

# Package ‘moonBook’

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**Title** Functions and Datasets for the Book by Keon-Woong Moon

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**URL** <https://github.com/cardiomoon/moonBook>

**BugReports** <https://github.com/cardiomoon/moonBook/issues>

**Description** Several analysis-related functions for the book entitled “R statistics and graph for medical articles” (written in Korean), version 1, by Keon-Woong Moon with Korean demographic data with several plot functions.

**Depends** R (>= 3.1.2)

**License** GPL-2

**LazyData** true

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**Imports** nortest, survival, sjmisc, stringr, magrittr, crayon

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acs

*Demographic data of 857 patients with ACS***Description**

A dataset containing demographic data and laboratory data of 857 patients with acute coronary syndrome(ACS).

**Format**

A data frame with 857 rows and 17 variables:

**age** patient age in years

**sex** "Male" or "Female"

**cardiogenicShock** "No" or "Yes"

**entry** vascular access route, either "Femoral" or "Radial"

**Dx** Final diagnosis, One of the followings : STEMI, NSTEMI or Unstable Angina

**EF** ejection fraction, percentage by echocardiography

**height** height in centimeter

**weight** weight in kilogram

**BMI** body mass index in kg/m2

**obesity** obesity, "No" or "Yes"

**TC** total cholesterol level in mg/dL

**LDLC** low density lipoprotein cholesterol level in mg/dL

**HDLC** high density lipoprotein cholesterol level in mg/dL

**TG** triglyceride level in mg/dL

**DM** history of diabetes mellitus,"No" or "Yes"

**HBP** history of hypertension,"No" or "Yes"

**smoking** history of smoking, One of the followings : "Never","Ex-smoker","Smoker"

addComma

*Change numbers into formatted numbers***Description**

Change numbers into formatted numbers

## Usage

```
addComma(x)

## S3 method for class 'mytable'
addComma(x)

## S3 method for class 'mytable.df'
addComma(x)

## S3 method for class 'cbind.mytable'
addComma(x)

## S3 method for class 'data.frame'
addComma(x)

## S3 method for class 'character'
addComma(x)
```

## Arguments

x                    An object

## Methods (by class)

- mytable: S3 method for class mytable
- mytable.df: S3 method for class mytable.df
- cbind.mytable: S3 method for class cbind.mytable
- data.frame: S3 method for class data.frame
- character: S3 method for class character

## Examples

```
## Not run:
require(stringr)
require(magrittr)
require(ggplot2)
mytable(cut~., data=diamonds) %>% addComma
x=mytable(Dx~sex, data=acs)
addComma(x)

## End(Not run)
```

---

addLabelDf	<i>Add value labels to the data.frame</i>
------------	---

---

**Description**

Add value labels to the data.frame

**Usage**

```
addLabelDf(data, mapping = NULL)
```

**Arguments**

data	A data.frame
mapping	Set of aesthetic mappings created by aes or aes_.

---

cat.test	<i>Perform chisq.test or fisher test</i>
----------	--

---

**Description**

Perform chisq.test or fisher test

**Usage**

```
cat.test(x, mode = 1, ...)
```

**Arguments**

x	a numeric vector or matrix. x and y can also both be factors.
mode	An integer. If 1(default), perform chisq.test first, If 2, perform fisher.test first
...	Further arguments to be passed to chisq.test or fisher.test

`cbind.mytable`            *cbind function for class "mytable"*

---

### Description

cbind function for class "mytable"

### Usage

```
## S3 method for class 'mytable'  
cbind(..., caption, y = NULL)
```

### Arguments

<code>...</code>	Objects of class "mytable", a result of a call to <a href="#">mytable</a>
<code>caption</code>	Unique values of grouping variables used for column name of table
<code>y</code>	Names of grouping variables used for caption of table

---

`centerprint`            *Internal mytable functions*

---

### Description

Internal mytable functions These are not to be called by the user

### Usage

```
centerprint(x, ..., width = 10)
```

### Arguments

<code>x</code>	a character vector
<code>...</code>	further arguments passed to or from other methods.
<code>width</code>	an integer

