeNA</code>	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
<code>test</code>	If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed, Default: T
<code>testApprox</code>	A function used to perform the large sample approximation based tests. The default is <code>chisq.test</code> . This is not recommended when some of the cell have small counts like fewer than 5, Default: <code>chisq.test</code>
<code>argsApprox</code>	A named list of arguments passed to the function specified in <code>testApprox</code> . The default is <code>list(correct = TRUE)</code> , which turns on the continuity correction for <code>chisq.test</code> , Default: <code>list(correct = TRUE)</code>
<code>testExact</code>	A function used to perform the exact tests. The default is <code>fisher.test</code> . If the cells have large numbers, it will fail because of memory limitation. In this situation, the large sample approximation based should suffice., Default: <code>fisher.test</code>
<code>argsExact</code>	A named list of arguments passed to the function specified in <code>testExact</code> . The default is <code>list(workspace = 2 * 10^5)</code> , which specifies the memory space allocated for <code>fisher.test</code> , Default: <code>list(workspace = 2 * 10^5)</code>
<code>testNormal</code>	A function used to perform the normal assumption based tests. The default is <code>oneway.test</code> . This is equivalent of the t-test when there are only two groups, Default: <code>oneway.test</code>
<code>argsNormal</code>	A named list of arguments passed to the function specified in <code>testNormal</code> . The default is <code>list(var.equal = TRUE)</code> , which makes it the ordinary ANOVA that assumes equal variance across groups., Default: <code>list(var.equal = F)</code>
<code>testNonNormal</code>	A function used to perform the nonparametric tests. The default is <code>kruskal.test</code> (Kruskal-Wallis Rank Sum Test). This is equivalent of the <code>wilcox.test</code> (Mann-Whitney U test) when there are only two groups, Default: <code>kruskal.test</code>
<code>argsNonNormal</code>	A named list of arguments passed to the function specified in <code>testNonNormal</code> . The default is <code>list(NULL)</code> , which is just a placeholder., Default: <code>list(NULL)</code>

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
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
normalityTest	Logical, perform the Shapiro test for all variables. 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	<i>extractAIC.coxme: Extract AIC from coxme.object</i>
------------------	--

---

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

---

**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**

y	Dependant variable
x	Independent variable
data	Data
id.vec	Vector of id (should be ordered)
family	Family: "gaussian", "binomial", "poisson", "quasipoisson", etc...
cor.type	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

*glmshow.display: Show summary table of glm object.*

---

## 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	<i>LabeljsCox: Apply label information to cox2.display object using label data</i>
------------	--

---

**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

*LabeljsGeeglm: Apply label information to geeglm.display object using label data*

---

**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**

obj.table      table of geeglm.display, lmer.display, coxme.display  
 ref            Label data made by mk.lev 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	<i>Export label and level: multiple variable</i>
--------	--

---

**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

*Export label and level: one variable*

---

**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)  
})
```

---

mort	<i>DATASET_TITLE</i>
------	----------------------

---

**Description**

DATASET\_DESCRIPTION

**Usage**

mort

**Format**

A data frame with 17562 rows and 24 variables:

```

ccode integer COLUMN_DESCRIPTION
cname character COLUMN_DESCRIPTION
yy integer COLUMN_DESCRIPTION
mm integer COLUMN_DESCRIPTION
dd integer COLUMN_DESCRIPTION
date character COLUMN_DESCRIPTION
nonacc integer COLUMN_DESCRIPTION
cardio integer COLUMN_DESCRIPTION
respir integer COLUMN_DESCRIPTION
influenza integer COLUMN_DESCRIPTION
meanpm10 double COLUMN_DESCRIPTION
meanso2 double COLUMN_DESCRIPTION
meanno2 double COLUMN_DESCRIPTION
meanco double COLUMN_DESCRIPTION
maxco double COLUMN_DESCRIPTION
maxo3 double COLUMN_DESCRIPTION
meantemp double COLUMN_DESCRIPTION
maxtemp double COLUMN_DESCRIPTION
mintemp double COLUMN_DESCRIPTION
meanhumi double COLUMN_DESCRIPTION
meanpress double COLUMN_DESCRIPTION
season integer COLUMN_DESCRIPTION
dow integer COLUMN_DESCRIPTION
sn integer COLUMN_DESCRIPTION

```

**Details**

DETAILS



---

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	<i>datable option for ROC result(DT package)</i>
---------	--

---

**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	<i>datable option for simple download(DT package)</i>
-------------------	---

---

**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	<i>datable option for table 1(DT package)</i>
---------	---

---

**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                    *svycoxph.display: table for svycoxph.object in survey package.*

---

**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 = dpbc
)
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.

<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>factorVars</code>	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 <code>vars</code> argument.
<code>includeNA</code>	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
<code>test</code>	If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed, Default: T
<code>showAllLevels</code>	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
<code>printToggle</code>	Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned., Default: F
<code>quote</code>	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
<code>smd</code>	If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated, Default: F
<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>Labels</code>	Use Label, Default: F
<code>labeldata</code>	labeldata to use, Default: NULL
<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(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     *svyCreateTableOneJS: Modified CreateTableOne function in tableone package*

---

**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

<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.
<code>factorVars</code>	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 <code>vars</code> argument.
<code>includeNA</code>	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
<code>test</code>	If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed, Default: T
<code>showAllLevels</code>	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
<code>printToggle</code>	Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned., Default: F
<code>quote</code>	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
<code>smd</code>	If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated, Default: F
<code>Labels</code>	Use Label, Default: F
<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



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,
  cluster = NULL,
  strata = NULL,
  weights = NULL
)

```

**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_entraterate	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
cluster	Cluster variable for coxph, Default: NULL
strata	Strata variable for coxph, Default: NULL
weights	Weights variable for coxph, Default: NULL

**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_entraterate = 100)
TableSubgroupCox(Surv(time, status) ~ sex,
  var_subgroup = "kk", data = lung,
  time_entraterate = 100
)

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

---

TableSubgroupGLM	<i>TableSubgroupGLM: Sub-group analysis table for GLM.</i>
------------------	--

---

**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" or 'poisson' or 'quasipoisson'
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](#)

**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,
  cluster = NULL,
  strata = NULL,
  weights = NULL
)

```

**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
cluster	Cluster variable for coxph, Default: NULL
strata	Strata variable for coxph, Default: NULL
weights	Weights variable for coxph, Default: NULL

### 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" or 'poisson' or 'quasipoisson'
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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