Package ‘jstable’

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Title Create Tables from Different Types of Regression

Version 1.2.5

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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)

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Encoding UTF-8

RoxygenNote 7.3.1

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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Repository CRAN

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R topics documented:

`coefNA` *coefNA: make coefficient table with NA*

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` *cox2.display: table for coxph.object with model option: TRUE - allow "frailty" or "cluster" model*

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` *coxExp: transform the unit of coefficients in cox model(internal function)*

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 transforemed coefficients(95

Examples

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

`coxme.display` *coxme.display: table for coxme.object (coxme package)*

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 *CreateTableOne2: Modified CreateTableOne function in tableone package*

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 (Man-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 ± 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 stratifed clolumns. Default: F

Details

DETAILS

Value

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

Examples

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

`CreateTableOneJS` *CreateTableOneJS: Modified CreateTableOne function in tableone package*

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

`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
`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 (Man-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
`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 ± 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 stratifed clolumns. 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 assinged 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 transforemed 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` *LabelepiDisplay: Apply label information to epiDisplay object using label data*

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` *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` *LabeljsMetric: Apply label information to jstable metric object using label data*

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` *LabeljsMixed: Apply label information to jstable object using label data*

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` *LabeljsRanef: Apply label information to jstable random effect object using label data*

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` *LabeljsTable: Apply label information to jstable object using label data*

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` *lmer.display: table for "lmerMod" or "glmerMod" object (lme4 package)*

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` *lmerExp: transform the unit of coefficients (internal function)*

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 transforemed 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` *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` *DATASET_TITLE*

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` *datable option for data(DT package)*

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.simpledown` *datable option for simple download(DT package)*

Description

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

Usage

```
opt.simpledown(fname)
```

Arguments

`fname`	File name to download

Details

DETAILS

Value

datatable option object

Examples

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

`opt.tb1` *datable 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` *datable option for regression table(DT package)*

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

dpbc <- 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.

`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 ± 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 stratifed clolumns. Default: F

Details

DETAILS

Value

A matrix object containing what you see is also invisibly returned. This can be assinged 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

`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 ± 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 stratifed clolumns. Default: F

Details

DETAILS

Value

A matrix object containing what you see is also invisibly returned. This can be assinged 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
)
```

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
`cluster`	Cluster 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_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" 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
)
```

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

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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