---

`changeColnameLabel`      *Change column names with labels*

---

**Description**

Change column names with labels

**Usage**

`changeColnameLabel(data)`

**Arguments**

`data`                  A data.frame

---

`comma`                      *Convert number to formatted number*

---

**Description**

Convert number to formatted number

**Usage**

`comma(x, ...)`

**Arguments**

`x`                          A numeric vector

`...`                      Further arguments to be passed to function format

---

 compress

*Compress an object of class mytable or cbind.mytable*


---

### Description

Compress an object of class mytable or cbind.mytable

### Usage

```
compress(x, no = 2, add.label = TRUE)

## S3 method for class 'mytable'
compress(x, no = 2, add.label = TRUE)

## S3 method for class 'cbind.mytable'
compress(x, no = 2, add.label = TRUE)

## S3 method for class 'data.frame'
compress(x, no = 2, add.label = TRUE)
```

### Arguments

x	An object of class mytable or cbind.mytable
no	Representative group of two groups
add.label	Logical. Whether or not add representative group name

### Methods (by class)

- mytable: S3 method for class mytable
- cbind.mytable: S3 method for class cbind.mytable
- data.frame: S3 method for class data.frame

### Examples

```
require(stringr)
require(magrittr)
mytable(acs) %>% compress
mytable(Dx~.,data=acs) %>% compress
## Not run:
require(ztable)
mytable(Dx~.,data=acs) %>% compress %>% ztable
mytable(Dx+sex~.,data=acs) %>% compress

## End(Not run)
```



---

deleteRows	<i>Delete rows of class mytable object</i>
------------	--

---

**Description**

Delete rows of class mytable object

**Usage**

```
deleteRows(x, rows)
```

**Arguments**

x	An object of class mytable or cbind.mytable
rows	rows to delete

---

densityplot	<i>Make Kernel density plot</i>
-------------	---------------------------------

---

**Description**

Make Kernel density plot

**Usage**

```
densityplot(formula, data, main = "", xlab = "", ylab = "", ...)
```

**Arguments**

formula	an R model formula, of the form ~ variable to estimate the unconditional density of variable, or variable ~ factor to estimate the density of variable within each level of factor.
data	an optional data frame containing the data.
main	main title of plot
xlab	label for the horizontal-axis; defaults to the name of the variable x.
ylab	label for the vertical axis; defaults to "Density".
...	arguments to be passed to plot

**Value**

This function return NULL invisibly and draw graphs.

**Examples**

```
require(moonBook)
data(acs)
densityplot(age~Dx,data=acs)
```

---

extractHR	<i>Extract hazard ratio from a data.frame</i>
-----------	---

---

**Description**

Extract hazard ratio from a data.frame

**Usage**

```
extractHR(x, digits = 2)
```

**Arguments**

x	an object of class coxph
digits	An integer indicating the number of decimal places (round) or significant digits to be used. Default value is 2.

**Value**

a data.frame consist of hazard ratio and 95 the p values.

**Examples**

```
require(survival)
data(cancer)
fit=coxph(Surv(time,status)~age+sex+obstruct+perfor,data=colon)
extractHR(fit)
```

---

extractKind	<i>Extract kind of an object of class mytable</i>
-------------	---

---

**Description**

Extract kind of an object of class mytable

**Usage**

```
extractKind(df)
```

**Arguments**

df	An object of class mytable or cbind.mytable
----	---

---

extractOR	<i>Extract the odds ratios from a S3 object of glm</i>
-----------	--

---

**Description**

Extract the odds ratios from a S3 object of glm

**Usage**

```
extractOR(x, digits = 2, method = "default")
```

**Arguments**

x	A S3 object of glm
digits	An integer indicating the number of decimal places (round) or significant digits to be used. Default value is 2.
method	Method to compute confidence interval. Choices are one of c("default", "LRT").

**Value**

A data.frame consist of odds ratios and 95 p values

**Examples**

```
data(cancer, package="survival")
x=glm(status~rx+sex+age+obstruct+nodes, data=colon, family="binomial")
extractOR(x)
```

---

getLabel	<i>Add column labels to the data.frame</i>
----------	--

---

**Description**

Add column labels to the data.frame

**Usage**

```
getLabel(data, colname, use.column.label = TRUE)
```

**Arguments**

data	A data.frame
colname	character. column name
use.column.label	Logical. Whether or not use column labels.

getMapping *extract variable name from mapping, aes*

---

**Description**

extract variable name from mapping, aes

**Usage**

```
getMapping(mapping, varname)
```

**Arguments**

mapping	aesthetic mapping
varname	variable name to extract

**Value**

variable name in character

**Examples**

```
require(ggplot2)
mapping=aes(colour=sex)
getMapping(mapping,"colour")
getMapping(mapping,"x")
```

---

HRplot *Draw a hazard ratio plot*

---

**Description**

Draw a hazard ratio plot

**Usage**

```
HRplot(
  out,
  type = 1,
  xlab = "",
  ylab = "",
  show.OR = TRUE,
  show.CI = FALSE,
  sig.level = 1,
  cex = 1.2,
  lwd = 2,
```

```

    pch = 18,
    col = NULL,
    ...
)

```

### Arguments

out	an object of class coxph or a resultant data.frame of mycph function
type	an integer indicating the type of plot. Default value is 1
xlab	a title for the x axis
ylab	a title for the y axis
show.OR	a logical vector indicating whether or not show the text indicating the p value
show.CI	a logical vector indicating whether or not show the text indicating the confidence interval
sig.level	a numeric value of upper limit of p value of showing variables
cex	A numerical value giving the amount by which plotting OR/HR symbols should be magnified relative to the default, defaulting 1.2.
lwd	The line width, a positive number, defaulting to 2.
pch	Either an integer specifying a symbol or a single character to be used as the default in plotting OR/HR points.
col	A specification for the default plotting color.
...	arguments to be passed to plot

### Value

This function return NULL invisibly and draw graphs

### Examples

```

require(survival)
attach(colon)
colon$TS=Surv(time,status==1)
out=mycph(TS~.,data=colon)
out
HRplot(out)
## Not run:
HRplot(out,type=1,pch=2,col=c("blue","red"))
HRplot(out,type=2,show.CI=TRUE,pch=2,cex=2,main="Hazard ratios of all individual variables")

## End(Not run)

```

---

my.chisq.test                      *Internal mytable functions*

---

### Description

Internal mytable functions These are not to be called by the user

### Usage

```
my.chisq.test(x, y, mydata, catMethod = 2)
```

### Arguments

x	a vector
y	a vector
mydata	A data.frame
catMethod	An integer indicating methods for categorical variables. Possible values in methods are <ul style="list-style-type: none"> <li><b>0</b> Perform chisq.test first. If warning present, perform fisher.test</li> <li><b>1</b> Perform chisq.test without continuity correction</li> <li><b>2</b> Perform chisq.test with continuity correction</li> <li><b>3</b> perform fisher.test</li> <li><b>4</b> perform prop.trend test</li> </ul> Default value is 2.

---

my.t.test                              *Internal mytable functions*

---

### Description

Internal mytable functions These are not to be called by the user

### Usage

```
my.t.test(y, x)
```

### Arguments

y	a vector
x	a numeric vector

---

mycph	<i>Perform coxph of individual expecting variables</i>
-------	--

---

**Description**

Perform coxph of individual expecting variables

**Usage**

```
mycph(formula, data, digits = 2)
```

**Arguments**

formula	An object of class "formula". Left side of ~ must be a variable of class Surv and the right side of ~ must have variables in an additive way.
data	A data.frame contains data for analysis.
digits	An integer indicating the number of decimal places (round) or significant digits to be used. Default value is 2.

**Value**

a data.frame consist of hazard ratio and 95% confidence intervals and the p values.

**Examples**

```
require(survival)
data(cancer)
attach(colon)
colon$TS=Surv(time,status==1)
out=mycph(TS~.,data=colon)
out
HRplot(out,type=2,show.CI=TRUE,main="Hazard ratios of all individual variables")
```

---

mycsv	<i>Export to csv file for class "mytable" or "cbind.mytable"</i>
-------	--

---

**Description**

Export to csv file for class "mytable" or "cbind.mytable"

**Usage**

```
mycsv(x, row.names = FALSE, ...)
```

**Arguments**

x                    An object of class "mytable" or "cbind.mytable"

row.names           either a logical value indicating whether the row names of x are to be written along with x, or a character vector of row names to be written.

...                  further arguments passed to or from other methods.

**Examples**

```
## Not run:
require(moonBook)
res=mytable(sex~age+DM,data=acs)
mycsv(res,file="test.csv")
mycsv(summary(res),file="testsummary.csv")

## End(Not run)
```

---

mycsv.cbind.mytable    *Export to csv file for class "cbind.mytable"*

---

**Description**

Export to csv file for class "cbind.mytable"

**Usage**

```
## S3 method for class 'cbind.mytable'
mycsv(x, row.names = FALSE, ...)
```

**Arguments**

x                    An object of class "cbind.mytable" a result of a call to [mytable](#)

row.names           either a logical value indicating whether the row names of x are to be written along with x, or a character vector of row names to be written.

...                  further arguments passed to or from other methods.

**Examples**

```
## Not run:
require(moonBook)
res1=mytable(sex+Dx~age+DM,data=acs)
mycsv(res1,file="test1.csv")
mycsv(summary(res1),file="testsummary1.csv")

## End(Not run)
```



---

mycsv.mytable	<i>Export to csv file for class "mytable"</i>
---------------	---

---

**Description**

Export to csv file for class "mytable"

**Usage**

```
## S3 method for class 'mytable'
mycsv(x, row.names = FALSE, ...)
```

**Arguments**

x	An object of class "mytable" a result of a call to <a href="#">mytable</a>
row.names	either a logical value indicating whether the row names of x are to be written along with x, or a character vector of row names to be written.
...	further arguments passed to or from other methods.

**Examples**

```
## Not run:
require(moonBook)
res=mytable(sex~age+DM,data=acs)
mycsv(res,file="test.csv")
mycsv(summary(res),file="testsummary.csv")
mycsv=function(x,row.names=FALSE) UseMethod("mycsv")

## End(Not run)
```

---

myhtml	<i>Export to html file for class "mytable" or "cbind.mytable" of "data.frame"</i>
--------	---

---

**Description**

Export to html file for class "mytable" or "cbind.mytable" of "data.frame"

**Usage**

```
myhtml(x, caption = NULL, rownames = TRUE)

## Default S3 method:
myhtml(x, caption = NULL, rownames = TRUE)

## S3 method for class 'mytable'
```

```
myhtml(x, caption = NULL, rownames = TRUE)

## S3 method for class 'cbind.mytable'
myhtml(x, caption = NULL, rownames = TRUE)
```

### Arguments

x	An object of class "mytable" or "cbind.mytable"
caption	A character
rownames	A logical value whether or not include rownames in table

### Methods (by class)

- default:
- mytable:
- cbind.mytable:

### Examples

```
require(moonBook)
res=mytable(sex~age+Dx,data=acs)
myhtml(res)
res1=mytable(sex+Dx~.,data=acs)
myhtml(res1)
x=head(iris)
myhtml(x)
myhtml(x,caption="Table 1. myhtml Test")
myhtml(x,caption="Table 1. myhtml Test",rownames=FALSE)
```

---

myhtmlHead

*Print my html style*

---

### Description

Print my html style

### Usage

```
myhtmlHead()
```

---

`mylatex`*Exporting "cbind.mytable","mytable" to LaTeX format*

---

**Description**

Exporting "cbind.mytable","mytable" to LaTeX format

**Usage**

```
mylatex(  
  myobj,  
  size = 5,  
  caption = NULL,  
  caption.placement = "top",  
  caption.position = "c"  
)  
  
## Default S3 method:  
mylatex(  
  myobj,  
  size = 5,  
  caption = NULL,  
  caption.placement = "top",  
  caption.position = "c"  
)  
  
## S3 method for class 'mytable'  
mylatex(  
  myobj,  
  size = 5,  
  caption = NULL,  
  caption.placement = "top",  
  caption.position = "c"  
)  
  
## S3 method for class 'cbind.mytable'  
mylatex(  
  myobj,  
  size = 5,  
  caption = NULL,  
  caption.placement = "top",  
  caption.position = "c"  
)
```

**Arguments**

`myobj`            An object of class 'mytable'

**size**                    An integer indicating font size, defaulting is 5.  
**caption**                A character  
**caption.placement**  
                           The caption will be have placed at the top of the table if `caption.placement` is "top" and at the bottom of the table if it equals "bottom". Default value is "top".  
**caption.position**  
                           The caption will be have placed at the center of the table if `caption.position` is "center" or "c", and at the left side of the table if it equals "left" or "l", and at the right side of the table if it equals "right" or "r". Default value is "center".

### Methods (by class)

- `default`: Exporting "cbind.mytable", "mytable" to LaTeX format
- `mytable`: Exporting "cbind.mytable", "mytable" to LaTeX format
- `cbind.mytable`: Exporting "cbind.mytable", "mytable" to LaTeX format

### Examples

```
require(moonBook)
out=mytable(sex~.,data=acs)
mylatex(out)
out1=mytable(sex+Dx~.,data=acs)
mylatex(out1,size=6)
```

---

<code>mytable</code>	<i>Produce table for descriptive statistics</i>
----------------------	---

---

### Description

Produce table for descriptive statistics by groups for several variables easily. Depending on the nature of these variables, different descriptive statistical methods were used (t-test, ANOVA, Kruskal-Wallis, chisq, Fisher,...)

### Usage

```
mytable(x, ...)
```

```
## S3 method for class 'formula'
mytable(x, ...)
```

```
## S3 method for class 'data.frame'
mytable(x, ...)
```

### Arguments

**x**                    An R object, formula or data.frame  
**...**                arguments to be passed to `mytable_sub`

**Methods (by class)**

- formula: S3 method for formula
- data.frame: S3 method for data.frame

**Examples**

```
mytable(acs)
mytable(~age+sex,data=acs)
mytable(Dx~age+sex+height+weight+TC+TG+HDLc,data=acs,method=3,digits=2)
mytable(am+cyl~,data=mtcars)
out=mytable(sex~,data=acs)
out
summary(out)
## Not run:
require(ztable)
ztable(out)

## End(Not run)
mytable(acs)
```

---

mytable2

---

*Produce combined table for descriptive statistics*


---

**Description**

Produce table for descriptive statistics by two grouping variables for several variables easily. Depending on the nature of these variables, different descriptive statistical methods were used (t-test, ANOVA, Kruskal-Wallis, chisq, Fisher,...)

**Usage**

```
mytable2(
  formula,
  data,
  use.labels = TRUE,
  use.column.label = TRUE,
  max.ylev = 5,
  maxCatLevel = 20,
  digits = 2,
  method = 1,
  catMethod = 2,
  show.all = FALSE,
  exact = FALSE,
  show.total = FALSE,
  origData = NULL
)
```

**Arguments**

formula	An object of class "formula". Left side of ~ must contain two grouping variables in an additive way(e.g. sex+group~), and the right side of ~ must have variables in an additive way.
data	A data.frame contains data for analysis
use.labels	Logical. Whether or not use labels.
use.column.label	Logical. Whether or not use column labels.
max.ylev	An integer indicating the maximum number of levels of grouping variable ('y'). If a column have unique values less than max.ylev it is treated as a categorical variable. Default value is 5.
maxCatLevel	An integer indicating the maximum number of unique levels of categorical variable. If a column have unique values more than maxCatLevel, categorical summarization will not be performed.
digits	An integer indicating the number of decimal places (round) or significant digits to be used. Default value is 1.
method	An integer indicating methods for continuous variables. Possible values in methods are <b>1</b> forces analysis as normal-distributed <b>2</b> forces analysis as continuous non-normal <b>3</b> performs a Shapiro-Wilk test to decide between normal or non-normal Default value is 1.
catMethod	An integer indicating methods for categorical variables. Possible values in methods are <b>0</b> Perform chisq.test first. If warning present, perform fisher test <b>1</b> Perform chisq.test without continuity correction <b>2</b> Perform chisq.test with continuity correction <b>3</b> perform fisher.test <b>4</b> perform prop.trend test Default value is 2.
show.all	A logical value indicating whether or not all statistical values have to be shown in table. Default value is FALSE.
exact	A logical value indicating whether or not permit call with approximate parameter. If true, only exact column name permitted.Default value is FALSE.
show.total	A logical value indicating whether or not show total group value. Default value is FALSE.
origData	A data.frame contains data for analysis

**Value**

An object of class "cbind.mytable"

---

mytable2df	<i>Convert mytable object to data.frame</i>
------------	---

---

**Description**

Add N number into data.frame

**Usage**

```
mytable2df(x)
```

**Arguments**

x                    An object of class "mytable" a result of a call to [mytable](#)

**Value**

a data.frame with N number

---

mytable2html	<i>Prepare mytable object to data.frame ready to html</i>
--------------	---

---

**Description**

Add N number into data.frame

**Usage**

```
mytable2html(x)
```

**Arguments**

x                    An object of class "mytable" a result of a call to [mytable](#)

**Value**

a data.frame with N number

---

mytable_df	<i>make mytable from data.frame</i>
------------	-------------------------------------

---

**Description**

make mytable from data.frame

**Usage**

```
mytable_df(
  x,
  use.labels = TRUE,
  use.column.label = TRUE,
  max.ylev = 5,
  maxCatLevel = 20,
  digits = 1,
  method = 1,
  show.all = FALSE
)
```

**Arguments**

x	A data.frame
use.labels	Logical. Whether or not use labels.
use.column.label	Logical. Whether or not use column labels.
max.ylev	An integer indicating the maximum number of levels of grouping variable. If a column have unique values less than max.ylev it is treated as a categorical variable. Default value is 5.
maxCatLevel	An integer indicating the maximum number of unique levels of categorical variable. If a column have unique values more than maxCatLevel, categorical summarization will not be performed.
digits	An integer indicating the number of decimal places (round) or significant digits to be used. Default value is 1.
method	An integer indicating methods for continuous variables. Possible values in methods are <b>1</b> forces analysis as normal-distributed <b>2</b> forces analysis as continuous non-normal <b>3</b> performs a Shapiro-Wilk test to decide between normal or non-normal Default value is 1.
show.all	A logical value indicating whether or not all statistical values have to be shown in table. Default value is FALSE.

**Value**

An object of class "mytable.df". 'print' returns a table for descriptive statistics.



---

mytable\_sub

*Produce table for descriptive statistics*


---

### Description

Produce table for descriptive statistics by groups for several variables easily. Depending on the nature of these variables, different descriptive statistical methods were used (t-test, ANOVA, Kruskal-Wallis, chisq, Fisher,...)

### Usage

```
mytable_sub(
  x,
  data,
  use.labels = TRUE,
  use.column.label = TRUE,
  max.ylev = 5,
  maxCatLevel = 20,
  digits = 1,
  method = 1,
  catMethod = 2,
  show.all = FALSE,
  exact = FALSE,
  show.total = FALSE,
  missing = FALSE
)
```

### Arguments

x	An object of class "formula". Left side of ~ must contain the name of one grouping variable or two grouping variables in an additive way (e.g. sex+group~), and the right side of ~ must have variables in an additive way.
data	A data.frame contains data for analysis
use.labels	Logical. Whether or not use labels.
use.column.label	Logical. Whether or not use column labels.
max.ylev	An integer indicating the maximum number of levels of grouping variable ('y'). If a column have unique values less than max.ylev it is treated as a categorical variable. Default value is 5.
maxCatLevel	An integer indicating the maximum number of unique levels of categorical variable. If a column have unique values more than maxCatLevel, categorical summarization will not be performed.
digits	An integer indicating the number of decimal places (round) or significant digits to be used. Default value is 1.

method	An integer indicating methods for continuous variables. Possible values in methods are <b>1</b> forces analysis as normal-distributed <b>2</b> forces analysis as continuous non-normal <b>3</b> performs a Shapiro-Wilk test to decide between normal or non-normal Default value is 1.
catMethod	An integer indicating methods for categorical variables. Possible values in methods are <b>0</b> Perform chisq.test first. If warning present, perform fisher test <b>1</b> Perform chisq.test without continuity correction <b>2</b> Perform chisq.test with continuity correction <b>3</b> perform fisher.test <b>4</b> perform prop.trend test Default value is 2.
show.all	A logical value indicating whether or not all statistical values have to be shown in table. Default value is FALSE.
exact	A logical value indicating whether or not permit call with approximate parameter. If true, only exact column name permitted. Default value is FALSE.
show.total	A logical value indicating whether or not show total group value. Default value is FALSE.
missing	A logical value indicating whether or not perform missing data analysis. Default value is FALSE.

**Value**

An object of class "mytable". 'print' returns a table for descriptive statistics. 'summary' returns a table with all statistical values.

---

mytable\_sub2

*Internal mytable functions*


---

**Description**

Internal mytable functions These are not to be called by the user

**Usage**

```
mytable_sub2(
  y,
  x,
  data,
  max.ylev = 5,
  maxCatLevel = 20,
```

```

    method = 1,
    catMethod = 2,
    show.total = FALSE,
    origData
  )

```

### Arguments

y	a vector
x	a vector
data	a data.frame
max.ylev	an integer
maxCatLevel	an integer
method	an integer
catMethod	an integer
show.total	a logical value
origData	a data.frame

---

num_summary	<i>Internal mytable functions</i>
-------------	-----------------------------------

---

### Description

Internal mytable functions These are not to be called by the user

### Usage

```
num_summary(x)
```

### Arguments

x	a numeric vector
---	------------------

---

obj2linecount	<i>Internal mytable functions</i>
---------------	-----------------------------------

---

### Description

Internal mytable functions These are not to be called by the user

### Usage

```
obj2linecount(myobj)
```

### Arguments

myobj	an R object
-------	-------------

---

 ORplot

*Plot for odds ratios for a S3 object of glm*


---

**Description**

Plot for odds ratios for a S3 object of glm

**Usage**

```
ORplot(
  x,
  type = 1,
  xlab = "",
  ylab = "",
  show.OR = TRUE,
  show.CI = FALSE,
  sig.level = 1,
  cex = 1.2,
  lwd = 2,
  pch = 18,
  col = NULL,
  ...
)
```

**Arguments**

x	A S3 object of glm
type	an integer defining the shape of plots; default value is 1
xlab	label for the horizontal-axis; defaults to "Odds Ratios"
ylab	label for the vertical axis; defaults to "".
show.OR	A logical value; Whether or not show p values on plot
show.CI	A logical value; Whether or not show 95% CI values on plot
sig.level	A numeric value of upper limit of p value of showing variables
cex	A numerical value giving the amount by which plotting OR/HR symbols should be magnified relative to the default, defaulting 1.2.
lwd	The line width, a positive number, defaulting to 2.
pch	Either an integer specifying a symbol or a single character to be used as the default in plotting OR/HR points.
col	A specification for the default plotting color.
...	arguments to be passed to plot

**Value**

This function return NULL invisibly and draw graphs

**Examples**

```

require(survival)
data(colon)
out1=glm(status~sex+age+rx+obstruct+node4,data=colon)
out2=glm(status~rx+node4,data=colon)
ORplot(out1,type=2,show.CI=TRUE,xlab="This is xlab",main="Main Title")
ORplot(out2,type=1,main="Main Title")
ORplot(out1,type=2,show.CI=TRUE,main="Main Title")
ORplot(out1,type=3,show.CI=TRUE,main="Main Title",sig.level=0.05)
ORplot(out1,type=3,show.CI=TRUE,main="Main Title",sig.level=0.05,
       pch=1,cex=2,lwd=4,col=c("red","blue"))

```

ORplot.sub

*A sub function for ORplot and HRplot***Description**

Plot for odds ratios for a S3 object of glm

**Usage**

```

ORplot.sub(
  result,
  type = 1,
  xlab = "",
  ylab = "",
  show.OR = TRUE,
  show.CI = FALSE,
  sig.level = 1,
  cex = 1.2,
  lwd = 2,
  pch = 18,
  col = NULL,
  ...
)

```

**Arguments**

result	A resultant data.frame of function extractOR
type	an integer defining the shape of plots; default value is 1
xlab	label for the horizontal-axis; defaults to "Odds Ratios"
ylab	label for the vertical axis; defaults to "".
show.OR	A logical value; Whether or not show p values on plot
show.CI	A logical value; Whether or not show 95% CI values on plot
sig.level	A numeric value of upper limit of p value of showing variables

<code>cex</code>	A numerical value giving the amount by which plotting OR/HR symbols should be magnified relative to the default, defaulting 1.2.
<code>lwd</code>	The line width, a positive number, defaulting to 2.
<code>pch</code>	Either an integer specifying a symbol or a single character to be used as the default in plotting OR/HR points.
<code>col</code>	A specification for the default plotting color.
<code>...</code>	Further arguments to be passed to plot

**Value**

This function return `NULL` invisibly and draw graphs

---

`p2sig`                      *Internal mytable functions*

---

**Description**

Internal mytable functions These are not to be called by the user

**Usage**

```
p2sig(value)
```

**Arguments**

`value`                      a numeric vector

---

`print.cbind.mytable`      *Print function for class "cbind.mytable"*

---

**Description**

Print function for class "cbind.mytable"

**Usage**

```
## S3 method for class 'cbind.mytable'
print(x, ...)
```

**Arguments**

`x`                              an object of class "cbind.mytable", a result of a call to `cbind.mytable`

`...`                          further arguments passed to or from other methods.

---

print.mytable	<i>Print function for class "mytable"</i>
---------------	---

---

**Description**

Print function for class "mytable"

**Usage**

```
## S3 method for class 'mytable'  
print(x, ...)
```

**Arguments**

x	An object of class "mytable", a result of a call to <a href="#">mytable</a>
...	further arguments passed to or from other methods.

---

print.mytable.df	<i>Print an object of mytable.df</i>
------------------	--------------------------------------

---

**Description**

Print an object of mytable.df

**Usage**

```
## S3 method for class 'mytable.df'  
print(x, ...)
```

**Arguments**

x	An object of class mytable.df
...	Further arguments

---

printmytable2	<i>Internal mytable functions</i>
---------------	-----------------------------------

---

**Description**

Internal mytable functions These are not to be called by the user

**Usage**

```
printmytable2(obj, digits = 1)
```

**Arguments**

obj	an object
digits	an integer

---

r	<i>Subfunction used in mylatex</i>
---	------------------------------------

---

**Description**

Subfunction used in mylatex

**Usage**

```
r(string)
```

**Arguments**

string	a character vector
--------	--------------------

---

radial	<i>Demographic data of 115 patients performing IVUS(intravascular ultrasound) examination of a radial artery.</i>
--------	---

---

**Description**

A dataset containing demographic data and laboratory data of 115 patients performing IVUS(intravascular ultrasound) examination of a radial artery after tansradial coronary angiography.



**Format**

A data frame with 115 rows and 15 variables:

**male** if Male, 1; if Female 0

**age** patient age in years

**height** height in centimeter

**weight** weight in kilogram

**HBP** history of hypertension, 1 for yes or 0 for no

**DM** history of diabetes mellitus, 1 for yes or 0 for no

**smoking** history of smoking, One of the followings : "non-smoker", "ex-smoker", "smoker"

**TC** total cholesterol level in mg/dL

**TG** triglyceride level in mg/dL

**HDL** high density lipoprotein cholesterol level in mg/dL

**LDL** low density lipoprotein cholesterol level in mg/dL

**hsCRP** high-sensitive C reactive protein

**NTAV** normalized total atheroma volume measured by IVUS in cubic mm

**PAV** percent atheroma volume in percentage

**sex** Factor with two levels; "Male" or "Female"

---

rank2group

*rank a numeric vector and returns a new ordinal vector*

---

**Description**

rank a numeric vector and returns a new ordinal vector

**Usage**

```
rank2group(y, k = 4)
```

**Arguments**

y                    a numeric vector

k                    a integer specifies how many groups you want to classify. default value is 4

**Value**

a ordinal vector(numeric) with the same length of y

**Examples**

```

require(ggplot2)
data(diamonds)
diamonds$PriceGroup=rank2group(diamonds$price,4)
table(diamonds$PriceGroup)
aggregate(price~PriceGroup,data=diamonds,range)

diamonds$PriceGroup3=rank2group(diamonds$price,3)
table(diamonds$PriceGroup3)
aggregate(price~PriceGroup3,data=diamonds,range)
diamonds$PriceGroup5=rank2group(diamonds$price,5)
table(diamonds$PriceGroup5)
aggregate(price~PriceGroup5,data=diamonds,range)

```

---

```
reprint
```

*Internal mytable functions*

---

**Description**

Internal mytable functions These are not to be called by the user

**Usage**

```
reprint(x, times)
```

**Arguments**

x	a character vector
times	an integer

---

```
space
```

*Internal mytable functions*

---

**Description**

Internal mytable functions These are not to be called by the user

**Usage**

```
space(num)
```

**Arguments**

num	an integer
-----	------------

---

summary.cbind.mytable *Summarizing function for class "cbind.mytable"*

---

### Description

Summarizing function for class "cbind.mytable"

### Usage

```
## S3 method for class 'cbind.mytable'  
summary(object, ...)
```

### Arguments

object            An object of class "cbind.mytable", a result of a call [mytable](#)  
...               further arguments passed to or from other methods.

### Examples

```
out=mytable(am+cyl~.,data=mtcars)  
summary(out)
```

---

summary.mytable            *Summarizing function for class "mytable"*

---

### Description

Summarizing function for class "mytable"

### Usage

```
## S3 method for class 'mytable'  
summary(object, ...)
```

### Arguments

object            An object of class "mytable", a result of a call [mytable](#)  
...               further arguments passed to or from other methods.

### Examples

```
out=mytable(am~.,data=mtcars)  
summary(out)
```

---

validColname	<i>Find valid string among character vector from approximate string</i>
--------------	---

---

**Description**

Find valid string among character vector from approximate string

**Usage**

```
validColname(pattern, x)
```

**Arguments**

pattern	character string to be matched in the given character
x	a character vector where matches are sought

**Value**

returns NA in case of no matched string found or a character string in string vector x

**Examples**

```
a="dx"  
b=c("Age", "Sex", "Dx")  
validColname(a,b)
```

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